



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 01:58 PM UTC

PDB ID : 1U2J / pdb_00001u2j
Title : Crystal structure of the C-terminal domain from the catalase-peroxidase KatG of Escherichia coli (P21 21 21)
Authors : Carpena, X.; Melik-Adamyany, W.; Loewen, P.C.; Fita, I.
Deposited on : 2004-07-19
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

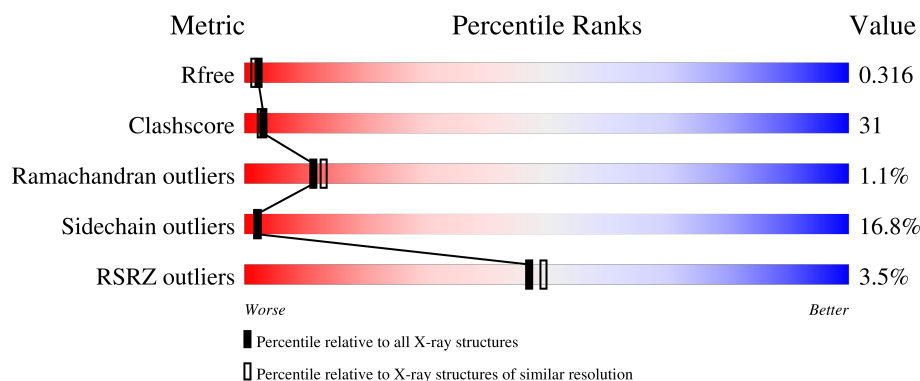
1 Overall quality at a glance

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	326	2% 49% 34% 6% 10%
1	B	326	% 56% 29% 6% 10%
1	C	326	2% 58% 27% 6% 10%
1	D	326	% 51% 31% 8% 10%
1	E	326	4% 51% 32% 8% 10%

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Mol	Chain	Length	Quality of chain
1	F	326	7% 39% 40% 11% 10%
1	G	326	3% 46% 36% 8% 10%
1	H	326	5% 44% 34% 12% 10%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 18136 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 Peroxidase/catalase HPI.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	295	Total	C	N	O	S	0	0	0
			2267	1435	391	435	6			
1	B	295	Total	C	N	O	S	0	0	0
			2267	1435	391	435	6			
1	C	295	Total	C	N	O	S	0	0	0
			2267	1435	391	435	6			
1	D	295	Total	C	N	O	S	0	0	0
			2267	1435	391	435	6			
1	E	295	Total	C	N	O	S	0	0	0
			2267	1435	391	435	6			
1	F	295	Total	C	N	O	S	0	0	0
			2267	1435	391	435	6			
1	G	295	Total	C	N	O	S	0	0	0
			2267	1435	391	435	6			
1	H	295	Total	C	N	O	S	0	0	0
			2267	1435	391	435	6			

There are 168 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	401	MET	-	expression tag	UNP P13029
A	402	GLY	-	expression tag	UNP P13029
A	403	SER	-	expression tag	UNP P13029
A	404	SER	-	expression tag	UNP P13029
A	405	HIS	-	expression tag	UNP P13029
A	406	HIS	-	expression tag	UNP P13029
A	407	HIS	-	expression tag	UNP P13029
A	408	HIS	-	expression tag	UNP P13029
A	409	HIS	-	expression tag	UNP P13029
A	410	HIS	-	expression tag	UNP P13029
A	411	SER	-	expression tag	UNP P13029
A	412	SER	-	expression tag	UNP P13029
A	413	GLY	-	expression tag	UNP P13029

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Chain	Residue	Modelled	Actual	Comment	Reference
A	414	LEU	-	expression tag	UNP P13029
A	415	VAL	-	expression tag	UNP P13029
A	416	PRO	-	expression tag	UNP P13029
A	417	ARG	-	expression tag	UNP P13029
A	418	GLY	-	expression tag	UNP P13029
A	419	SER	-	expression tag	UNP P13029
A	420	HIS	-	expression tag	UNP P13029
A	421	MET	-	expression tag	UNP P13029
B	401	MET	-	expression tag	UNP P13029
B	402	GLY	-	expression tag	UNP P13029
B	403	SER	-	expression tag	UNP P13029
B	404	SER	-	expression tag	UNP P13029
B	405	HIS	-	expression tag	UNP P13029
B	406	HIS	-	expression tag	UNP P13029
B	407	HIS	-	expression tag	UNP P13029
B	408	HIS	-	expression tag	UNP P13029
B	409	HIS	-	expression tag	UNP P13029
B	410	HIS	-	expression tag	UNP P13029
B	411	SER	-	expression tag	UNP P13029
B	412	SER	-	expression tag	UNP P13029
B	413	GLY	-	expression tag	UNP P13029
B	414	LEU	-	expression tag	UNP P13029
B	415	VAL	-	expression tag	UNP P13029
B	416	PRO	-	expression tag	UNP P13029
B	417	ARG	-	expression tag	UNP P13029
B	418	GLY	-	expression tag	UNP P13029
B	419	SER	-	expression tag	UNP P13029
B	420	HIS	-	expression tag	UNP P13029
B	421	MET	-	expression tag	UNP P13029
C	401	MET	-	expression tag	UNP P13029
C	402	GLY	-	expression tag	UNP P13029
C	403	SER	-	expression tag	UNP P13029
C	404	SER	-	expression tag	UNP P13029
C	405	HIS	-	expression tag	UNP P13029
C	406	HIS	-	expression tag	UNP P13029
C	407	HIS	-	expression tag	UNP P13029
C	408	HIS	-	expression tag	UNP P13029
C	409	HIS	-	expression tag	UNP P13029
C	410	HIS	-	expression tag	UNP P13029
C	411	SER	-	expression tag	UNP P13029
C	412	SER	-	expression tag	UNP P13029
C	413	GLY	-	expression tag	UNP P13029

