



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 12, 2026 – 02:41 PM UTC

PDB ID : 5ERB / pdb_00005erb
Title : Ketosynthase from module 5 of the bacillaene synthase from *Bacillus amyloliquefaciens* FZB42
Authors : Wagner, D.T.; Gay, D.C.; Keatinge-Clay, A.T.; Meinke, J.
Deposited on : 2015-11-13
Resolution : 4.20 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

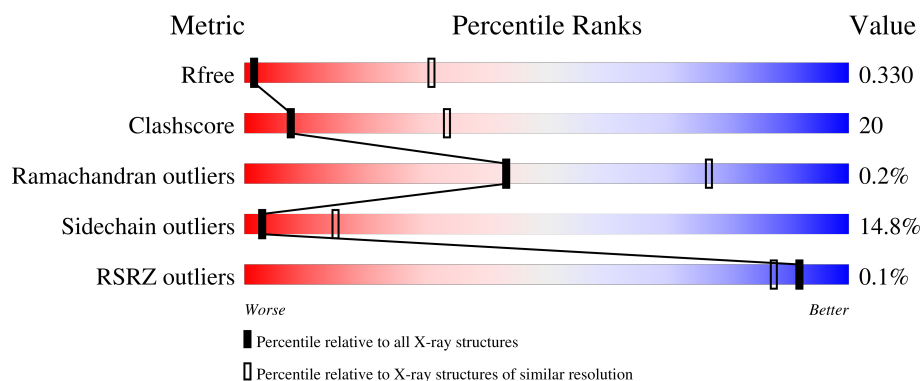
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.20 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	1004 (4.52-3.88)
Clashscore	190562	1019 (4.50-3.90)
Ramachandran outliers	187476	1020 (4.56-3.84)
Sidechain outliers	187428	1006 (4.56-3.84)
RSRZ outliers	180081	1001 (4.52-3.88)

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	640	58% 26% 6% • 9%
1	B	640	58% 25% 8% • 7%
1	C	640	58% 23% 8% • 8%
1	D	640	57% 26% 7% • 8%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 18315 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 Polyketide synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	584	Total	C	N	O	S	0	0	0
			4543	2859	790	873	21			
1	B	593	Total	C	N	O	S	0	0	0
			4618	2907	798	892	21			
1	C	586	Total	C	N	O	S	0	0	0
			4562	2872	792	878	20			
1	D	590	Total	C	N	O	S	0	0	0
			4592	2886	797	888	21			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP Q1RS72
A	-18	GLY	-	expression tag	UNP Q1RS72
A	-17	SER	-	expression tag	UNP Q1RS72
A	-16	SER	-	expression tag	UNP Q1RS72
A	-15	HIS	-	expression tag	UNP Q1RS72
A	-14	HIS	-	expression tag	UNP Q1RS72
A	-13	HIS	-	expression tag	UNP Q1RS72
A	-12	HIS	-	expression tag	UNP Q1RS72
A	-11	HIS	-	expression tag	UNP Q1RS72
A	-10	HIS	-	expression tag	UNP Q1RS72
A	-9	SER	-	expression tag	UNP Q1RS72
A	-8	SER	-	expression tag	UNP Q1RS72
A	-7	GLY	-	expression tag	UNP Q1RS72
A	-6	LEU	-	expression tag	UNP Q1RS72
A	-5	VAL	-	expression tag	UNP Q1RS72
A	-4	PRO	-	expression tag	UNP Q1RS72
A	-3	ARG	-	expression tag	UNP Q1RS72
A	-2	GLY	-	expression tag	UNP Q1RS72
A	-1	SER	-	expression tag	UNP Q1RS72
A	0	SER	-	expression tag	UNP Q1RS72
B	-19	MET	-	initiating methionine	UNP Q1RS72

