



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 10:30 PM UTC

PDB ID : 9H68 / pdb_00009h68
Title : Crystal Structure of the spore germination lytic transglycosylase SleC from *Clostridioides difficile* in its zymogenic form (prepro-SleC)
Authors : Molina, R.; Garay-Alvarez, A.; Hermoso, J.A.
Deposited on : 2024-10-23
Resolution : 2.10 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

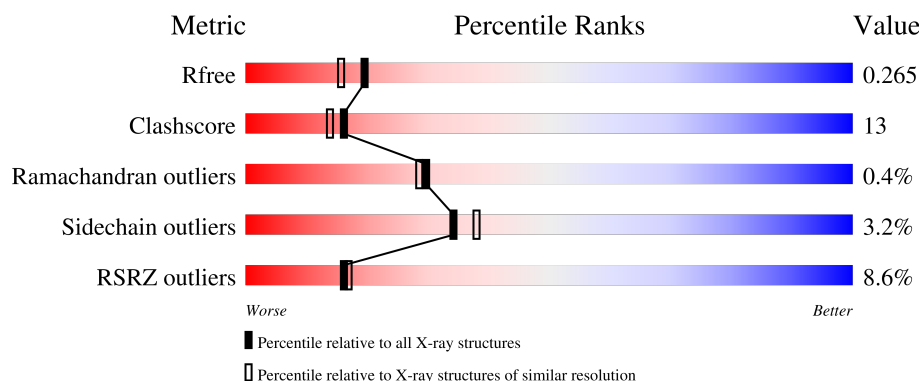
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	480	5% 65% 19% • 14%
1	B	480	3% 63% 21% • 15%
1	C	480	12% 65% 18% • 15%
1	D	480	10% 61% 22% • 16%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 13534 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 Spore cortex-lytic enzyme pre-pro-form.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	412	Total	C	N	O	S	0	0	0
			3274	2102	533	633	6			
1	D	404	Total	C	N	O	S	0	0	0
			3199	2052	520	621	6			
1	B	410	Total	C	N	O	S	0	0	0
			3256	2090	530	630	6			
1	C	406	Total	C	N	O	S	0	0	0
			3216	2061	525	624	6			

There are 228 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-56	MET	-	initiating methionine	UNP Q188Z5
A	-55	GLY	-	expression tag	UNP Q188Z5
A	-54	SER	-	expression tag	UNP Q188Z5
A	-53	SER	-	expression tag	UNP Q188Z5
A	-52	HIS	-	expression tag	UNP Q188Z5
A	-51	HIS	-	expression tag	UNP Q188Z5
A	-50	HIS	-	expression tag	UNP Q188Z5
A	-49	HIS	-	expression tag	UNP Q188Z5
A	-48	HIS	-	expression tag	UNP Q188Z5
A	-47	HIS	-	expression tag	UNP Q188Z5
A	-46	SER	-	expression tag	UNP Q188Z5
A	-45	SER	-	expression tag	UNP Q188Z5
A	-44	GLY	-	expression tag	UNP Q188Z5
A	-43	SER	-	expression tag	UNP Q188Z5
A	-42	ALA	-	expression tag	UNP Q188Z5
A	-41	TRP	-	expression tag	UNP Q188Z5
A	-40	SER	-	expression tag	UNP Q188Z5
A	-39	HIS	-	expression tag	UNP Q188Z5
A	-38	PRO	-	expression tag	UNP Q188Z5
A	-37	GLN	-	expression tag	UNP Q188Z5
A	-36	PHE	-	expression tag	UNP Q188Z5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-35	GLU	-	expression tag	UNP Q188Z5
A	-34	LYS	-	expression tag	UNP Q188Z5
A	-33	GLY	-	expression tag	UNP Q188Z5
A	-32	GLY	-	expression tag	UNP Q188Z5
A	-31	GLY	-	expression tag	UNP Q188Z5
A	-30	SER	-	expression tag	UNP Q188Z5
A	-29	GLY	-	expression tag	UNP Q188Z5
A	-28	GLY	-	expression tag	UNP Q188Z5
A	-27	GLY	-	expression tag	UNP Q188Z5
A	-26	SER	-	expression tag	UNP Q188Z5
A	-25	GLY	-	expression tag	UNP Q188Z5
A	-24	GLY	-	expression tag	UNP Q188Z5
A	-23	SER	-	expression tag	UNP Q188Z5
A	-22	ALA	-	expression tag	UNP Q188Z5
A	-21	TRP	-	expression tag	UNP Q188Z5
A	-20	SER	-	expression tag	UNP Q188Z5
A	-19	HIS	-	expression tag	UNP Q188Z5
A	-18	PRO	-	expression tag	UNP Q188Z5
A	-17	GLN	-	expression tag	UNP Q188Z5
A	-16	PHE	-	expression tag	UNP Q188Z5
A	-15	GLU	-	expression tag	UNP Q188Z5
A	-14	LYS	-	expression tag	UNP Q188Z5
A	-13	SER	-	expression tag	UNP Q188Z5
A	-12	ASN	-	expression tag	UNP Q188Z5
A	-11	ASN	-	expression tag	UNP Q188Z5
A	-10	ASN	-	expression tag	UNP Q188Z5
A	-9	LEU	-	expression tag	UNP Q188Z5
A	-8	GLY	-	expression tag	UNP Q188Z5
A	-7	GLU	-	expression tag	UNP Q188Z5
A	-6	ASN	-	expression tag	UNP Q188Z5
A	-5	LEU	-	expression tag	UNP Q188Z5
A	-4	TYR	-	expression tag	UNP Q188Z5
A	-3	PHE	-	expression tag	UNP Q188Z5
A	-2	GLN	-	expression tag	UNP Q188Z5
A	-1	GLY	-	expression tag	UNP Q188Z5
A	0	HIS	-	expression tag	UNP Q188Z5
D	-56	MET	-	initiating methionine	UNP Q188Z5
D	-55	GLY	-	expression tag	UNP Q188Z5
D	-54	SER	-	expression tag	UNP Q188Z5
D	-53	SER	-	expression tag	UNP Q188Z5
D	-52	HIS	-	expression tag	UNP Q188Z5
D	-51	HIS	-	expression tag	UNP Q188Z5

