



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:19 AM UTC

PDB ID : 5YPT / pdb_00005ypt
Title : Crystal structure of Marchantia paleacea chalone synthase like 1 (CHSL1)
Authors : Lou, H.X.; Yu, H.
Deposited on : 2017-11-03
Resolution : 2.39 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

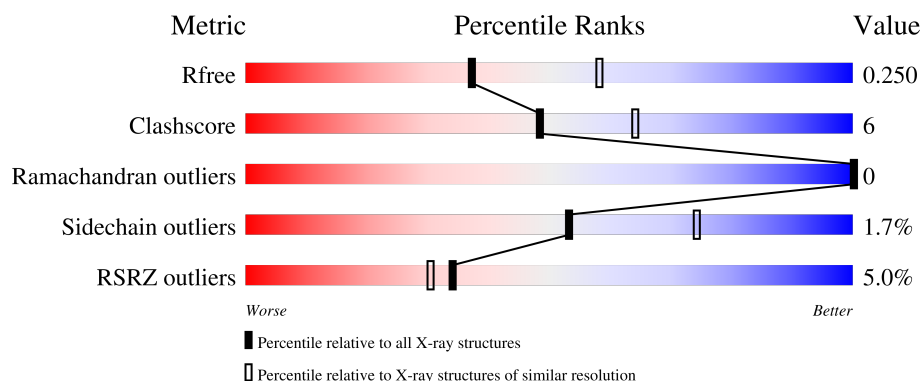
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.39 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	429	 3% 78% 11% 10%
1	B	429	 2% 77% 12% 11%
1	C	429	 4% 77% 12% 10%
1	D	429	 4% 77% 12% 10%
1	E	429	 5% 76% 14% 10%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	429	9% 72% 16% • 10%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 18274 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 Stilbenecarboxylate synthase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	384	Total	C	N	O	S	0	2	0
			2959	1873	518	556	12			
1	B	383	Total	C	N	O	S	0	0	0
			2937	1858	515	552	12			
1	C	384	Total	C	N	O	S	0	0	0
			2949	1867	516	554	12			
1	D	384	Total	C	N	O	S	0	0	0
			2949	1867	516	554	12			
1	E	384	Total	C	N	O	S	0	0	0
			2949	1867	516	554	12			
1	F	384	Total	C	N	O	S	0	0	0
			2949	1867	516	554	12			

There are 216 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-35	GLY	-	expression tag	UNP Q5I6Y2
A	-34	SER	-	expression tag	UNP Q5I6Y2
A	-33	GLY	-	expression tag	UNP Q5I6Y2
A	-32	MET	-	expression tag	UNP Q5I6Y2
A	-31	LYS	-	expression tag	UNP Q5I6Y2
A	-30	GLU	-	expression tag	UNP Q5I6Y2
A	-29	THR	-	expression tag	UNP Q5I6Y2
A	-28	ALA	-	expression tag	UNP Q5I6Y2
A	-27	ALA	-	expression tag	UNP Q5I6Y2
A	-26	ALA	-	expression tag	UNP Q5I6Y2
A	-25	LYS	-	expression tag	UNP Q5I6Y2
A	-24	PHE	-	expression tag	UNP Q5I6Y2
A	-23	GLU	-	expression tag	UNP Q5I6Y2
A	-22	ARG	-	expression tag	UNP Q5I6Y2
A	-21	GLN	-	expression tag	UNP Q5I6Y2
A	-20	HIS	-	expression tag	UNP Q5I6Y2
A	-19	MET	-	expression tag	UNP Q5I6Y2

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	ASP	-	expression tag	UNP Q5I6Y2
A	-17	SER	-	expression tag	UNP Q5I6Y2
A	-16	PRO	-	expression tag	UNP Q5I6Y2
A	-15	ASP	-	expression tag	UNP Q5I6Y2
A	-14	LEU	-	expression tag	UNP Q5I6Y2
A	-13	GLY	-	expression tag	UNP Q5I6Y2
A	-12	THR	-	expression tag	UNP Q5I6Y2
A	-11	ASP	-	expression tag	UNP Q5I6Y2
A	-10	ASP	-	expression tag	UNP Q5I6Y2
A	-9	ASP	-	expression tag	UNP Q5I6Y2
A	-8	ASP	-	expression tag	UNP Q5I6Y2
A	-7	LYS	-	expression tag	UNP Q5I6Y2
A	-6	ALA	-	expression tag	UNP Q5I6Y2
A	-5	MET	-	expression tag	UNP Q5I6Y2
A	-4	ALA	-	expression tag	UNP Q5I6Y2
A	-3	ASP	-	expression tag	UNP Q5I6Y2
A	-2	ILE	-	expression tag	UNP Q5I6Y2
A	-1	GLY	-	expression tag	UNP Q5I6Y2
A	0	SER	-	expression tag	UNP Q5I6Y2
B	-35	GLY	-	expression tag	UNP Q5I6Y2
B	-34	SER	-	expression tag	UNP Q5I6Y2
B	-33	GLY	-	expression tag	UNP Q5I6Y2
B	-32	MET	-	expression tag	UNP Q5I6Y2
B	-31	LYS	-	expression tag	UNP Q5I6Y2
B	-30	GLU	-	expression tag	UNP Q5I6Y2
B	-29	THR	-	expression tag	UNP Q5I6Y2
B	-28	ALA	-	expression tag	UNP Q5I6Y2
B	-27	ALA	-	expression tag	UNP Q5I6Y2
B	-26	ALA	-	expression tag	UNP Q5I6Y2
B	-25	LYS	-	expression tag	UNP Q5I6Y2
B	-24	PHE	-	expression tag	UNP Q5I6Y2
B	-23	GLU	-	expression tag	UNP Q5I6Y2
B	-22	ARG	-	expression tag	UNP Q5I6Y2
B	-21	GLN	-	expression tag	UNP Q5I6Y2
B	-20	HIS	-	expression tag	UNP Q5I6Y2
B	-19	MET	-	expression tag	UNP Q5I6Y2
B	-18	ASP	-	expression tag	UNP Q5I6Y2
B	-17	SER	-	expression tag	UNP Q5I6Y2
B	-16	PRO	-	expression tag	UNP Q5I6Y2
B	-15	ASP	-	expression tag	UNP Q5I6Y2
B	-14	LEU	-	expression tag	UNP Q5I6Y2
B	-13	GLY	-	expression tag	UNP Q5I6Y2