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	GLY	-	expression tag	UNP Q1RS72
B	-17	SER	-	expression tag	UNP Q1RS72
B	-16	SER	-	expression tag	UNP Q1RS72
B	-15	HIS	-	expression tag	UNP Q1RS72
B	-14	HIS	-	expression tag	UNP Q1RS72
B	-13	HIS	-	expression tag	UNP Q1RS72
B	-12	HIS	-	expression tag	UNP Q1RS72
B	-11	HIS	-	expression tag	UNP Q1RS72
B	-10	HIS	-	expression tag	UNP Q1RS72
B	-9	SER	-	expression tag	UNP Q1RS72
B	-8	SER	-	expression tag	UNP Q1RS72
B	-7	GLY	-	expression tag	UNP Q1RS72
B	-6	LEU	-	expression tag	UNP Q1RS72
B	-5	VAL	-	expression tag	UNP Q1RS72
B	-4	PRO	-	expression tag	UNP Q1RS72
B	-3	ARG	-	expression tag	UNP Q1RS72
B	-2	GLY	-	expression tag	UNP Q1RS72
B	-1	SER	-	expression tag	UNP Q1RS72
B	0	SER	-	expression tag	UNP Q1RS72
C	-19	MET	-	initiating methionine	UNP Q1RS72
C	-18	GLY	-	expression tag	UNP Q1RS72
C	-17	SER	-	expression tag	UNP Q1RS72
C	-16	SER	-	expression tag	UNP Q1RS72
C	-15	HIS	-	expression tag	UNP Q1RS72
C	-14	HIS	-	expression tag	UNP Q1RS72
C	-13	HIS	-	expression tag	UNP Q1RS72
C	-12	HIS	-	expression tag	UNP Q1RS72
C	-11	HIS	-	expression tag	UNP Q1RS72
C	-10	HIS	-	expression tag	UNP Q1RS72
C	-9	SER	-	expression tag	UNP Q1RS72
C	-8	SER	-	expression tag	UNP Q1RS72
C	-7	GLY	-	expression tag	UNP Q1RS72
C	-6	LEU	-	expression tag	UNP Q1RS72
C	-5	VAL	-	expression tag	UNP Q1RS72
C	-4	PRO	-	expression tag	UNP Q1RS72
C	-3	ARG	-	expression tag	UNP Q1RS72
C	-2	GLY	-	expression tag	UNP Q1RS72
C	-1	SER	-	expression tag	UNP Q1RS72
C	0	SER	-	expression tag	UNP Q1RS72
D	-19	MET	-	initiating methionine	UNP Q1RS72
D	-18	GLY	-	expression tag	UNP Q1RS72
D	-17	SER	-	expression tag	UNP Q1RS72

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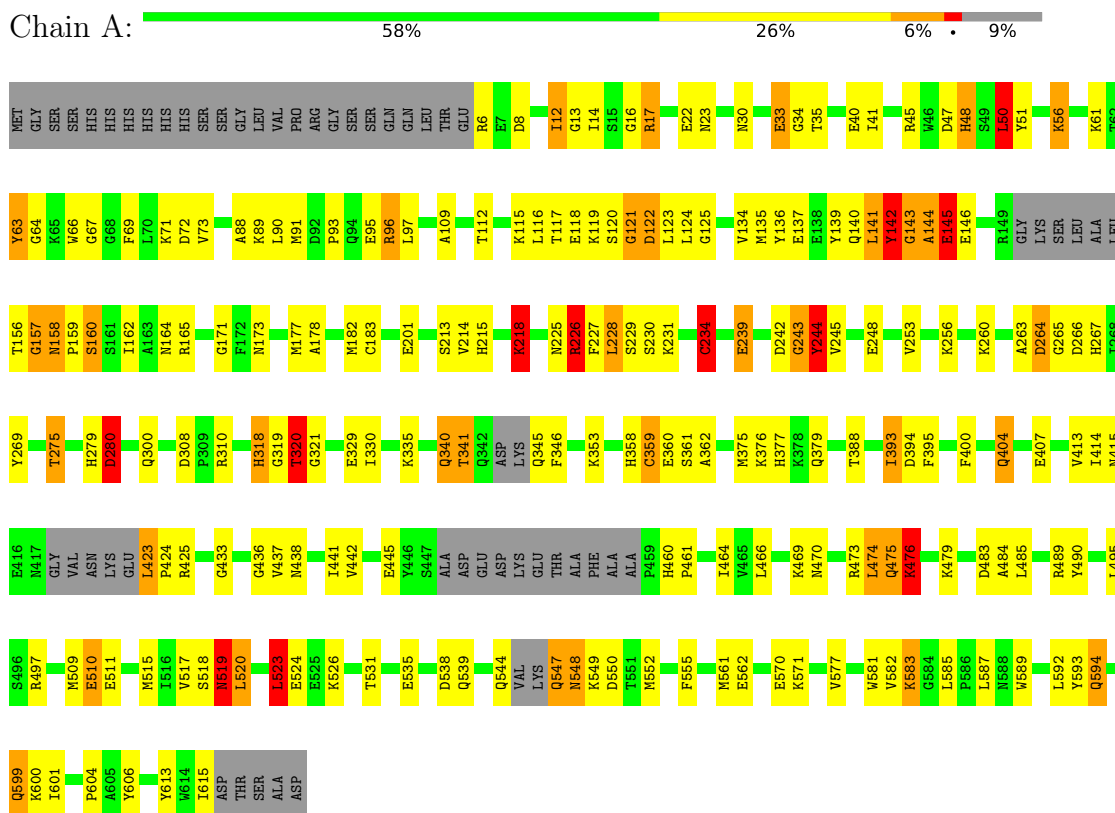
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Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	SER	-	expression tag	UNP Q1RS72
D	-15	HIS	-	expression tag	UNP Q1RS72
D	-14	HIS	-	expression tag	UNP Q1RS72
D	-13	HIS	-	expression tag	UNP Q1RS72
D	-12	HIS	-	expression tag	UNP Q1RS72
D	-11	HIS	-	expression tag	UNP Q1RS72
D	-10	HIS	-	expression tag	UNP Q1RS72
D	-9	SER	-	expression tag	UNP Q1RS72
D	-8	SER	-	expression tag	UNP Q1RS72
D	-7	GLY	-	expression tag	UNP Q1RS72
D	-6	LEU	-	expression tag	UNP Q1RS72
D	-5	VAL	-	expression tag	UNP Q1RS72
D	-4	PRO	-	expression tag	UNP Q1RS72
D	-3	ARG	-	expression tag	UNP Q1RS72
D	-2	GLY	-	expression tag	UNP Q1RS72
D	-1	SER	-	expression tag	UNP Q1RS72
D	0	SER	-	expression tag	UNP Q1RS72