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-50	HIS	-	expression tag	UNP Q188Z5
D	-49	HIS	-	expression tag	UNP Q188Z5
D	-48	HIS	-	expression tag	UNP Q188Z5
D	-47	HIS	-	expression tag	UNP Q188Z5
D	-46	SER	-	expression tag	UNP Q188Z5
D	-45	SER	-	expression tag	UNP Q188Z5
D	-44	GLY	-	expression tag	UNP Q188Z5
D	-43	SER	-	expression tag	UNP Q188Z5
D	-42	ALA	-	expression tag	UNP Q188Z5
D	-41	TRP	-	expression tag	UNP Q188Z5
D	-40	SER	-	expression tag	UNP Q188Z5
D	-39	HIS	-	expression tag	UNP Q188Z5
D	-38	PRO	-	expression tag	UNP Q188Z5
D	-37	GLN	-	expression tag	UNP Q188Z5
D	-36	PHE	-	expression tag	UNP Q188Z5
D	-35	GLU	-	expression tag	UNP Q188Z5
D	-34	LYS	-	expression tag	UNP Q188Z5
D	-33	GLY	-	expression tag	UNP Q188Z5
D	-32	GLY	-	expression tag	UNP Q188Z5
D	-31	GLY	-	expression tag	UNP Q188Z5
D	-30	SER	-	expression tag	UNP Q188Z5
D	-29	GLY	-	expression tag	UNP Q188Z5
D	-28	GLY	-	expression tag	UNP Q188Z5
D	-27	GLY	-	expression tag	UNP Q188Z5
D	-26	SER	-	expression tag	UNP Q188Z5
D	-25	GLY	-	expression tag	UNP Q188Z5
D	-24	GLY	-	expression tag	UNP Q188Z5
D	-23	SER	-	expression tag	UNP Q188Z5
D	-22	ALA	-	expression tag	UNP Q188Z5
D	-21	TRP	-	expression tag	UNP Q188Z5
D	-20	SER	-	expression tag	UNP Q188Z5
D	-19	HIS	-	expression tag	UNP Q188Z5
D	-18	PRO	-	expression tag	UNP Q188Z5
D	-17	GLN	-	expression tag	UNP Q188Z5
D	-16	PHE	-	expression tag	UNP Q188Z5
D	-15	GLU	-	expression tag	UNP Q188Z5
D	-14	LYS	-	expression tag	UNP Q188Z5
D	-13	SER	-	expression tag	UNP Q188Z5
D	-12	ASN	-	expression tag	UNP Q188Z5
D	-11	ASN	-	expression tag	UNP Q188Z5
D	-10	ASN	-	expression tag	UNP Q188Z5
D	-9	LEU	-	expression tag	UNP Q188Z5

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-8	GLY	-	expression tag	UNP Q188Z5
D	-7	GLU	-	expression tag	UNP Q188Z5
D	-6	ASN	-	expression tag	UNP Q188Z5
D	-5	LEU	-	expression tag	UNP Q188Z5
D	-4	TYR	-	expression tag	UNP Q188Z5
D	-3	PHE	-	expression tag	UNP Q188Z5
D	-2	GLN	-	expression tag	UNP Q188Z5
D	-1	GLY	-	expression tag	UNP Q188Z5
D	0	HIS	-	expression tag	UNP Q188Z5
B	-56	MET	-	initiating methionine	UNP Q188Z5
B	-55	GLY	-	expression tag	UNP Q188Z5
B	-54	SER	-	expression tag	UNP Q188Z5
B	-53	SER	-	expression tag	UNP Q188Z5
B	-52	HIS	-	expression tag	UNP Q188Z5
B	-51	HIS	-	expression tag	UNP Q188Z5
B	-50	HIS	-	expression tag	UNP Q188Z5
B	-49	HIS	-	expression tag	UNP Q188Z5
B	-48	HIS	-	expression tag	UNP Q188Z5
B	-47	HIS	-	expression tag	UNP Q188Z5
B	-46	SER	-	expression tag	UNP Q188Z5
B	-45	SER	-	expression tag	UNP Q188Z5
B	-44	GLY	-	expression tag	UNP Q188Z5
B	-43	SER	-	expression tag	UNP Q188Z5
B	-42	ALA	-	expression tag	UNP Q188Z5
B	-41	TRP	-	expression tag	UNP Q188Z5
B	-40	SER	-	expression tag	UNP Q188Z5
B	-39	HIS	-	expression tag	UNP Q188Z5
B	-38	PRO	-	expression tag	UNP Q188Z5
B	-37	GLN	-	expression tag	UNP Q188Z5
B	-36	PHE	-	expression tag	UNP Q188Z5
B	-35	GLU	-	expression tag	UNP Q188Z5
B	-34	LYS	-	expression tag	UNP Q188Z5
B	-33	GLY	-	expression tag	UNP Q188Z5
B	-32	GLY	-	expression tag	UNP Q188Z5
B	-31	GLY	-	expression tag	UNP Q188Z5
B	-30	SER	-	expression tag	UNP Q188Z5
B	-29	GLY	-	expression tag	UNP Q188Z5
B	-28	GLY	-	expression tag	UNP Q188Z5
B	-27	GLY	-	expression tag	UNP Q188Z5
B	-26	SER	-	expression tag	UNP Q188Z5
B	-25	GLY	-	expression tag	UNP Q188Z5
B	-24	GLY	-	expression tag	UNP Q188Z5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-23	SER	-	expression tag	UNP Q188Z5
B	-22	ALA	-	expression tag	UNP Q188Z5
B	-21	TRP	-	expression tag	UNP Q188Z5
B	-20	SER	-	expression tag	UNP Q188Z5
B	-19	HIS	-	expression tag	UNP Q188Z5
B	-18	PRO	-	expression tag	UNP Q188Z5
B	-17	GLN	-	expression tag	UNP Q188Z5
B	-16	PHE	-	expression tag	UNP Q188Z5
B	-15	GLU	-	expression tag	UNP Q188Z5
B	-14	LYS	-	expression tag	UNP Q188Z5
B	-13	SER	-	expression tag	UNP Q188Z5
B	-12	ASN	-	expression tag	UNP Q188Z5
B	-11	ASN	-	expression tag	UNP Q188Z5
B	-10	ASN	-	expression tag	UNP Q188Z5
B	-9	LEU	-	expression tag	UNP Q188Z5
B	-8	GLY	-	expression tag	UNP Q188Z5
B	-7	GLU	-	expression tag	UNP Q188Z5
B	-6	ASN	-	expression tag	UNP Q188Z5
B	-5	LEU	-	expression tag	UNP Q188Z5
B	-4	TYR	-	expression tag	UNP Q188Z5
B	-3	PHE	-	expression tag	UNP Q188Z5
B	-2	GLN	-	expression tag	UNP Q188Z5
B	-1	GLY	-	expression tag	UNP Q188Z5
B	0	HIS	-	expression tag	UNP Q188Z5
C	-56	MET	-	initiating methionine	UNP Q188Z5
C	-55	GLY	-	expression tag	UNP Q188Z5
C	-54	SER	-	expression tag	UNP Q188Z5
C	-53	SER	-	expression tag	UNP Q188Z5
C	-52	HIS	-	expression tag	UNP Q188Z5
C	-51	HIS	-	expression tag	UNP Q188Z5
C	-50	HIS	-	expression tag	UNP Q188Z5
C	-49	HIS	-	expression tag	UNP Q188Z5
C	-48	HIS	-	expression tag	UNP Q188Z5
C	-47	HIS	-	expression tag	UNP Q188Z5
C	-46	SER	-	expression tag	UNP Q188Z5
C	-45	SER	-	expression tag	UNP Q188Z5
C	-44	GLY	-	expression tag	UNP Q188Z5
C	-43	SER	-	expression tag	UNP Q188Z5
C	-42	ALA	-	expression tag	UNP Q188Z5
C	-41	TRP	-	expression tag	UNP Q188Z5
C	-40	SER	-	expression tag	UNP Q188Z5
C	-39	HIS	-	expression tag	UNP Q188Z5