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	-12	THR	-	expression tag	UNP Q5I6Y2
B	-11	ASP	-	expression tag	UNP Q5I6Y2
B	-10	ASP	-	expression tag	UNP Q5I6Y2
B	-9	ASP	-	expression tag	UNP Q5I6Y2
B	-8	ASP	-	expression tag	UNP Q5I6Y2
B	-7	LYS	-	expression tag	UNP Q5I6Y2
B	-6	ALA	-	expression tag	UNP Q5I6Y2
B	-5	MET	-	expression tag	UNP Q5I6Y2
B	-4	ALA	-	expression tag	UNP Q5I6Y2
B	-3	ASP	-	expression tag	UNP Q5I6Y2
B	-2	ILE	-	expression tag	UNP Q5I6Y2
B	-1	GLY	-	expression tag	UNP Q5I6Y2
B	0	SER	-	expression tag	UNP Q5I6Y2
C	-35	GLY	-	expression tag	UNP Q5I6Y2
C	-34	SER	-	expression tag	UNP Q5I6Y2
C	-33	GLY	-	expression tag	UNP Q5I6Y2
C	-32	MET	-	expression tag	UNP Q5I6Y2
C	-31	LYS	-	expression tag	UNP Q5I6Y2
C	-30	GLU	-	expression tag	UNP Q5I6Y2
C	-29	THR	-	expression tag	UNP Q5I6Y2
C	-28	ALA	-	expression tag	UNP Q5I6Y2
C	-27	ALA	-	expression tag	UNP Q5I6Y2
C	-26	ALA	-	expression tag	UNP Q5I6Y2
C	-25	LYS	-	expression tag	UNP Q5I6Y2
C	-24	PHE	-	expression tag	UNP Q5I6Y2
C	-23	GLU	-	expression tag	UNP Q5I6Y2
C	-22	ARG	-	expression tag	UNP Q5I6Y2
C	-21	GLN	-	expression tag	UNP Q5I6Y2
C	-20	HIS	-	expression tag	UNP Q5I6Y2
C	-19	MET	-	expression tag	UNP Q5I6Y2
C	-18	ASP	-	expression tag	UNP Q5I6Y2
C	-17	SER	-	expression tag	UNP Q5I6Y2
C	-16	PRO	-	expression tag	UNP Q5I6Y2
C	-15	ASP	-	expression tag	UNP Q5I6Y2
C	-14	LEU	-	expression tag	UNP Q5I6Y2
C	-13	GLY	-	expression tag	UNP Q5I6Y2
C	-12	THR	-	expression tag	UNP Q5I6Y2
C	-11	ASP	-	expression tag	UNP Q5I6Y2
C	-10	ASP	-	expression tag	UNP Q5I6Y2
C	-9	ASP	-	expression tag	UNP Q5I6Y2
C	-8	ASP	-	expression tag	UNP Q5I6Y2
C	-7	LYS	-	expression tag	UNP Q5I6Y2

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	-6	ALA	-	expression tag	UNP Q5I6Y2
C	-5	MET	-	expression tag	UNP Q5I6Y2
C	-4	ALA	-	expression tag	UNP Q5I6Y2
C	-3	ASP	-	expression tag	UNP Q5I6Y2
C	-2	ILE	-	expression tag	UNP Q5I6Y2
C	-1	GLY	-	expression tag	UNP Q5I6Y2
C	0	SER	-	expression tag	UNP Q5I6Y2
D	-35	GLY	-	expression tag	UNP Q5I6Y2
D	-34	SER	-	expression tag	UNP Q5I6Y2
D	-33	GLY	-	expression tag	UNP Q5I6Y2
D	-32	MET	-	expression tag	UNP Q5I6Y2
D	-31	LYS	-	expression tag	UNP Q5I6Y2
D	-30	GLU	-	expression tag	UNP Q5I6Y2
D	-29	THR	-	expression tag	UNP Q5I6Y2
D	-28	ALA	-	expression tag	UNP Q5I6Y2
D	-27	ALA	-	expression tag	UNP Q5I6Y2
D	-26	ALA	-	expression tag	UNP Q5I6Y2
D	-25	LYS	-	expression tag	UNP Q5I6Y2
D	-24	PHE	-	expression tag	UNP Q5I6Y2
D	-23	GLU	-	expression tag	UNP Q5I6Y2
D	-22	ARG	-	expression tag	UNP Q5I6Y2
D	-21	GLN	-	expression tag	UNP Q5I6Y2
D	-20	HIS	-	expression tag	UNP Q5I6Y2
D	-19	MET	-	expression tag	UNP Q5I6Y2
D	-18	ASP	-	expression tag	UNP Q5I6Y2
D	-17	SER	-	expression tag	UNP Q5I6Y2
D	-16	PRO	-	expression tag	UNP Q5I6Y2
D	-15	ASP	-	expression tag	UNP Q5I6Y2
D	-14	LEU	-	expression tag	UNP Q5I6Y2
D	-13	GLY	-	expression tag	UNP Q5I6Y2
D	-12	THR	-	expression tag	UNP Q5I6Y2
D	-11	ASP	-	expression tag	UNP Q5I6Y2
D	-10	ASP	-	expression tag	UNP Q5I6Y2
D	-9	ASP	-	expression tag	UNP Q5I6Y2
D	-8	ASP	-	expression tag	UNP Q5I6Y2
D	-7	LYS	-	expression tag	UNP Q5I6Y2
D	-6	ALA	-	expression tag	UNP Q5I6Y2
D	-5	MET	-	expression tag	UNP Q5I6Y2
D	-4	ALA	-	expression tag	UNP Q5I6Y2
D	-3	ASP	-	expression tag	UNP Q5I6Y2
D	-2	ILE	-	expression tag	UNP Q5I6Y2
D	-1	GLY	-	expression tag	UNP Q5I6Y2

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	0	SER	-	expression tag	UNP Q5I6Y2
E	-35	GLY	-	expression tag	UNP Q5I6Y2
E	-34	SER	-	expression tag	UNP Q5I6Y2
E	-33	GLY	-	expression tag	UNP Q5I6Y2
E	-32	MET	-	expression tag	UNP Q5I6Y2
E	-31	LYS	-	expression tag	UNP Q5I6Y2
E	-30	GLU	-	expression tag	UNP Q5I6Y2
E	-29	THR	-	expression tag	UNP Q5I6Y2
E	-28	ALA	-	expression tag	UNP Q5I6Y2
E	-27	ALA	-	expression tag	UNP Q5I6Y2
E	-26	ALA	-	expression tag	UNP Q5I6Y2
E	-25	LYS	-	expression tag	UNP Q5I6Y2
E	-24	PHE	-	expression tag	UNP Q5I6Y2
E	-23	GLU	-	expression tag	UNP Q5I6Y2
E	-22	ARG	-	expression tag	UNP Q5I6Y2
E	-21	GLN	-	expression tag	UNP Q5I6Y2
E	-20	HIS	-	expression tag	UNP Q5I6Y2
E	-19	MET	-	expression tag	UNP Q5I6Y2
E	-18	ASP	-	expression tag	UNP Q5I6Y2
E	-17	SER	-	expression tag	UNP Q5I6Y2
E	-16	PRO	-	expression tag	UNP Q5I6Y2
E	-15	ASP	-	expression tag	UNP Q5I6Y2
E	-14	LEU	-	expression tag	UNP Q5I6Y2
E	-13	GLY	-	expression tag	UNP Q5I6Y2
E	-12	THR	-	expression tag	UNP Q5I6Y2
E	-11	ASP	-	expression tag	UNP Q5I6Y2
E	-10	ASP	-	expression tag	UNP Q5I6Y2
E	-9	ASP	-	expression tag	UNP Q5I6Y2
E	-8	ASP	-	expression tag	UNP Q5I6Y2
E	-7	LYS	-	expression tag	UNP Q5I6Y2
E	-6	ALA	-	expression tag	UNP Q5I6Y2
E	-5	MET	-	expression tag	UNP Q5I6Y2
E	-4	ALA	-	expression tag	UNP Q5I6Y2
E	-3	ASP	-	expression tag	UNP Q5I6Y2
E	-2	ILE	-	expression tag	UNP Q5I6Y2
E	-1	GLY	-	expression tag	UNP Q5I6Y2
E	0	SER	-	expression tag	UNP Q5I6Y2
F	-35	GLY	-	expression tag	UNP Q5I6Y2
F	-34	SER	-	expression tag	UNP Q5I6Y2
F	-33	GLY	-	expression tag	UNP Q5I6Y2
F	-32	MET	-	expression tag	UNP Q5I6Y2
F	-31	LYS	-	expression tag	UNP Q5I6Y2