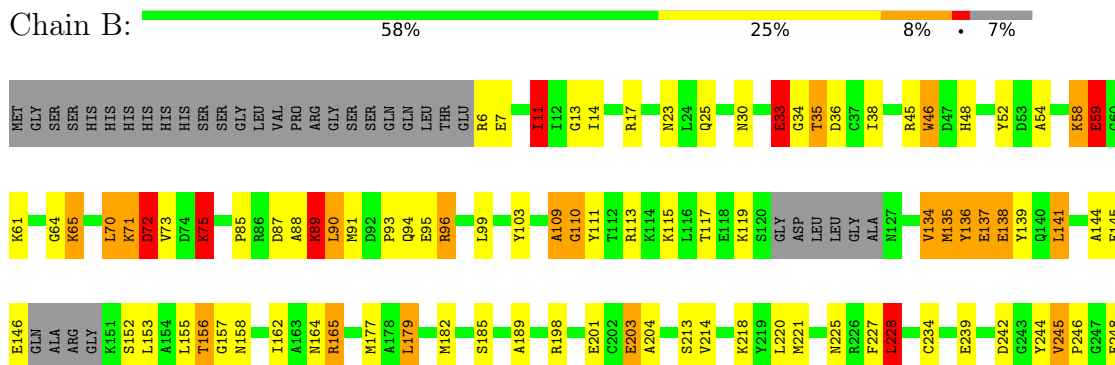
3 Residue-property plots

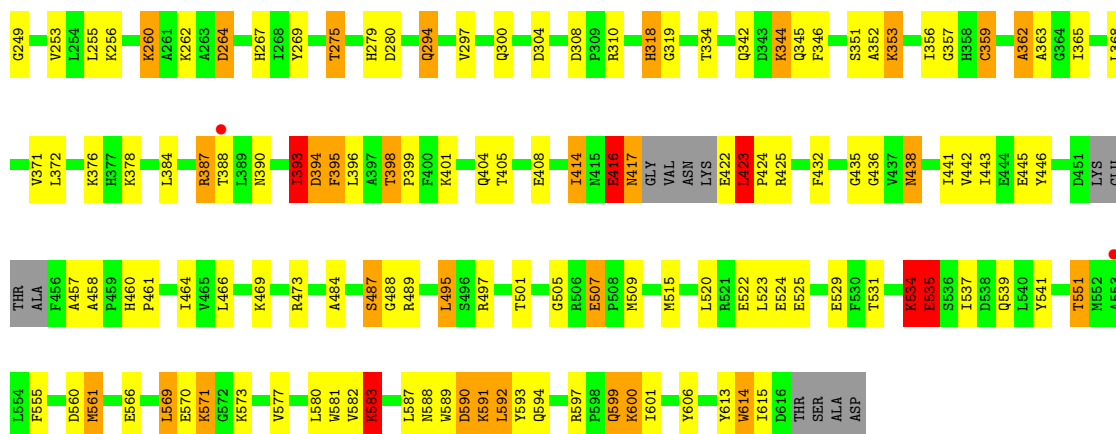
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Polyketide synthase