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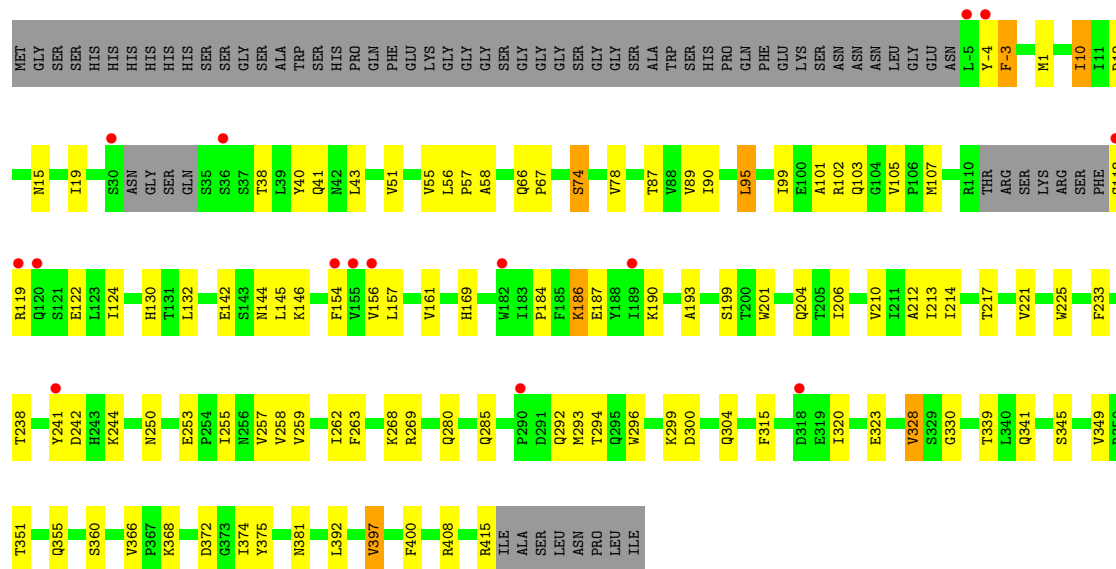
Chain	Residue	Modelled	Actual	Comment	Reference
C	-38	PRO	-	expression tag	UNP Q188Z5
C	-37	GLN	-	expression tag	UNP Q188Z5
C	-36	PHE	-	expression tag	UNP Q188Z5
C	-35	GLU	-	expression tag	UNP Q188Z5
C	-34	LYS	-	expression tag	UNP Q188Z5
C	-33	GLY	-	expression tag	UNP Q188Z5
C	-32	GLY	-	expression tag	UNP Q188Z5
C	-31	GLY	-	expression tag	UNP Q188Z5
C	-30	SER	-	expression tag	UNP Q188Z5
C	-29	GLY	-	expression tag	UNP Q188Z5
C	-28	GLY	-	expression tag	UNP Q188Z5
C	-27	GLY	-	expression tag	UNP Q188Z5
C	-26	SER	-	expression tag	UNP Q188Z5
C	-25	GLY	-	expression tag	UNP Q188Z5
C	-24	GLY	-	expression tag	UNP Q188Z5
C	-23	SER	-	expression tag	UNP Q188Z5
C	-22	ALA	-	expression tag	UNP Q188Z5
C	-21	TRP	-	expression tag	UNP Q188Z5
C	-20	SER	-	expression tag	UNP Q188Z5
C	-19	HIS	-	expression tag	UNP Q188Z5
C	-18	PRO	-	expression tag	UNP Q188Z5
C	-17	GLN	-	expression tag	UNP Q188Z5
C	-16	PHE	-	expression tag	UNP Q188Z5
C	-15	GLU	-	expression tag	UNP Q188Z5
C	-14	LYS	-	expression tag	UNP Q188Z5
C	-13	SER	-	expression tag	UNP Q188Z5
C	-12	ASN	-	expression tag	UNP Q188Z5
C	-11	ASN	-	expression tag	UNP Q188Z5
C	-10	ASN	-	expression tag	UNP Q188Z5
C	-9	LEU	-	expression tag	UNP Q188Z5
C	-8	GLY	-	expression tag	UNP Q188Z5
C	-7	GLU	-	expression tag	UNP Q188Z5
C	-6	ASN	-	expression tag	UNP Q188Z5
C	-5	LEU	-	expression tag	UNP Q188Z5
C	-4	TYR	-	expression tag	UNP Q188Z5
C	-3	PHE	-	expression tag	UNP Q188Z5
C	-2	GLN	-	expression tag	UNP Q188Z5
C	-1	GLY	-	expression tag	UNP Q188Z5
C	0	HIS	-	expression tag	UNP Q188Z5

- Molecule 2 is water.

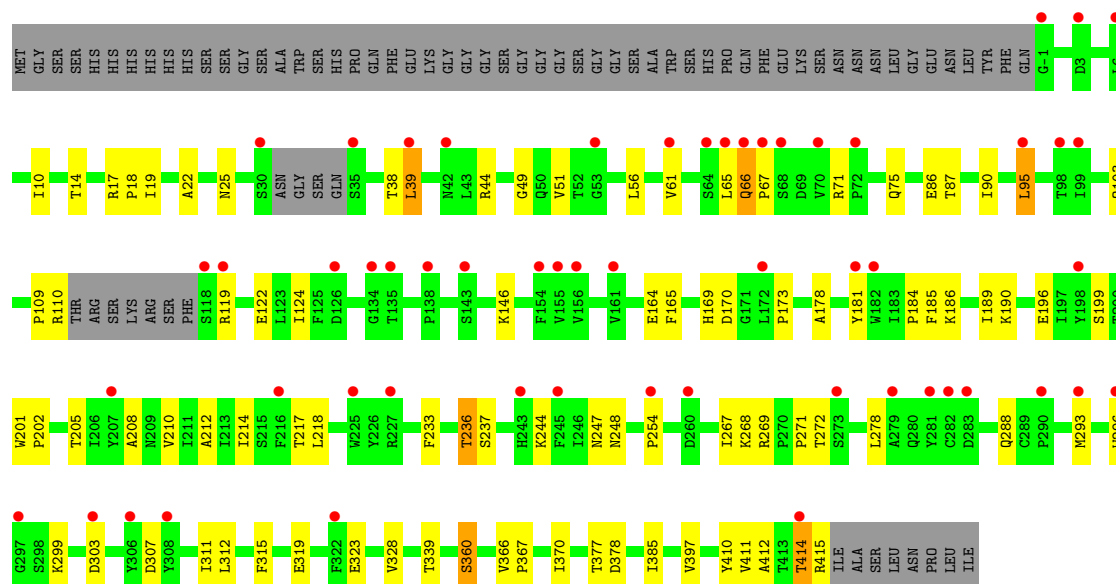
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	130	Total 130	O 130	0	0
2	D	143	Total 143	O 143	0	0
2	B	168	Total 168	O 168	0	0
2	C	148	Total 148	O 148	0	0



- Molecule 1: Spore cortex-lytic enzyme pre-pro-form



- Molecule 1: Spore cortex-lytic enzyme pre-pro-form



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	66.43Å 89.78Å 99.62Å 76.90° 75.87° 89.12°	Depositor
Resolution (Å)	72.90 – 2.10 72.90 – 2.10	Depositor EDS
% Data completeness (in resolution range)	57.3 (72.90-2.10) 57.3 (72.90-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.90 (at 2.10Å)	Xtriage
Refinement program	PHENIX 1.21.2_5419	Depositor
R, R_{free}	0.211 , 0.261 (Not available) , 0.265	Depositor DCC
R_{free} test set	3687 reflections (2.91%)	wwPDB-VP
Wilson B-factor (Å ²)	40.4	Xtriage
Anisotropy	0.135	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 41.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	13534	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.30% 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	0.42	0/3361	0.62	0/4595
1	B	0.42	0/3343	0.64	0/4570
1	C	0.37	1/3301 (0.0%)	0.55	0/4513
1	D	0.40	0/3284	0.60	0/4491
All	All	0.40	1/13289 (0.0%)	0.60	0/18169

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	66	GLN	CD-OE1	-6.15	1.11	1.23

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3274	0	3176	83	0
1	B	3256	0	3158	92	0
1	C	3216	0	3121	78	0
1	D	3199	0	3103	89	0
2	A	130	0	0	34	0
2	B	168	0	0	50	0
2	C	148	0	0	36	0
2	D	143	0	0	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	13534	0	12558	333	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 13.