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Chain	Residue	Modelled	Actual	Comment	Reference
C	414	LEU	-	expression tag	UNP P13029
C	415	VAL	-	expression tag	UNP P13029
C	416	PRO	-	expression tag	UNP P13029
C	417	ARG	-	expression tag	UNP P13029
C	418	GLY	-	expression tag	UNP P13029
C	419	SER	-	expression tag	UNP P13029
C	420	HIS	-	expression tag	UNP P13029
C	421	MET	-	expression tag	UNP P13029
D	401	MET	-	expression tag	UNP P13029
D	402	GLY	-	expression tag	UNP P13029
D	403	SER	-	expression tag	UNP P13029
D	404	SER	-	expression tag	UNP P13029
D	405	HIS	-	expression tag	UNP P13029
D	406	HIS	-	expression tag	UNP P13029
D	407	HIS	-	expression tag	UNP P13029
D	408	HIS	-	expression tag	UNP P13029
D	409	HIS	-	expression tag	UNP P13029
D	410	HIS	-	expression tag	UNP P13029
D	411	SER	-	expression tag	UNP P13029
D	412	SER	-	expression tag	UNP P13029
D	413	GLY	-	expression tag	UNP P13029
D	414	LEU	-	expression tag	UNP P13029
D	415	VAL	-	expression tag	UNP P13029
D	416	PRO	-	expression tag	UNP P13029
D	417	ARG	-	expression tag	UNP P13029
D	418	GLY	-	expression tag	UNP P13029
D	419	SER	-	expression tag	UNP P13029
D	420	HIS	-	expression tag	UNP P13029
D	421	MET	-	expression tag	UNP P13029
E	401	MET	-	expression tag	UNP P13029
E	402	GLY	-	expression tag	UNP P13029
E	403	SER	-	expression tag	UNP P13029
E	404	SER	-	expression tag	UNP P13029
E	405	HIS	-	expression tag	UNP P13029
E	406	HIS	-	expression tag	UNP P13029
E	407	HIS	-	expression tag	UNP P13029
E	408	HIS	-	expression tag	UNP P13029
E	409	HIS	-	expression tag	UNP P13029
E	410	HIS	-	expression tag	UNP P13029
E	411	SER	-	expression tag	UNP P13029
E	412	SER	-	expression tag	UNP P13029
E	413	GLY	-	expression tag	UNP P13029

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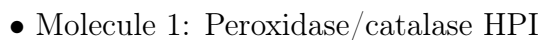
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E	414	LEU	-	expression tag	UNP P13029
E	415	VAL	-	expression tag	UNP P13029
E	416	PRO	-	expression tag	UNP P13029
E	417	ARG	-	expression tag	UNP P13029
E	418	GLY	-	expression tag	UNP P13029
E	419	SER	-	expression tag	UNP P13029
E	420	HIS	-	expression tag	UNP P13029
E	421	MET	-	expression tag	UNP P13029
F	401	MET	-	expression tag	UNP P13029
F	402	GLY	-	expression tag	UNP P13029
F	403	SER	-	expression tag	UNP P13029
F	404	SER	-	expression tag	UNP P13029
F	405	HIS	-	expression tag	UNP P13029
F	406	HIS	-	expression tag	UNP P13029
F	407	HIS	-	expression tag	UNP P13029
F	408	HIS	-	expression tag	UNP P13029
F	409	HIS	-	expression tag	UNP P13029
F	410	HIS	-	expression tag	UNP P13029
F	411	SER	-	expression tag	UNP P13029
F	412	SER	-	expression tag	UNP P13029
F	413	GLY	-	expression tag	UNP P13029
F	414	LEU	-	expression tag	UNP P13029
F	415	VAL	-	expression tag	UNP P13029
F	416	PRO	-	expression tag	UNP P13029
F	417	ARG	-	expression tag	UNP P13029
F	418	GLY	-	expression tag	UNP P13029
F	419	SER	-	expression tag	UNP P13029
F	420	HIS	-	expression tag	UNP P13029
F	421	MET	-	expression tag	UNP P13029
G	401	MET	-	expression tag	UNP P13029
G	402	GLY	-	expression tag	UNP P13029
G	403	SER	-	expression tag	UNP P13029
G	404	SER	-	expression tag	UNP P13029
G	405	HIS	-	expression tag	UNP P13029
G	406	HIS	-	expression tag	UNP P13029
G	407	HIS	-	expression tag	UNP P13029
G	408	HIS	-	expression tag	UNP P13029
G	409	HIS	-	expression tag	UNP P13029
G	410	HIS	-	expression tag	UNP P13029
G	411	SER	-	expression tag	UNP P13029
G	412	SER	-	expression tag	UNP P13029
G	413	GLY	-	expression tag	UNP P13029