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
F	-30	GLU	-	expression tag	UNP Q5I6Y2
F	-29	THR	-	expression tag	UNP Q5I6Y2
F	-28	ALA	-	expression tag	UNP Q5I6Y2
F	-27	ALA	-	expression tag	UNP Q5I6Y2
F	-26	ALA	-	expression tag	UNP Q5I6Y2
F	-25	LYS	-	expression tag	UNP Q5I6Y2
F	-24	PHE	-	expression tag	UNP Q5I6Y2
F	-23	GLU	-	expression tag	UNP Q5I6Y2
F	-22	ARG	-	expression tag	UNP Q5I6Y2
F	-21	GLN	-	expression tag	UNP Q5I6Y2
F	-20	HIS	-	expression tag	UNP Q5I6Y2
F	-19	MET	-	expression tag	UNP Q5I6Y2
F	-18	ASP	-	expression tag	UNP Q5I6Y2
F	-17	SER	-	expression tag	UNP Q5I6Y2
F	-16	PRO	-	expression tag	UNP Q5I6Y2
F	-15	ASP	-	expression tag	UNP Q5I6Y2
F	-14	LEU	-	expression tag	UNP Q5I6Y2
F	-13	GLY	-	expression tag	UNP Q5I6Y2
F	-12	THR	-	expression tag	UNP Q5I6Y2
F	-11	ASP	-	expression tag	UNP Q5I6Y2
F	-10	ASP	-	expression tag	UNP Q5I6Y2
F	-9	ASP	-	expression tag	UNP Q5I6Y2
F	-8	ASP	-	expression tag	UNP Q5I6Y2
F	-7	LYS	-	expression tag	UNP Q5I6Y2
F	-6	ALA	-	expression tag	UNP Q5I6Y2
F	-5	MET	-	expression tag	UNP Q5I6Y2
F	-4	ALA	-	expression tag	UNP Q5I6Y2
F	-3	ASP	-	expression tag	UNP Q5I6Y2
F	-2	ILE	-	expression tag	UNP Q5I6Y2
F	-1	GLY	-	expression tag	UNP Q5I6Y2
F	0	SER	-	expression tag	UNP Q5I6Y2

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	161	Total O 161 161	0	0
2	B	127	Total O 127 127	0	0
2	C	56	Total O 56 56	0	0
2	D	99	Total O 99 99	0	0

Continued on next page...

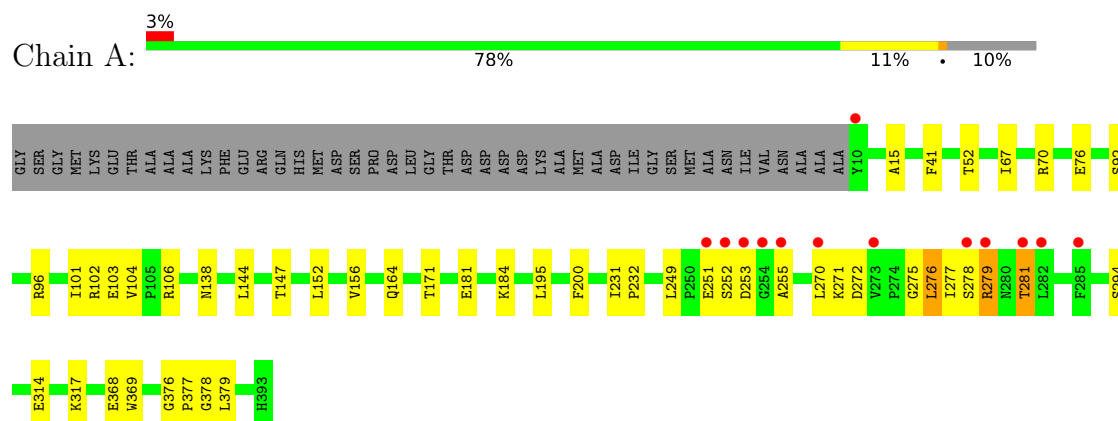
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	E	66	Total 66	O 66	0	0
2	F	73	Total 73	O 73	0	0

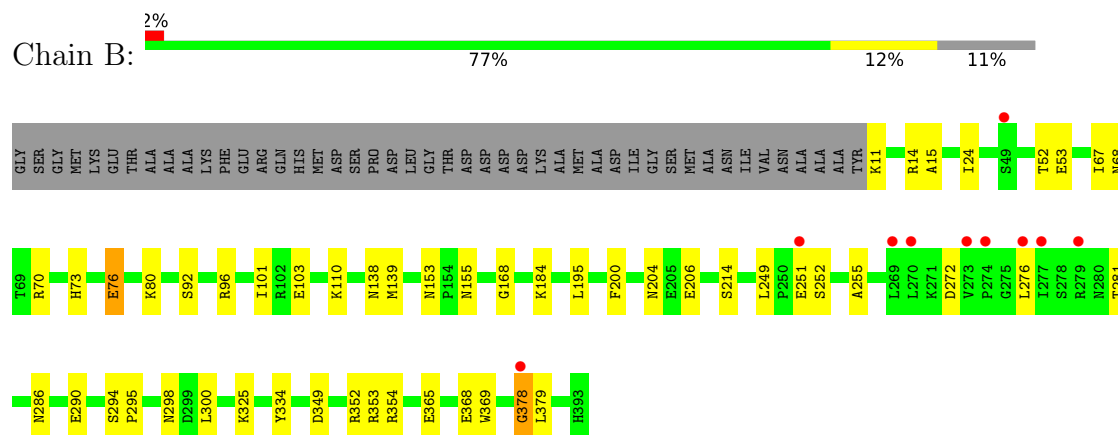
3 Residue-property plots [i](#)

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.