All (333) 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:D:294:THR:HG22	1:D:297:GLY:H	1.25	1.02
1:A:259:VAL:HG11	2:A:502:HOH:O	1.66	0.94
1:D:267:ILE:HD11	1:D:312:LEU:HD13	1.56	0.87
1:A:268:LYS:HD3	1:A:323:GLU:HG3	1.55	0.86
1:A:146:LYS:HE2	1:A:278:LEU:HD22	1.56	0.86
1:B:130:HIS:HD2	1:B:132:LEU:H	1.22	0.84
1:B:268:LYS:HD3	1:B:323:GLU:HG3	1.62	0.81
1:D:351:THR:HB	2:D:502:HOH:O	1.83	0.78
1:A:336:PRO:HD3	2:A:598:HOH:O	1.83	0.77
1:D:75:GLN:HG2	2:D:548:HOH:O	1.85	0.77
1:D:218:LEU:HB2	2:D:573:HOH:O	1.85	0.76
1:B:328:VAL:HG23	2:B:514:HOH:O	1.86	0.76
1:D:163:PRO:HD2	2:D:635:HOH:O	1.87	0.74
1:D:266:PHE:HA	2:D:503:HOH:O	1.86	0.73
1:C:267:ILE:HD11	1:C:312:LEU:HD13	1.69	0.73
1:D:410:TYR:HB2	2:D:567:HOH:O	1.89	0.73
1:B:130:HIS:CD2	1:B:132:LEU:H	2.06	0.73
1:D:130:HIS:HD2	1:D:132:LEU:H	1.37	0.72
1:D:220:ARG:HG2	2:D:504:HOH:O	1.89	0.72
1:D:73:TYR:HD1	2:D:548:HOH:O	1.72	0.72
1:C:173:PRO:HG3	1:C:236:THR:HG21	1.72	0.72
1:C:109:PRO:HD3	2:C:505:HOH:O	1.91	0.70
1:C:87:THR:HB	1:C:122:GLU:HG2	1.76	0.68
1:D:355:GLN:HB3	2:D:567:HOH:O	1.94	0.68
1:B:58:ALA:HA	1:B:74:SER:OG	1.94	0.68
1:A:267:ILE:HA	2:A:538:HOH:O	1.94	0.67
1:B:12:ASP:HA	2:B:540:HOH:O	1.94	0.67
1:D:269:ARG:HG2	1:D:269:ARG:HH11	1.58	0.67
1:D:415:ARG:HB2	1:C:415:ARG:HD3	1.77	0.67
1:D:191:ASN:HA	2:D:606:HOH:O	1.94	0.67
1:B:341:GLN:HB3	1:B:397:VAL:HG22	1.76	0.67
1:A:130:HIS:CD2	1:A:132:LEU:H	2.13	0.66
1:A:324:ARG:HD2	2:A:615:HOH:O	1.94	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:190:LYS:HG3	2:A:502:HOH:O	1.95	0.66
1:A:218:LEU:HB2	2:A:571:HOH:O	1.94	0.66
1:A:130:HIS:HD2	1:A:132:LEU:H	1.41	0.66
1:B:296:TRP:HA	2:B:641:HOH:O	1.95	0.65
1:A:215:SER:HA	2:A:571:HOH:O	1.96	0.65
1:B:57:PRO:HD2	2:B:565:HOH:O	1.97	0.65
1:C:146:LYS:HE2	1:C:278:LEU:HD22	1.77	0.65
1:A:235:ILE:HG22	2:A:501:HOH:O	1.98	0.64
1:B:293:MET:HG3	1:B:315:PHE:CD2	2.32	0.64
1:C:75:GLN:HG3	2:C:523:HOH:O	1.98	0.64
1:D:89:VAL:HB	1:D:124:ILE:HD13	1.80	0.64
1:B:58:ALA:HB3	2:B:506:HOH:O	1.98	0.63
1:C:367:PRO:HD2	2:C:538:HOH:O	1.97	0.62
1:C:25:ASN:HB3	2:C:511:HOH:O	1.98	0.62
1:B:345:SER:HA	2:B:512:HOH:O	1.98	0.62
1:D:381:ASN:HB2	2:D:609:HOH:O	1.98	0.62
1:D:215:SER:HA	2:D:573:HOH:O	1.98	0.62
1:C:67:PRO:HD3	1:C:296:TRP:CD2	2.35	0.61
1:A:204:GLN:HA	2:A:508:HOH:O	2.01	0.61
1:C:360:SER:HB2	1:C:366:VAL:O	2.00	0.61
1:A:295:GLN:HB3	2:A:507:HOH:O	2.00	0.61
1:D:415:ARG:HH11	1:C:415:ARG:HB3	1.66	0.60
1:B:269:ARG:HB2	1:B:320:ILE:HG22	1.84	0.60
1:C:185:PHE:HD2	2:C:542:HOH:O	1.85	0.60
1:C:212:ALA:HA	2:C:534:HOH:O	2.01	0.60
1:A:39:LEU:HB3	2:A:608:HOH:O	2.01	0.60
1:A:197:ILE:HG22	2:A:507:HOH:O	2.01	0.59
1:B:293:MET:HE1	2:B:503:HOH:O	2.01	0.59
1:A:266:PHE:CD1	1:A:276:PRO:HB3	2.36	0.59
1:A:189:ILE:HG22	2:A:520:HOH:O	2.02	0.59
1:B:56:LEU:HB2	1:B:95:LEU:HD22	1.85	0.59
1:B:214:ILE:HD11	2:B:634:HOH:O	2.01	0.59
1:D:130:HIS:CD2	1:D:132:LEU:H	2.20	0.59
1:A:259:VAL:HG12	2:A:558:HOH:O	2.03	0.59
1:C:311:ILE:HG22	2:C:513:HOH:O	2.03	0.59
1:B:107:MET:HB2	2:B:540:HOH:O	2.03	0.58
1:B:258:VAL:HB	2:B:584:HOH:O	2.04	0.58
1:C:385:ILE:HB	2:C:538:HOH:O	2.04	0.58
1:C:201:TRP:HB3	2:C:605:HOH:O	2.03	0.58
1:B:244:LYS:HD3	2:B:501:HOH:O	2.04	0.58
1:C:14:THR:HG23	2:C:505:HOH:O	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:178:ALA:HB1	2:C:502:HOH:O	2.05	0.57
1:B:206:ILE:HD11	2:B:515:HOH:O	2.05	0.57
1:B:381:ASN:HB2	2:B:640:HOH:O	2.04	0.57
1:C:271:PRO:HG3	1:C:319:GLU:O	2.05	0.56
1:B:10:ILE:HD13	1:B:105:VAL:HB	1.87	0.56
1:C:119:ARG:H	1:C:119:ARG:HD2	1.70	0.56
1:D:301:LEU:HB3	1:D:306:TYR:HD2	1.68	0.56
1:D:360:SER:HB2	1:D:366:VAL:O	2.05	0.56