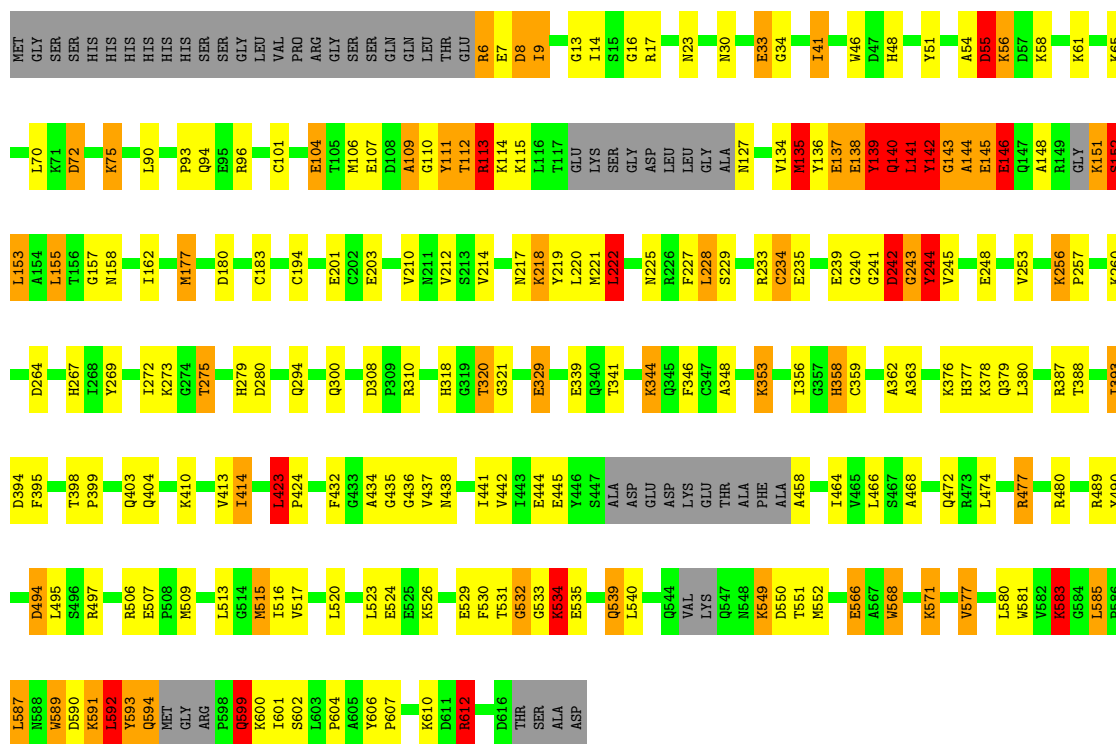
• Molecule 1: Polyketide synthase





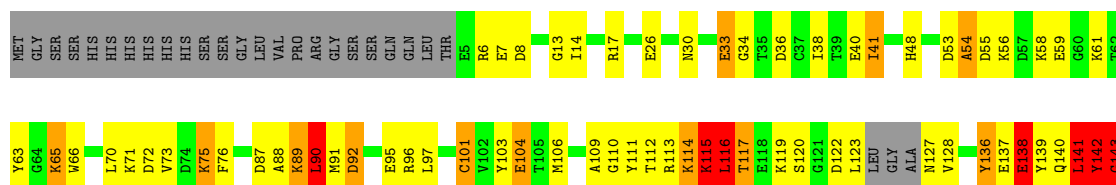
• Molecule 1: Polyketide synthase

Chain C: 58% 23% 8% 8%



• Molecule 1: Polyketide synthase

Chain D: 57% 26% 7% 8%





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	70.76Å 319.13Å 103.47Å 90.00° 110.26° 90.00°	Depositor
Resolution (Å)	97.07 – 4.20 97.07 – 4.20	Depositor EDS
% Data completeness (in resolution range)	79.9 (97.07-4.20) 78.8 (97.07-4.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.19 (at 4.14Å)	Xtriage
Refinement program	REFMAC 5.8.0107	Depositor
R, R_{free}	0.288 , 0.341 0.281 , 0.330	Depositor DCC
R_{free} test set	1279 reflections (4.09%)	wwPDB-VP
Wilson B-factor (Å ²)	168.6	Xtriage
Anisotropy	0.045	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 600.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.115 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	18315	wwPDB-VP
Average B, all atoms (Å ²)	198.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.12% 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	0.86	5/4632 (0.1%)	1.53	80/6245 (1.3%)
1	B	0.87	12/4709 (0.3%)	1.72	91/6351 (1.4%)
1	C	0.86	10/4651 (0.2%)	1.73	104/6272 (1.7%)
1	D	0.87	8/4681 (0.2%)	1.60	85/6312 (1.3%)
All	All	0.86	35/18673 (0.2%)	1.65	360/25180 (1.4%)

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	0	8
1	B	0	3
1	C	0	7
1	D	0	2
All	All	0	20

The worst 5 of 35 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	152	SER	C-N	-7.73	1.22	1.33
1	A	121	GLY	C-N	-7.69	1.23	1.33
1	D	143	GLY	C-N	-7.63	1.23	1.33
1	B	393	ILE	CA-CB	7.26	1.64	1.53
1	B	488	GLY	C-N	6.99	1.43	1.33

The worst 5 of 360 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	144	ALA	N-CA-C	41.87	156.92	111.28
1	C	142	TYR	CA-C-N	27.64	150.75	121.45
1	C	142	TYR	C-N-CA	27.64	150.75	121.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	89	LYS	N-CA-C	-26.83	73.32	110.35
1	A	583	LYS	N-CA-C	-26.17	71.79	110.52

There are no chirality outliers.

5 of 20 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	121	GLY	Mainchain
1	A	157	GLY	Mainchain
1	A	244	TYR	Mainchain
1	A	475	GLN	Peptide