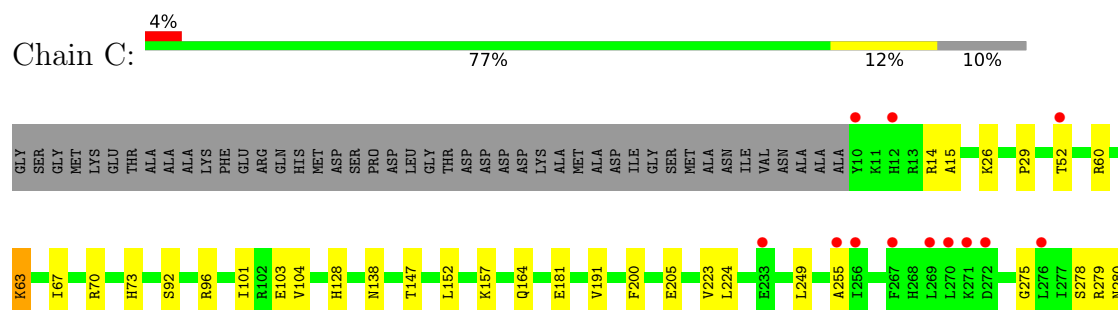
• Molecule 1: Stilbenecarboxylate synthase 1



• Molecule 1: Stilbenecarboxylate synthase 1

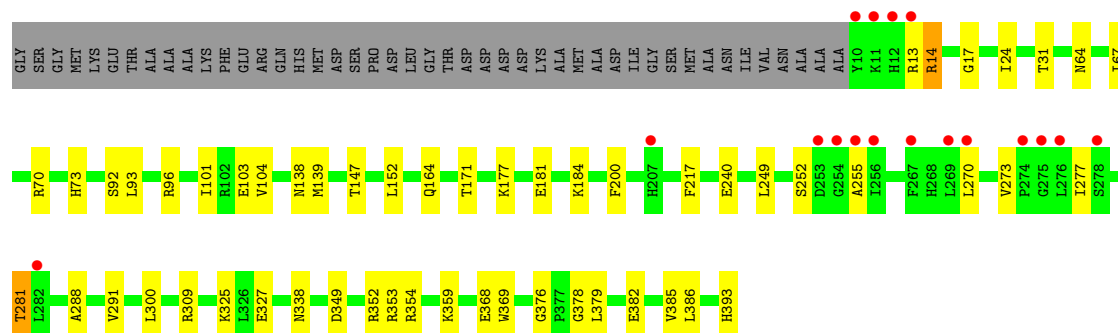
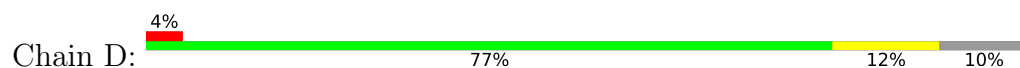


• Molecule 1: Stilbenecarboxylate synthase 1

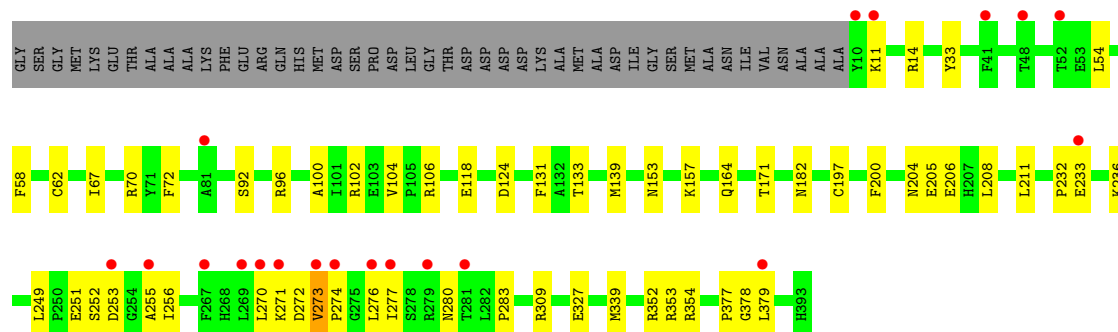
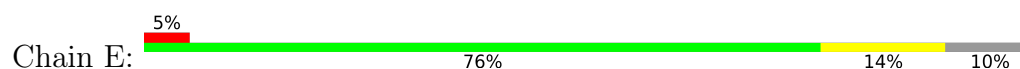




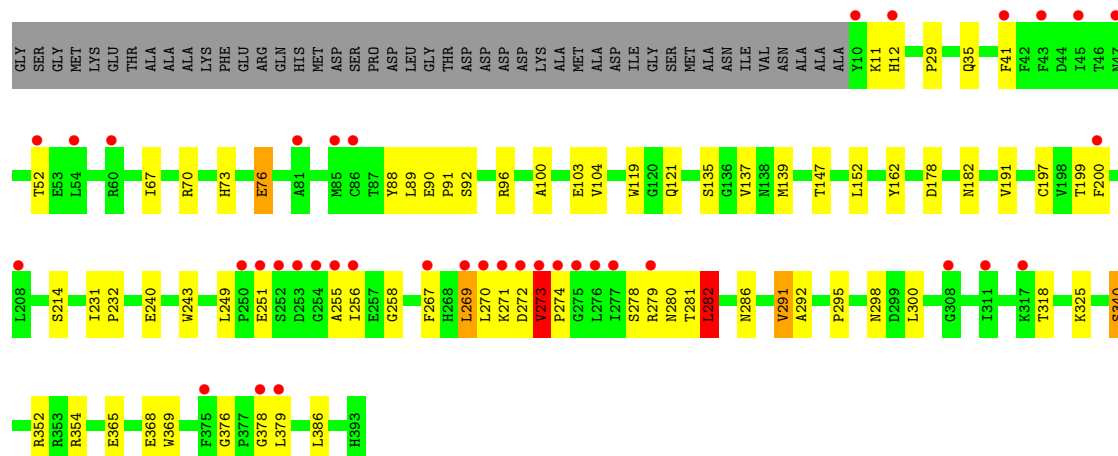
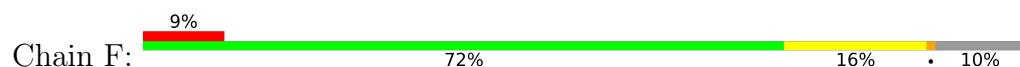
• Molecule 1: Stilbenecarboxylate synthase 1