1:B:103:GLN:HG2	2:B:508:HOH:O	2.05	0.56
1:A:25:ASN:HB3	2:A:530:HOH:O	2.06	0.56
1:D:86:GLU:HG2	1:D:122:GLU:HA	1.87	0.56
1:D:97:ALA:HB1	2:D:534:HOH:O	2.06	0.55
1:D:379:THR:HB	2:D:501:HOH:O	2.06	0.55
1:D:238:THR:HG22	1:D:240:ALA:H	1.70	0.55
1:C:210:VAL:O	1:C:214:ILE:HG13	2.06	0.55
1:D:301:LEU:HB3	1:D:306:TYR:CD2	2.42	0.55
1:B:204:GLN:HA	2:B:538:HOH:O	2.06	0.55
1:D:415:ARG:HB2	1:C:415:ARG:CD	2.36	0.54
1:B:184:PRO:HB2	1:B:187:GLU:HG2	1.90	0.54
1:B:66:GLN:HG3	1:B:67:PRO:HD2	1.88	0.54
1:D:268:LYS:HD3	1:D:273:SER:HB2	1.89	0.53
1:D:271:PRO:HB3	1:D:321:VAL:HG11	1.91	0.53
1:C:65:LEU:HA	2:C:503:HOH:O	2.09	0.53
1:B:351:THR:O	1:B:355:GLN:HG3	2.09	0.53
1:A:56:LEU:HB2	1:A:95:LEU:HD22	1.91	0.53
1:B:415:ARG:HH11	1:B:415:ARG:C	2.16	0.53
1:C:244:LYS:HA	2:C:507:HOH:O	2.08	0.53
1:A:241:TYR:HB2	2:A:504:HOH:O	2.10	0.52
1:A:28:SER:HB3	1:A:39:LEU:HD11	1.90	0.52
1:D:106:PRO:HD2	2:D:604:HOH:O	2.07	0.52
1:B:241:TYR:HB2	2:B:502:HOH:O	2.08	0.52
1:A:14:THR:O	1:A:416:ILE:HG21	2.10	0.52
1:D:206:ILE:HG22	1:D:258:VAL:HG11	1.91	0.52
1:B:294:THR:HG21	2:B:533:HOH:O	2.10	0.52
1:D:357:ASN:HA	2:D:537:HOH:O	2.08	0.52
1:B:360:SER:HB2	1:B:366:VAL:O	2.09	0.52
1:A:416:ILE:HA	2:A:587:HOH:O	2.10	0.51
1:C:189:ILE:HD13	2:C:632:HOH:O	2.10	0.51
1:A:124:ILE:HD11	2:A:599:HOH:O	2.10	0.51
1:D:208:ALA:HA	2:D:546:HOH:O	2.08	0.51
1:C:411:VAL:HG13	1:C:415:ARG:CZ	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:163:PRO:HG2	2:D:589:HOH:O	2.09	0.51
1:B:349:VAL:HG11	2:B:512:HOH:O	2.11	0.51
1:C:170:ASP:HB2	1:C:181:TYR:HE2	1.75	0.51
1:C:254:PRO:HG2	2:C:539:HOH:O	2.08	0.51
1:B:400:PHE:HA	2:B:624:HOH:O	2.11	0.51
1:B:78:VAL:HB	2:B:508:HOH:O	2.10	0.51
1:B:89:VAL:HB	1:B:124:ILE:HD13	1.93	0.51
1:C:38:THR:HG23	2:C:511:HOH:O	2.11	0.51
1:D:216:PHE:CD1	1:D:278:LEU:HG	2.46	0.51
1:D:341:GLN:HB3	1:D:397:VAL:HG22	1.93	0.51
1:C:307:ASP:O	1:C:311:ILE:HG13	2.11	0.50
1:A:405:GLU:OE2	1:A:405:GLU:HA	2.11	0.50
1:B:1:MET:HE3	1:B:57:PRO:HB2	1.93	0.50
1:B:293:MET:HE2	2:B:510:HOH:O	2.11	0.50
1:A:271:PRO:HB3	1:A:321:VAL:HG13	1.93	0.50
1:D:185:PHE:HB2	2:D:589:HOH:O	2.10	0.50
1:B:19:ILE:HD11	2:B:540:HOH:O	2.11	0.50
1:B:55:VAL:HG12	2:B:614:HOH:O	2.11	0.50
1:D:132:LEU:HD23	2:D:516:HOH:O	2.11	0.50
1:B:132:LEU:HD12	2:B:505:HOH:O	2.12	0.50
1:A:255:ILE:O	1:A:259:VAL:HG23	2.12	0.50
1:D:173:PRO:HG3	1:D:236:THR:HG21	1.93	0.50
1:B:144:ASN:O	1:B:145:LEU:HD23	2.11	0.50
1:A:132:LEU:HD13	2:A:593:HOH:O	2.10	0.49
1:A:40:TYR:HB3	1:A:43:LEU:HD11	1.94	0.49
1:A:157:LEU:HD11	1:B:368:LYS:HD2	1.95	0.49
1:A:342:VAL:HA	1:A:375:TYR:O	2.11	0.49
1:C:411:VAL:O	1:C:415:ARG:HG3	2.12	0.49
1:A:92:GLY:O	1:A:94:GLN:HG3	2.13	0.49
1:A:120:GLN:HB2	1:D:124:ILE:O	2.12	0.49
1:A:385:ILE:HB	2:A:509:HOH:O	2.13	0.49
1:B:101:ALA:HB1	1:B:250:ASN:HD22	1.77	0.49
1:D:322:PHE:HE1	2:D:522:HOH:O	1.95	0.49
1:C:51:VAL:HG23	2:C:562:HOH:O	2.12	0.49
1:B:154:PHE:HA	2:B:563:HOH:O	2.13	0.49
1:C:67:PRO:HD3	1:C:296:TRP:CE3	2.48	0.49
1:D:290:PRO:O	1:D:291:ASP:HB3	2.13	0.48
1:B:87:THR:HB	1:B:122:GLU:HG2	1.94	0.48
1:D:174:GLU:CD	1:D:174:GLU:H	2.21	0.48
1:B:210:VAL:HG21	2:B:584:HOH:O	2.13	0.48
1:B:299:LYS:HB3	2:B:641:HOH:O	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:268:LYS:HD3	1:C:323:GLU:HG3	1.95	0.48
1:C:71:ARG:HD3	2:C:523:HOH:O	2.13	0.48
1:A:189:ILE:HB	2:A:502:HOH:O	2.13	0.48
1:A:162:VAL:O	1:A:328:VAL:HG13	2.14	0.48
1:B:212:ALA:HB2	2:B:503:HOH:O	2.14	0.48
1:B:55:VAL:HG13	2:B:518:HOH:O	2.13	0.48
1:A:288:GLN:HG2	1:A:289:CYS:N	2.29	0.48
1:A:366:VAL:HA	2:A:509:HOH:O	2.13	0.48
1:C:17:ARG:HG2	1:C:18:PRO:HD2	1.96	0.47
1:A:283:ASP:HA	1:A:295:GLN:HB2	1.95	0.47