1	A	72	ASP	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	4543	0	4470	158	0
1	B	4618	0	4540	154	1
1	C	4562	0	4491	265	0
1	D	4592	0	4505	211	1
All	All	18315	0	18006	730	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 20.

The worst 5 of 730 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:A:141:LEU:HD21	1:A:215:HIS:CE1	1.26	1.63
1:D:142:TYR:CE2	1:D:615:ILE:HG12	1.29	1.56
1:D:142:TYR:CE2	1:D:615:ILE:CG1	1.77	1.56
1:C:135:MET:CG	1:D:159:PRO:HD2	1.18	1.52
1:C:458:ALA:N	1:C:594:GLN:HB3	1.30	1.46

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the sym-

metry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:387:ARG:O	1:D:405:THR:OG1[2_646]	2.01	0.19

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	572/640 (89%)	529 (92%)	40 (7%)	3 (0%)	24	62
1	B	583/640 (91%)	543 (93%)	38 (6%)	2 (0%)	36	71
1	C	574/640 (90%)	533 (93%)	41 (7%)	0	100	100
1	D	578/640 (90%)	543 (94%)	35 (6%)	0	100	100
All	All	2307/2560 (90%)	2148 (93%)	154 (7%)	5 (0%)	43	77

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	538	ASP
1	A	141	LEU
1	A	142	TYR
1	B	113	ARG
1	B	246	PRO

5.3.2 Protein sidechains [i](#)

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	479/524 (91%)	416 (87%)	63 (13%)	4	17
1	B	488/524 (93%)	407 (83%)	81 (17%)	2	12
1	C	482/524 (92%)	412 (86%)	70 (14%)	3	15
1	D	484/524 (92%)	412 (85%)	72 (15%)	3	15
All	All	1933/2096 (92%)	1647 (85%)	286 (15%)	3	15

5 of 286 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	138	GLU
1	D	158	ASN
1	D	469	LYS
1	B	280	ASP
1	B	260	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	415	ASN
1	D	215	HIS
1	C	417	ASN
1	D	158	ASN
1	D	267	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no 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	584/640 (91%)	-0.54	0 100 100	23, 191, 295, 377	0
1	B	593/640 (92%)	-0.59	2 (0%) 90 80	30, 189, 285, 364	0
1	C	586/640 (91%)	-0.60	0 100 100	23, 193, 285, 402	0
1	D	590/640 (92%)	-0.64	1 (0%) 91 83	23, 191, 285, 399	0
All	All	2353/2560 (91%)	-0.59	3 (0%) 92 87	23, 191, 290, 402	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	388	THR	2.4
1	B	553	ALA	2.2
1	D	556	THR	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.