• Molecule 1: Stilbenecarboxylate synthase 1



• Molecule 1: Stilbenecarboxylate synthase 1



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	128.18Å 74.58Å 262.15Å 90.00° 104.04° 90.00°	Depositor
Resolution (Å)	48.25 – 2.39 48.25 – 2.39	Depositor EDS
% Data completeness (in resolution range)	98.5 (48.25-2.39) 98.6 (48.25-2.39)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.12 (at 2.39Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.194 , 0.248 0.197 , 0.250	Depositor DCC
R_{free} test set	4702 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	33.9	Xtriage
Anisotropy	0.721	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 43.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.014 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	18274	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.03% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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	0.69	2/3027 (0.1%)	0.92	6/4113 (0.1%)
1	B	0.61	0/2998	0.91	4/4072 (0.1%)
1	C	0.57	1/3011 (0.0%)	0.91	4/4090 (0.1%)
1	D	0.60	1/3011 (0.0%)	0.92	6/4090 (0.1%)
1	E	0.61	0/3011	0.90	2/4090 (0.0%)
1	F	0.59	1/3011 (0.0%)	0.92	9/4090 (0.2%)
All	All	0.61	5/18069 (0.0%)	0.91	31/24545 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	104	VAL	CA-CB	10.55	1.60	1.54
1	C	104	VAL	CA-CB	9.09	1.59	1.54
1	D	104	VAL	CA-CB	8.13	1.58	1.54
1	A	104	VAL	CA-CB	7.83	1.58	1.54
1	A	156	VAL	CA-CB	5.81	1.60	1.54

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	378	GLY	N-CA-C	-8.11	105.43	115.08
1	A	376	GLY	CA-C-N	7.70	127.74	119.89
1	A	376	GLY	C-N-CA	7.70	127.74	119.89
1	D	378	GLY	N-CA-C	-6.94	106.82	115.08
1	C	378	GLY	N-CA-C	-6.74	107.06	115.08
1	A	294	SER	CA-C-N	-6.67	113.80	120.21
1	A	294	SER	C-N-CA	-6.67	113.80	120.21
1	F	378	GLY	N-CA-C	-6.62	106.60	115.21
1	F	376	GLY	CA-C-N	6.61	126.63	119.89
1	F	376	GLY	C-N-CA	6.61	126.63	119.89
1	B	378	GLY	N-CA-C	-6.54	106.70	115.21
1	B	294	SER	CA-C-N	-6.54	113.93	120.21
1	B	294	SER	C-N-CA	-6.54	113.93	120.21

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	17	GLY	CA-C-N	6.09	126.00	119.85
1	D	17	GLY	C-N-CA	6.09	126.00	119.85
1	F	340	SER	CB-CA-C	-5.60	110.10	116.54
1	B	52	THR	N-CA-C	5.57	117.80	111.11
1	C	52	THR	N-CA-C	5.55	117.77	111.11
1	D	376	GLY	CA-C-N	5.55	125.55	119.89
1	D	376	GLY	C-N-CA	5.55	125.55	119.89
1	A	52	THR	N-CA-C	5.38	117.56	111.11
1	C	340	SER	CB-CA-C	-5.35	110.39	116.54
1	C	29	PRO	O-C-N	5.33	123.76	121.31
1	F	273	VAL	N-CA-C	5.31	120.36	108.88
1	E	277	ILE	N-CA-C	5.27	115.48	110.53
1	E	378	GLY	N-CA-C	-5.26	108.45	115.40
1	F	29	PRO	O-C-N	5.19	123.70	121.31
1	F	191	VAL	N-CA-C	5.12	115.28	108.11
1	D	31	THR	N-CA-C	5.04	116.96	109.25
1	F	282	LEU	CA-C-N	-5.03	113.74	118.97
1	F	282	LEU	C-N-CA	-5.03	113.74	118.97

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	2959	0	2970	28	0
1	B	2937	0	2949	34	0
1	C	2949	0	2958	34	0
1	D	2949	0	2958	33	0
1	E	2949	0	2958	37	0
1	F	2949	0	2958	39	0
2	A	161	0	0	1	0
2	B	127	0	0	3	0
2	C	56	0	0	2	0
2	D	99	0	0	1	0
2	E	66	0	0	2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	73	0	0	0	0
All	All	18274	0	17751	195	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.