1:D:38:THR:HG23	2:D:524:HOH:O	2.15	0.47
1:C:296:TRP:HZ3	2:C:503:HOH:O	1.97	0.47
1:D:253:GLU:HB3	1:D:254:PRO:HD3	1.96	0.47
1:D:284:GLY:HA3	1:D:294:THR:HG23	1.97	0.47
1:A:-6:ASN:HD22	1:A:-5:LEU:HD23	1.78	0.47
1:A:10:ILE:HG22	2:A:506:HOH:O	2.13	0.47
1:A:186:LYS:HA	2:A:613:HOH:O	2.14	0.47
1:A:263:PHE:HB2	2:A:613:HOH:O	2.15	0.47
1:B:99:ILE:HG21	2:B:519:HOH:O	2.15	0.47
1:D:267:ILE:HG22	1:D:277:LEU:HB3	1.97	0.47
1:C:412:ALA:HB2	2:C:603:HOH:O	2.14	0.47
1:A:123:LEU:HD23	1:D:121:SER:HB3	1.97	0.47
1:A:186:LYS:HD2	2:A:558:HOH:O	2.15	0.47
1:D:207:TYR:CD2	1:D:262:ILE:HD13	2.50	0.47
1:A:360:SER:OG	1:A:368:LYS:HE2	2.15	0.47
1:D:157:LEU:HA	2:D:617:HOH:O	2.14	0.47
1:C:202:PRO:HD2	2:C:605:HOH:O	2.15	0.47
1:C:19:ILE:O	1:C:49:GLY:HA2	2.15	0.46
1:D:293:MET:HE1	1:D:312:LEU:HD22	1.96	0.46
1:D:415:ARG:HB2	1:C:415:ARG:NE	2.30	0.46
1:B:408:ARG:HA	2:B:547:HOH:O	2.14	0.46
1:C:201:TRP:NE1	2:C:503:HOH:O	2.48	0.46
1:B:300:ASP:O	1:B:304:GLN:HG3	2.16	0.46
1:A:269:ARG:HG3	1:A:320:ILE:HG22	1.97	0.46
1:D:268:LYS:O	1:D:320:ILE:HA	2.15	0.46
1:A:86:GLU:HB3	2:A:540:HOH:O	2.14	0.46
1:A:130:HIS:CD2	1:A:132:LEU:HB2	2.50	0.46
1:D:259:VAL:HG13	2:D:626:HOH:O	2.15	0.46
1:B:90:ILE:HD13	1:B:103:GLN:NE2	2.31	0.46
1:B:142:GLU:HG2	1:B:146:LYS:NZ	2.31	0.46
1:B:169:HIS:HB2	1:B:233:PHE:CG	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:166:ILE:HG22	2:A:501:HOH:O	2.15	0.46
1:C:90:ILE:HG21	1:C:103:GLN:NE2	2.30	0.46
1:A:190:LYS:N	2:A:502:HOH:O	2.49	0.46
1:C:312:LEU:HG	2:C:501:HOH:O	2.15	0.46
1:B:142:GLU:HG2	1:B:146:LYS:HZ3	1.81	0.45
1:A:308:TYR:HD2	2:A:508:HOH:O	1.99	0.45
1:A:20:GLN:HG3	1:A:21:ASN:N	2.30	0.45
1:A:103:GLN:OE1	1:A:250:ASN:HB3	2.17	0.45
1:D:256:ASN:HB3	2:D:527:HOH:O	2.15	0.45
1:A:130:HIS:HD2	1:A:132:LEU:N	2.13	0.45
1:D:251:LEU:HD23	2:D:606:HOH:O	2.17	0.45
1:C:217:THR:HG22	2:C:540:HOH:O	2.15	0.45
1:A:201:TRP:HZ2	2:A:593:HOH:O	1.98	0.45
1:A:352:ILE:HD11	1:A:403:TRP:CE3	2.52	0.45
1:D:132:LEU:HD12	2:D:508:HOH:O	2.17	0.45
1:C:39:LEU:HD13	1:C:56:LEU:HD22	1.97	0.45
1:D:269:ARG:HB2	1:D:320:ILE:HG22	1.98	0.45
1:B:263:PHE:HA	2:B:634:HOH:O	2.16	0.45
1:A:99:ILE:HD13	1:A:99:ILE:HA	1.78	0.45
1:A:352:ILE:HD13	1:A:352:ILE:HA	1.68	0.45
1:D:294:THR:HG22	1:D:297:GLY:N	2.09	0.45
1:C:370:ILE:HD13	1:C:370:ILE:HA	1.90	0.45
1:D:62:ASP:HA	1:D:65:LEU:HD12	1.99	0.45
1:A:199:SER:HB3	1:A:255:ILE:HG13	1.99	0.44
1:A:239:THR:HG23	1:A:244:LYS:HB2	1.98	0.44
1:A:278:LEU:HD23	2:A:517:HOH:O	2.16	0.44
1:A:293:MET:HE2	1:A:316:TYR:CE2	2.51	0.44
1:D:221:VAL:HG22	1:D:234:THR:HG21	1.99	0.44
1:A:122:GLU:HB2	2:A:599:HOH:O	2.17	0.44
1:A:341:GLN:O	1:A:342:VAL:C	2.61	0.44
1:B:40:TYR:HB3	1:B:43:LEU:HD11	1.99	0.44
1:B:339:THR:CG2	1:B:397:VAL:HG13	2.47	0.44
1:D:309:GLU:HB3	2:D:522:HOH:O	2.17	0.44
1:C:205:THR:O	1:C:208:ALA:HB3	2.16	0.44
1:B:217:THR:O	1:B:221:VAL:HG23	2.17	0.44
1:C:86:GLU:HA	1:C:110:ARG:CZ	2.48	0.44
1:C:196:GLU:HG2	2:C:537:HOH:O	2.16	0.44
1:D:339:THR:CG2	1:D:397:VAL:HG13	2.48	0.44
1:C:61:VAL:O	1:C:65:LEU:HD12	2.18	0.44
1:C:319:GLU:HG2	2:C:567:HOH:O	2.17	0.44
1:C:185:PHE:HE1	2:C:540:HOH:O	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:199:SER:HB3	2:C:539:HOH:O	2.18	0.44
1:C:267:ILE:HD12	2:C:534:HOH:O	2.17	0.43
1:D:56:LEU:HB2	1:D:95:LEU:CD2	2.48	0.43
1:D:58:ALA:HA	1:D:74:SER:OG	2.18	0.43
1:D:99:ILE:HD12	1:D:254:PRO:HG2	2.00	0.43
1:B:259:VAL:HA	2:B:634:HOH:O	2.17	0.43
1:D:258:VAL:O	1:D:262:ILE:HG12	2.18	0.43
1:C:267:ILE:HG12	2:C:546:HOH:O	2.18	0.43
1:D:4:GLY:HA2	2:D:517:HOH:O	2.17	0.43
1:C:184:PRO:HD2	2:C:640:HOH:O	2.19	0.43
1:D:25:ASN:HB3	2:D:524:HOH:O	2.19	0.43
1:C:164:GLU:HB3	1:C:165:PHE:CD1	2.54	0.43
1:A:19:ILE:O	1:A:49:GLY:HA2	2.19	0.43
1:D:266:PHE:HB3	2:D:580:HOH:O	2.18	0.43
1:B:193:ALA:HB2	2:B:529:HOH:O	2.19	0.43
1:B:12:ASP:HB3	1:B:15:ASN:OD1	2.18	0.43
1:B:102:ARG:NH1	2:B:511:HOH:O	2.52	0.43
1:D:270:PRO:HG2	1:D:272:THR:HG22	2.02	0.42
1:B:280:GLN:O	1:B:292:GLN:HG2	2.19	0.42
1:A:260:ASP:HB3	1:A:401:LYS:HB2	2.01	0.42
1:A:384:LYS:HG3	1:A:396:GLY:CA	2.49	0.42
1:B:130:HIS:CD2	1:B:132:LEU:HB2	2.54	0.42
1:B:199:SER:HB2	2:B:504:HOH:O	2.18	0.42
1:B:206:ILE:HD13	1:B:206:ILE:HG21	1.77	0.42
1:A:271:PRO:HB3	1:A:321:VAL:CG1	2.49	0.42
1:B:119:ARG:NH1	1:C:178:ALA:HA	2.33	0.42
1:A:266:PHE:HE2	1:A:325:ALA:HB2	1.84	0.42
1:A:339:THR:HG23	1:A:397:VAL:HG13	2.01	0.42
1:D:298:SER:HB2	1:D:311:ILE:HG21	2.01	0.42
1:B:392:LEU:HB3	2:B:548:HOH:O	2.19	0.42
1:C:269:ARG:HA	2:C:567:HOH:O	2.19	0.42
1:A:89:VAL:HB	1:A:124:ILE:HD13	2.02	0.42
1:D:7:THR:HG22	2:D:514:HOH:O	2.18	0.42
1:D:162:VAL:O	1:D:328:VAL:HG12	2.19	0.42
1:B:242:ASP:N	2:B:502:HOH:O	2.52	0.42
1:A:207:TYR:HB2	2:A:508:HOH:O	2.19	0.42
1:C:288:GLN:HA	2:C:536:HOH:O	2.18	0.42
1:D:197:ILE:HG21	1:D:209:ASN:OD1	2.20	0.42
1:C:39:LEU:HA	1:C:39:LEU:HD23	1.84	0.42
1:C:299:LYS:HE2	1:C:303:ASP:OD1	2.19	0.42
1:B:38:THR:HG21	1:B:41:GLN:OE1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:375:TYR:N	2:B:512:HOH:O	2.52	0.42
1:B:415:ARG:HB3	2:B:545:HOH:O	2.18	0.42
1:A:11:ILE:O	1:A:11:ILE:HG13	2.20	0.42
1:A:345:SER:HA	1:A:373:GLY:O	2.20	0.41
1:D:342:VAL:HG23	2:D:543:HOH:O	2.20	0.41
1:B:253:GLU:O	1:B:257:VAL:HG23	2.20	0.41
1:B:339:THR:HG23	1:B:397:VAL:HG13	2.02	0.41
1:C:190:LYS:HG3	2:C:518:HOH:O	2.19	0.41
1:D:281:TYR:HE2	2:D:590:HOH:O	2.01	0.41
1:C:218:LEU:HD23	1:C:218:LEU:HA	1.95	0.41
1:C:366:VAL:HA	2:C:538:HOH:O	2.19	0.41
1:C:169:HIS:HB2	1:C:233:PHE:CG	2.55	0.41
1:B:253:GLU:HG3	2:B:557:HOH:O	2.20	0.41
1:D:293:MET:HE3	1:D:316:TYR:HE2	1.84	0.41
1:B:90:ILE:HB	2:B:508:HOH:O	2.21	0.41
1:C:170:ASP:HA	1:C:237:SER:OG	2.21	0.41
1:D:169:HIS:HE1	2:D:506:HOH:O	2.04	0.41
1:B:213:ILE:HG21	2:B:529:HOH:O	2.20	0.41
1:B:299:LYS:CB	2:B:641:HOH:O	2.68	0.41
1:C:22:ALA:O	1:C:44:ARG:HA	2.21	0.41
1:D:146:LYS:HD2	1:D:225:TRP:CZ3	2.55	0.41
1:D:160:PRO:HD3	1:D:274:ARG:O	2.21	0.41
1:B:157:LEU:HD13	2:B:648:HOH:O	2.19	0.41
1:C:410:TYR:O	1:C:414:THR:HB	2.20	0.41
1:D:87:THR:O	1:D:122:GLU:HB2	2.20	0.41
1:D:259:VAL:O	1:D:263:PHE:HB3	2.21	0.41
1:D:411:VAL:HG12	1:D:415:ARG:HD3	2.03	0.41
1:C:56:LEU:HB2	1:C:95:LEU:CD2	2.51	0.41
1:C:208:ALA:HA	2:C:501:HOH:O	2.21	0.41
1:D:132:LEU:HD11	1:D:201:TRP:CH2	2.56	0.41
1:B:262:ILE:HB	2:B:647:HOH:O	2.20	0.41
1:B:330:GLY:N	2:B:514:HOH:O	2.53	0.41
1:C:66:GLN:OE1	1:C:67:PRO:HD2	2.21	0.41
1:C:119:ARG:HD2	1:C:119:ARG:N	2.34	0.41
1:C:247:ASN:O	1:C:248:ASN:HB2	2.20	0.41
1:D:345:SER:HA	1:D:373:GLY:O	2.21	0.41
1:B:67:PRO:HG2	1:B:285:GLN:NE2	2.35	0.41
1:B:122:GLU:CD	1:C:124:ILE:HG13	2.46	0.41
1:B:132:LEU:HA	1:B:132:LEU:HD23	1.76	0.41
1:B:255:ILE:HA	2:B:584:HOH:O	2.21	0.41
1:B:51:VAL:HB	2:B:665:HOH:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:372:ASP:OD2	1:B:374:ILE:HB	2.21	0.40
1:C:293:MET:HA	1:C:315:PHE:CD1	2.57	0.40
1:D:74:SER:C	2:D:548:HOH:O	2.64	0.40
1:A:164:GLU:HB2	1:A:328:VAL:HG22	2.03	0.40
1:B:146:LYS:HD2	1:B:225:TRP:CZ3	2.57	0.40
1:B:186:LYS:O	1:B:190:LYS:HG3	2.21	0.40
1:B:201:TRP:N	2:B:515:HOH:O	2.54	0.40
1:A:154:PHE:O	1:A:156:VAL:N	2.54	0.40
1:A:166:ILE:HG23	1:A:166:ILE:HD12	1.82	0.40
1:A:259:VAL:O	1:A:263:PHE:HB3	2.21	0.40
1:A:307:ASP:O	1:A:311:ILE:HG13	2.22	0.40
1:A:360:SER:HB2	1:A:366:VAL:O	2.21	0.40
1:D:20:GLN:HG3	1:D:46:ASN:O	2.22	0.40