All (195) 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:96:ARG:NH2	1:B:200:PHE:O	2.06	0.88
1:F:96:ARG:NH2	1:F:200:PHE:O	2.09	0.85
1:D:96:ARG:NH2	1:D:200:PHE:O	2.11	0.82
1:E:96:ARG:NH2	1:E:200:PHE:O	2.12	0.81
1:C:96:ARG:NH2	1:C:200:PHE:O	2.15	0.80
1:A:96:ARG:NH2	1:A:200:PHE:O	2.16	0.77
1:C:298:ASN:HB3	1:C:322:LYS:HE2	1.70	0.73
1:C:15:ALA:O	1:D:14:ARG:NH1	2.23	0.72
1:E:249:LEU:HD12	1:E:379:LEU:HD13	1.71	0.72
1:B:255:ALA:HB3	1:B:379:LEU:HD23	1.72	0.71
1:E:280:ASN:O	1:E:283:PRO:HD2	1.91	0.70
1:E:252:SER:HB2	1:E:379:LEU:HB2	1.77	0.67
1:F:90:GLU:HG3	1:F:91:PRO:HD2	1.76	0.66
1:F:251:GLU:O	1:F:251:GLU:HG2	1.94	0.66
1:D:255:ALA:HB3	1:D:379:LEU:HD23	1.78	0.66
1:C:92:SER:O	1:C:96:ARG:HG3	1.96	0.66
1:E:67:ILE:HG21	1:E:70:ARG:HD2	1.78	0.65
1:F:92:SER:O	1:F:96:ARG:HG3	1.96	0.65
1:E:54:LEU:HD11	1:E:211:LEU:HD11	1.78	0.64
1:A:102:ARG:NH2	1:A:106:ARG:HH22	1.96	0.64
1:E:182:ASN:ND2	1:F:178:ASP:OD1	2.31	0.63
1:B:252:SER:HB2	1:B:379:LEU:HB2	1.79	0.63
1:A:70:ARG:HD3	2:A:471:HOH:O	1.99	0.63
1:A:255:ALA:HB3	1:A:379:LEU:HD23	1.81	0.62
1:E:271:LYS:HG3	1:E:272:ASP:H	1.64	0.61
1:D:92:SER:O	1:D:96:ARG:HG3	2.00	0.60
1:A:255:ALA:HB2	1:A:271:LYS:HD2	1.82	0.60
1:C:249:LEU:HD12	1:C:379:LEU:HD12	1.84	0.60
1:A:314:GLU:OE2	1:A:317:LYS:NZ	2.31	0.60
1:B:204:ASN:OD1	1:B:206:GLU:HG3	2.02	0.59
1:D:252:SER:HB2	1:D:379:LEU:HB2	1.84	0.59
1:E:92:SER:O	1:E:96:ARG:HG3	2.02	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:92:SER:O	1:B:96:ARG:HG3	2.03	0.59
1:F:35:GLN:OE1	1:F:70:ARG:NH1	2.35	0.58
1:A:92:SER:O	1:A:96:ARG:HG3	2.04	0.58
1:F:255:ALA:HB3	1:F:379:LEU:HD23	1.87	0.57
1:F:278:SER:OG	1:F:318:THR:OG1	2.19	0.57
1:E:118:GLU:O	1:E:236:LYS:NZ	2.25	0.57
1:D:147:THR:HG23	1:D:152:LEU:HB2	1.88	0.56
1:F:270:LEU:C	1:F:271:LYS:HD3	2.30	0.56
1:C:164:GLN:NE2	2:C:401:HOH:O	2.23	0.56
1:E:272:ASP:HA	1:E:274:PRO:HD2	1.88	0.56
1:A:272:ASP:O	1:A:276:LEU:HB2	2.05	0.55
1:D:67:ILE:HG21	1:D:70:ARG:HD2	1.89	0.55
1:A:103:GLU:HB2	1:A:195:LEU:HD11	1.89	0.55
1:F:147:THR:HG23	1:F:152:LEU:HB2	1.89	0.55
1:C:300:LEU:O	1:C:325:LYS:NZ	2.39	0.54
1:D:64:ASN:O	1:D:309:ARG:NH1	2.38	0.54
1:A:277:ILE:O	1:A:281:THR:OG1	2.25	0.54
1:A:249:LEU:HD12	1:A:379:LEU:HD12	1.90	0.54
1:B:249:LEU:HD12	1:B:379:LEU:HD12	1.88	0.54
1:B:70:ARG:HD3	2:B:472:HOH:O	2.08	0.54
1:A:101:ILE:HG12	1:A:138:ASN:HB2	1.89	0.54
1:C:368:GLU:HG3	1:C:369:TRP:CD1	2.43	0.54
1:D:73:HIS:NE2	1:D:103:GLU:HG3	2.22	0.53
1:A:275:GLY:O	1:A:279:ARG:HB3	2.08	0.53
1:F:255:ALA:HB3	1:F:379:LEU:CD2	2.38	0.53
1:B:110:LYS:NZ	2:B:402:HOH:O	2.21	0.52
1:E:232:PRO:O	1:E:233:GLU:HB3	2.09	0.52
1:B:295:PRO:HG2	1:B:300:LEU:HD21	1.91	0.52
1:E:256:ILE:HB	1:E:377:PRO:HA	1.92	0.52
1:C:70:ARG:HD3	2:C:430:HOH:O	2.10	0.52
1:E:327:GLU:HB3	1:E:354:ARG:NH2	2.25	0.52
1:A:377:PRO:HG2	1:B:139:MET:HE2	1.93	0.51
1:A:252:SER:HB2	1:A:379:LEU:HB2	1.92	0.51
1:E:102:ARG:HH12	1:E:106:ARG:NH1	2.08	0.51
1:D:327:GLU:HB3	1:D:354:ARG:NH2	2.25	0.51
1:D:255:ALA:HB3	1:D:379:LEU:CD2	2.41	0.51
1:A:252:SER:HB2	1:A:379:LEU:CB	2.41	0.50
1:B:352:ARG:HG2	1:B:353:ARG:N	2.26	0.50
1:F:271:LYS:HD3	1:F:271:LYS:N	2.25	0.50
1:D:277:ILE:O	1:D:281:THR:HG23	2.11	0.50
1:B:67:ILE:HG21	1:B:70:ARG:HD2	1.92	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:295:PRO:HG2	1:C:300:LEU:HD21	1.93	0.50
1:E:204:ASN:OD1	1:E:206:GLU:HG3	2.11	0.50
1:F:12:HIS:HE1	1:F:182:ASN:O	1.93	0.50
1:D:24:ILE:HG21	1:D:349:ASP:HB2	1.94	0.49
1:B:251:GLU:CD	1:B:251:GLU:O	2.55	0.49
1:A:67:ILE:HG21	1:A:70:ARG:HD2	1.94	0.49
1:D:300:LEU:O	1:D:325:LYS:NZ	2.41	0.48
1:F:282:LEU:O	1:F:286:ASN:ND2	2.47	0.48
1:D:270:LEU:O	1:D:273:VAL:HG23	2.14	0.48
1:E:131:PHE:HE2	1:E:133:THR:HB	1.79	0.48
1:C:278:SER:OG	1:C:318:THR:OG1	2.30	0.48
1:F:67:ILE:HG21	1:F:70:ARG:HD2	1.96	0.48
1:C:147:THR:HG23	1:C:152:LEU:HB2	1.95	0.47
1:F:41:PHE:HE1	1:F:76:GLU:HG3	1.79	0.47
1:B:153:ASN:OD1	1:B:155:ASN:HB2	2.15	0.47
1:D:177:LYS:NZ	1:D:181:GLU:OE1	2.47	0.47
1:C:249:LEU:HD22	1:C:280:ASN:HB3	1.96	0.47
1:A:181:GLU:O	1:B:14:ARG:NH1	2.44	0.47
1:C:181:GLU:O	1:D:14:ARG:NH1	2.48	0.47
1:D:13:ARG:HG3	1:D:184:LYS:HB2	1.97	0.47
1:E:256:ILE:HG12	1:E:270:LEU:HD13	1.97	0.47
1:E:273:VAL:N	1:E:274:PRO:HD2	2.30	0.47
1:D:382:GLU:OE1	2:D:401:HOH:O	2.20	0.46
1:E:157:LYS:HE3	2:E:405:HOH:O	2.14	0.46
1:E:251:GLU:O	1:E:251:GLU:HG3	2.15	0.46
1:B:251:GLU:OE1	1:B:276:LEU:HD21	2.15	0.46
1:F:298:ASN:HA	1:F:325:LYS:HD2	1.96	0.46
1:C:255:ALA:HB3	1:C:379:LEU:HD23	1.97	0.46
1:A:41:PHE:HE1	1:A:76:GLU:HG2	1.81	0.46
1:B:298:ASN:HA	1:B:325:LYS:HD2	1.98	0.46
1:C:67:ILE:HG21	1:C:70:ARG:HD2	1.96	0.46
1:E:58:PHE:CE2	1:E:62:CYS:SG	3.09	0.46
1:D:352:ARG:HG2	1:D:353:ARG:N	2.31	0.46
1:B:76:GLU:HG3	1:B:80:LYS:HE2	1.98	0.45
1:E:271:LYS:HG3	1:E:272:ASP:N	2.31	0.45
1:E:273:VAL:N	1:E:274:PRO:CD	2.78	0.45
1:F:88:TYR:O	1:F:89:LEU:HD23	2.17	0.45
1:C:101:ILE:HG12	1:C:138:ASN:HB2	1.98	0.45
1:B:73:HIS:NE2	1:B:103:GLU:HG3	2.30	0.45
1:B:252:SER:HB2	1:B:379:LEU:CB	2.45	0.45
1:F:70:ARG:NH2	1:F:214:SER:O	2.48	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:295:PRO:HG2	1:F:300:LEU:HD21	1.99	0.45
1:B:354:ARG:NH1	1:B:365:GLU:OE2	2.47	0.45
1:C:298:ASN:HA	1:C:325:LYS:HD2	1.98	0.45
1:D:379:LEU:HD13	1:D:379:LEU:HA	1.81	0.45
1:F:256:ILE:HG23	1:F:269:LEU:HD22	1.99	0.45
1:D:217:PHE:HA	1:D:338:ASN:O	2.16	0.44
1:E:100:ALA:HB2	1:E:197:CYS:SG	2.57	0.44
1:B:70:ARG:NH2	1:B:214:SER:O	2.47	0.44
1:D:101:ILE:HG12	1:D:138:ASN:HB2	1.99	0.44
1:E:377:PRO:HG2	1:F:139:MET:HE2	1.98	0.44
1:C:298:ASN:HB3	1:C:322:LYS:CE	2.44	0.44
1:E:124:ASP:O	1:E:153:ASN:ND2	2.42	0.44
1:D:252:SER:CB	1:D:379:LEU:HB2	2.47	0.44
1:F:255:ALA:HA	1:F:271:LYS:H	1.82	0.44
1:C:340:SER:OG	1:C:341:GLY:N	2.51	0.44
1:A:231:ILE:HA	1:A:232:PRO:HD3	1.86	0.44
1:E:33:TYR:CD2	1:E:72:PHE:HD2	2.36	0.44
1:F:368:GLU:HG3	1:F:369:TRP:CD1	2.52	0.44
1:A:15:ALA:HA	1:A:184:LYS:HD2	2.00	0.44
1:A:164:GLN:NE2	1:A:171:THR:HG21	2.33	0.43
1:B:101:ILE:HG12	1:B:138:ASN:HB2	2.00	0.43
1:F:199:THR:HG21	1:F:267:PHE:HE2	1.84	0.43
1:F:354:ARG:NE	1:F:365:GLU:OE2	2.41	0.43
1:C:191:VAL:HG22	1:C:223:VAL:HG22	2.00	0.43
1:B:272:ASP:O	1:B:276:LEU:HB2	2.19	0.43
1:C:223:VAL:C	1:C:224:LEU:HD12	2.43	0.42
1:F:243:TRP:HB2	1:F:291:VAL:HG21	2.01	0.42
1:A:147:THR:HG23	1:A:152:LEU:HB2	2.00	0.42
1:A:251:GLU:O	1:A:251:GLU:CD	2.62	0.42
1:B:68:ASN:HB2	1:B:334:TYR:CZ	2.54	0.42
1:B:68:ASN:HB2	1:B:334:TYR:CE1	2.55	0.42
1:B:368:GLU:HG3	1:B:369:TRP:CD1	2.54	0.42
1:D:249:LEU:HB2	1:D:379:LEU:HB3	2.01	0.42
1:F:11:LYS:HG2	1:F:11:LYS:O	2.19	0.42
1:C:377:PRO:HG2	1:D:139:MET:HE2	1.99	0.42
1:C:73:HIS:NE2	1:C:103:GLU:HG3	2.35	0.42
1:E:14:ARG:HG2	2:E:409:HOH:O	2.20	0.42
1:F:73:HIS:NE2	1:F:103:GLU:HG3	2.35	0.42
1:F:292:ALA:HB1	1:F:369:TRP:CG	2.55	0.42
1:D:368:GLU:HG3	1:D:369:TRP:CD1	2.55	0.42
1:E:104:VAL:HG12	1:E:131:PHE:HZ	1.84	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:352:ARG:HG2	1:E:353:ARG:N	2.35	0.42
1:B:24:ILE:HG21	1:B:349:ASP:HB2	2.01	0.42
1:C:128:HIS:CD2	1:C:157:LYS:HB2	2.55	0.42
1:D:359:LYS:HA	1:D:393:HIS:ND1	2.35	0.42
1:A:102:ARG:NH2	1:A:106:ARG:NH2	2.65	0.42
1:B:15:ALA:HA	1:B:184:LYS:HD2	2.00	0.42
1:C:14:ARG:NH1	1:D:181:GLU:O	2.52	0.41
1:D:255:ALA:HA	1:D:270:LEU:HG	2.02	0.41
1:F:273:VAL:HG13	1:F:274:PRO:HD3	2.02	0.41
1:F:100:ALA:HB2	1:F:197:CYS:SG	2.60	0.41
1:B:168:GLY:HA3	2:B:482:HOH:O	2.21	0.41
1:D:240:GLU:O	1:D:386:LEU:HA	2.20	0.41
1:C:63:LYS:HE2	1:C:63:LYS:HB2	1.63	0.41
1:C:286:ASN:O	1:C:290:GLU:HG3	2.19	0.41
1:B:349:ASP:CG	1:B:353:ARG:HE	2.29	0.41
1:E:208:LEU:O	1:E:211:LEU:HB2	2.21	0.41
1:B:103:GLU:HB2	1:B:195:LEU:HD11	2.03	0.41
1:C:205:GLU:H	1:C:205:GLU:CD	2.24	0.41
1:F:119:TRP:CZ2	1:F:121:GLN:HB2	2.56	0.41
1:C:359:LYS:HG2	1:C:393:HIS:CE1	2.56	0.41
1:D:288:ALA:O	1:D:385:VAL:HG21	2.21	0.41
1:E:139:MET:HB2	1:F:258:GLY:HA3	2.02	0.41
1:E:164:GLN:NE2	1:E:171:THR:HG21	2.36	0.41
1:F:240:GLU:O	1:F:386:LEU:HA	2.21	0.41
1:F:249:LEU:HD22	1:F:280:ASN:HB3	2.03	0.41
1:F:278:SER:O	1:F:318:THR:HG21	2.21	0.41
1:A:253:ASP:O	1:A:271:LYS:NZ	2.54	0.41
1:C:26:LYS:NZ	1:C:349:ASP:OD2	2.38	0.41
1:C:275:GLY:HA3	1:C:279:ARG:HH21	1.86	0.41
1:C:379:LEU:HA	1:C:379:LEU:HD22	1.73	0.41
1:A:368:GLU:HG3	1:A:369:TRP:CD1	2.56	0.40
1:B:286:ASN:O	1:B:290:GLU:HG3	2.20	0.40
1:F:137:VAL:HA	1:F:162:TYR:CE1	2.56	0.40
1:A:144:LEU:HD13	1:B:378:GLY:HA3	2.03	0.40
1:D:164:GLN:NE2	1:D:171:THR:HG21	2.36	0.40
1:E:205:GLU:HA	1:E:208:LEU:HD21	2.02	0.40
1:C:224:LEU:HD12	1:C:224:LEU:N	2.37	0.40
1:E:253:ASP:C	1:E:255:ALA:H	2.29	0.40
1:E:339:MET:HE3	1:E:339:MET:HB2	1.98	0.40
1:F:231:ILE:HA	1:F:232:PRO:HD3	1.97	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	384/429 (90%)	378 (98%)	6 (2%)	0	100	100
1	B	381/429 (89%)	371 (97%)	10 (3%)	0	100	100
1	C	382/429 (89%)	374 (98%)	8 (2%)	0	100	100
1	D	382/429 (89%)	372 (97%)	10 (3%)	0	100	100
1	E	382/429 (89%)	369 (97%)	13 (3%)	0	100	100
1	F	382/429 (89%)	374 (98%)	8 (2%)	0	100	100
All	All	2293/2574 (89%)	2238 (98%)	55 (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	319/349 (91%)	314 (98%)	5 (2%)	55	76
1	B	316/349 (90%)	312 (99%)	4 (1%)	61	80
1	C	317/349 (91%)	313 (99%)	4 (1%)	61	80
1	D	317/349 (91%)	313 (99%)	4 (1%)	61	80
1	E	317/349 (91%)	313 (99%)	4 (1%)	61	80
1	F	317/349 (91%)	305 (96%)	12 (4%)	29	49
All	All	1903/2094 (91%)	1870 (98%)	33 (2%)	53	74