There are no symmetry-related clashes.

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	406/480 (85%)	386 (95%)	19 (5%)	1 (0%)	43	44
1	B	404/480 (84%)	388 (96%)	14 (4%)	2 (0%)	24	22
1	C	400/480 (83%)	377 (94%)	22 (6%)	1 (0%)	36	36
1	D	398/480 (83%)	379 (95%)	16 (4%)	3 (1%)	16	12
All	All	1608/1920 (84%)	1530 (95%)	71 (4%)	7 (0%)	30	28

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	-3	PHE
1	B	-4	TYR

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Mol	Chain	Res	Type
1	A	-6	ASN
1	C	339	THR
1	D	42	ASN
1	D	319	GLU
1	D	155	VAL

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	366/420 (87%)	350 (96%)	16 (4%)	25	26
1	B	365/420 (87%)	354 (97%)	11 (3%)	36	41
1	C	361/420 (86%)	349 (97%)	12 (3%)	33	37
1	D	359/420 (86%)	351 (98%)	8 (2%)	45	53
All	All	1451/1680 (86%)	1404 (97%)	47 (3%)	34	38

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	ILE
1	A	95	LEU
1	A	120	GLN
1	A	124	ILE
1	A	145	LEU
1	A	161	VAL
1	A	176	SER
1	A	199	SER
1	A	236	THR
1	A	272	THR
1	A	286	LYS
1	A	328	VAL
1	A	339	THR
1	A	352	ILE
1	A	397	VAL
1	A	416	ILE

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Mol	Chain	Res	Type
1	D	7	THR
1	D	10	ILE
1	D	124	ILE
1	D	232	ASN
1	D	283	ASP
1	D	341	GLN
1	D	360	SER
1	D	397	VAL
1	B	-3	PHE
1	B	10	ILE
1	B	74	SER
1	B	95	LEU
1	B	118	SER
1	B	156	VAL
1	B	161	VAL
1	B	186	LYS
1	B	238	THR
1	B	328	VAL
1	B	397	VAL
1	C	10	ILE
1	C	39	LEU
1	C	95	LEU
1	C	186	LYS
1	C	236	THR
1	C	272	THR
1	C	328	VAL
1	C	360	SER
1	C	377	THR
1	C	378	ASP
1	C	397	VAL
1	C	414	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	GLN
1	A	50	GLN
1	A	130	HIS
1	A	159	ASN
1	A	243	HIS
1	A	247	ASN
1	D	144	ASN

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Mol	Chain	Res	Type
1	D	394	GLN
1	B	120	GLN
1	B	130	HIS
1	B	243	HIS
1	C	2	GLN
1	C	16	ASN
1	C	21	ASN
1	C	103	GLN
1	C	144	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

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	412/480 (85%)	0.46	23 (5%)	30 32	31, 44, 71, 122	0
1	B	410/480 (85%)	0.46	15 (3%)	45 47	29, 43, 70, 110	0
1	C	406/480 (84%)	1.17	56 (13%)	6 6	37, 61, 94, 127	0
1	D	404/480 (84%)	0.90	46 (11%)	10 10	33, 55, 97, 127	0
All	All	1632/1920 (85%)	0.75	140 (8%)	16 17	29, 49, 88, 127	0

All (140) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	-5	LEU	6.4
1	A	-5	LEU	5.9
1	B	-4	TYR	5.7
1	A	416	ILE	5.2
1	D	182	TRP	4.9
1	A	417	ALA	4.9
1	D	30	SER	4.6
1	D	156	VAL	4.4
1	A	415	ARG	4.3
1	B	182	TRP	4.1
1	D	154	PHE	4.0
1	C	154	PHE	4.0
1	D	152	THR	3.9
1	D	293	MET	3.8
1	D	312	LEU	3.8
1	C	30	SER	3.6
1	C	-1	GLY	3.5
1	C	3	ASP	3.4
1	C	281	TYR	3.4
1	B	154	PHE	3.4
1	A	-4	TYR	3.3

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Mol	Chain	Res	Type	RSRZ
1	C	66	GLN	3.3
1	C	118	SER	3.2
1	D	205	THR	3.2
1	C	156	VAL	3.1
1	C	67	PRO	3.1
1	D	321	VAL	3.1
1	D	155	VAL	3.1
1	A	284	GLY	3.0
1	D	318	ASP	3.0
1	C	64	SER	3.0
1	D	272	THR	3.0
1	A	306	TYR	3.0
1	C	322	PHE	3.0
1	D	132	LEU	3.0
1	D	314	TYR	3.0
1	C	308	TYR	2.9
1	C	61	VAL	2.9
1	C	414	THR	2.9
1	D	271	PRO	2.9
1	C	182	TRP	2.9
1	C	134	GLY	2.9
1	A	119	ARG	2.9
1	B	189	ILE	2.9
1	D	198	TYR	2.8
1	C	306	TYR	2.8
1	A	290	PRO	2.8
1	B	156	VAL	2.8
1	C	296	TRP	2.8
1	A	232	ASN	2.7
1	B	118	SER	2.7
1	D	70	VAL	2.7
1	D	273	SER	2.7
1	C	216	PHE	2.7
1	A	155	VAL	2.7
1	D	199	SER	2.7
1	C	35	SER	2.7
1	D	-1	GLY	2.7
1	C	279	ALA	2.6
1	C	245	PHE	2.6
1	D	300	ASP	2.6
1	B	318	ASP	2.6
1	C	283	ASP	2.6

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Mol	Chain	Res	Type	RSRZ
1	D	149	PRO	2.6
1	D	290	PRO	2.6
1	A	287	SER	2.6
1	B	155	VAL	2.6
1	C	297	GLY	2.6
1	C	293	MET	2.6
1	C	243	HIS	2.6
1	C	65	LEU	2.6
1	C	207	TYR	2.5
1	A	300	ASP	2.5
1	D	135	THR	2.5
1	C	135	THR	2.5
1	D	281	TYR	2.5
1	C	126	ASP	2.5
1	B	30	SER	2.4
1	A	182	TRP	2.4
1	C	290	PRO	2.4
1	D	39	LEU	2.4
1	D	218	LEU	2.4
1	C	172	LEU	2.4
1	C	303	ASP	2.3
1	D	267	ILE	2.3
1	B	290	PRO	2.3
1	D	289	CYS	2.3
1	A	285	GLN	2.3
1	C	225	TRP	2.3
1	D	241	TYR	2.3
1	D	35	SER	2.3
1	C	143	SER	2.3
1	C	53	GLY	2.3
1	C	70	VAL	2.3
1	C	98	THR	2.3
1	C	6	LEU	2.3
1	C	198	TYR	2.3
1	D	225	TRP	2.3
1	A	154	PHE	2.2
1	A	156	VAL	2.2
1	C	227	ARG	2.2
1	A	-1	GLY	2.2
1	D	172	LEU	2.2
1	D	138	PRO	2.2
1	C	99	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	243	HIS	2.2
1	A	-3	PHE	2.2
1	C	254	PRO	2.2
1	C	155	VAL	2.2
1	D	279	ALA	2.2
1	C	282	CYS	2.2
1	A	64	SER	2.2
1	B	119	ARG	2.2
1	C	119	ARG	2.1
1	A	281	TYR	2.1
1	C	260	ASP	2.1
1	C	72	PRO	2.1
1	B	120	GLN	2.1
1	C	161	VAL	2.1
1	C	95	LEU	2.1
1	C	181	TYR	2.1
1	D	98	THR	2.1
1	D	285	GLN	2.1
1	D	415	ARG	2.1
1	D	319	GLU	2.1
1	B	241	TYR	2.1
1	D	322	PHE	2.1
1	B	36	SER	2.1
1	C	39	LEU	2.0
1	D	303	ASP	2.0
1	D	294	THR	2.0
1	C	138	PRO	2.0
1	D	306	TYR	2.0
1	D	316	TYR	2.0
1	D	311	ILE	2.0
1	C	68	SER	2.0
1	C	273	SER	2.0
1	C	42	ASN	2.0
1	A	303	ASP	2.0
1	D	243	HIS	2.0

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

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.