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	270	LEU
1	A	276	LEU
1	A	278	SER
1	A	279	ARG
1	A	281	THR
1	B	11	LYS
1	B	53	GLU
1	B	76	GLU
1	B	281	THR
1	C	60	ARG
1	C	63	LYS
1	C	309	ARG
1	C	361	ARG
1	D	14	ARG
1	D	93	LEU
1	D	281	THR
1	D	291	VAL
1	E	11	LYS
1	E	273	VAL
1	E	276	LEU
1	E	309	ARG
1	F	52	THR
1	F	76	GLU
1	F	135	SER
1	F	269	LEU
1	F	272	ASP
1	F	273	VAL
1	F	279	ARG
1	F	281	THR
1	F	282	LEU
1	F	291	VAL
1	F	340	SER
1	F	352	ARG

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

Mol	Chain	Res	Type
1	A	210	ASN
1	B	138	ASN
1	D	268	HIS
1	F	268	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 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

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	384/429 (89%)	-0.00	13 (3%)	48	44	18, 31, 58, 80	2 (0%)
1	B	383/429 (89%)	0.11	10 (2%)	57	53	19, 34, 60, 79	0
1	C	384/429 (89%)	0.46	18 (4%)	36	32	24, 44, 68, 89	0
1	D	384/429 (89%)	0.26	17 (4%)	39	34	22, 37, 69, 88	0
1	E	384/429 (89%)	0.52	20 (5%)	33	29	25, 43, 73, 94	0
1	F	384/429 (89%)	0.59	38 (9%)	13	9	25, 44, 77, 93	0
All	All	2303/2574 (89%)	0.32	116 (5%)	34	30	18, 38, 70, 94	2 (0%)

All (116) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	270	LEU	5.8
1	E	273	VAL	4.7
1	C	269	LEU	4.5
1	E	269	LEU	4.4
1	A	10	TYR	4.2
1	F	273	VAL	4.1
1	E	255	ALA	4.0
1	F	267	PHE	3.9
1	F	269	LEU	3.8
1	C	10	TYR	3.7
1	D	270	LEU	3.7
1	F	270	LEU	3.6
1	D	269	LEU	3.5
1	F	86	CYS	3.4
1	B	378	GLY	3.4
1	F	277	ILE	3.4
1	D	11	LYS	3.4
1	A	254	GLY	3.4
1	D	274	PRO	3.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	273	VAL	3.3
1	A	281	THR	3.2
1	F	43	PHE	3.2
1	B	273	VAL	3.1
1	F	271	LYS	3.0
1	F	276	LEU	3.0
1	D	10	TYR	3.0
1	E	279	ARG	2.9
1	F	251	GLU	2.9
1	C	276	LEU	2.9
1	D	255	ALA	2.9
1	F	52	THR	2.9
1	F	250	PRO	2.9
1	F	256	ILE	2.9
1	F	254	GLY	2.8
1	F	54	LEU	2.8
1	D	207	HIS	2.8
1	E	267	PHE	2.8
1	E	274	PRO	2.7
1	E	276	LEU	2.7
1	C	271	LYS	2.6
1	D	13	ARG	2.6
1	F	317	LYS	2.6
1	D	276	LEU	2.6
1	F	308	GLY	2.6
1	C	12	HIS	2.6
1	B	270	LEU	2.5
1	B	276	LEU	2.5
1	C	282	LEU	2.5
1	F	375	PHE	2.5
1	D	267	PHE	2.5
1	F	275	GLY	2.5
1	F	10	TYR	2.4
1	F	252	SER	2.4
1	F	379	LEU	2.4
1	C	361	ARG	2.4
1	E	253	ASP	2.4
1	F	253	ASP	2.4
1	B	274	PRO	2.4
1	F	255	ALA	2.4
1	E	52	THR	2.4
1	B	277	ILE	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	281	THR	2.4
1	E	41	PHE	2.4
1	B	279	ARG	2.3
1	F	12	HIS	2.3
1	F	279	ARG	2.3
1	C	270	LEU	2.3
1	F	81	ALA	2.3
1	A	251	GLU	2.3
1	E	379	LEU	2.3
1	F	208	LEU	2.3
1	A	253	ASP	2.3
1	D	253	ASP	2.3
1	A	270	LEU	2.3
1	A	282	LEU	2.3
1	E	48	THR	2.3
1	D	12	HIS	2.3
1	E	11	LYS	2.3
1	F	41	PHE	2.2
1	C	272	ASP	2.2
1	C	255	ALA	2.2
1	B	251	GLU	2.2
1	A	278	SER	2.2
1	F	47	ASN	2.2
1	D	254	GLY	2.2
1	D	275	GLY	2.2
1	F	60	ARG	2.1
1	C	256	ILE	2.1
1	F	311	ILE	2.1
1	F	85	MET	2.1
1	E	233	GLU	2.1
1	A	252	SER	2.1
1	B	269	LEU	2.1
1	F	272	ASP	2.1
1	A	285	PHE	2.1
1	F	200	PHE	2.1
1	F	274	PRO	2.1
1	B	49	SER	2.1
1	C	390	ALA	2.1
1	D	278	SER	2.1
1	C	52	THR	2.1
1	E	281	THR	2.1
1	A	255	ALA	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	E	81	ALA	2.1
1	C	233	GLU	2.1
1	D	256	ILE	2.1
1	C	267	PHE	2.1
1	C	379	LEU	2.0
1	D	282	LEU	2.0
1	E	277	ILE	2.0
1	F	45	ILE	2.0
1	E	10	TYR	2.0
1	F	378	GLY	2.0
1	C	292	ALA	2.0
1	A	279	ARG	2.0
1	E	271	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 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.