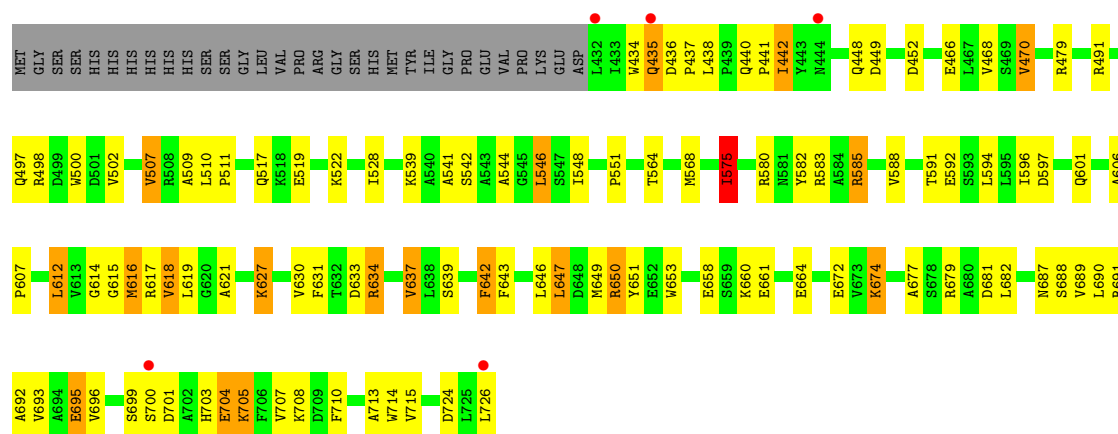
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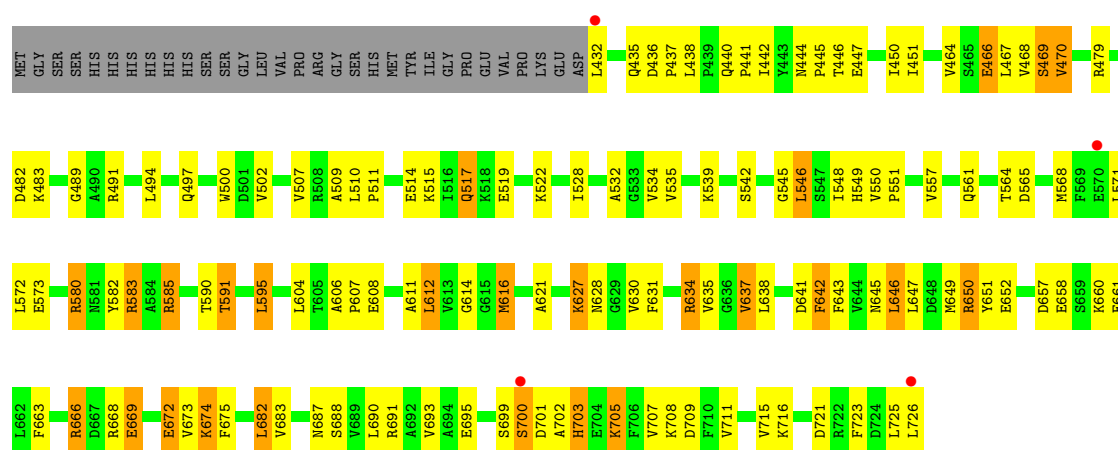
Chain	Residue	Modelled	Actual	Comment	Reference
G	414	LEU	-	expression tag	UNP P13029
G	415	VAL	-	expression tag	UNP P13029
G	416	PRO	-	expression tag	UNP P13029
G	417	ARG	-	expression tag	UNP P13029
G	418	GLY	-	expression tag	UNP P13029
G	419	SER	-	expression tag	UNP P13029
G	420	HIS	-	expression tag	UNP P13029
G	421	MET	-	expression tag	UNP P13029
H	401	MET	-	expression tag	UNP P13029
H	402	GLY	-	expression tag	UNP P13029
H	403	SER	-	expression tag	UNP P13029
H	404	SER	-	expression tag	UNP P13029
H	405	HIS	-	expression tag	UNP P13029
H	406	HIS	-	expression tag	UNP P13029
H	407	HIS	-	expression tag	UNP P13029
H	408	HIS	-	expression tag	UNP P13029
H	409	HIS	-	expression tag	UNP P13029
H	410	HIS	-	expression tag	UNP P13029
H	411	SER	-	expression tag	UNP P13029
H	412	SER	-	expression tag	UNP P13029
H	413	GLY	-	expression tag	UNP P13029
H	414	LEU	-	expression tag	UNP P13029
H	415	VAL	-	expression tag	UNP P13029
H	416	PRO	-	expression tag	UNP P13029
H	417	ARG	-	expression tag	UNP P13029
H	418	GLY	-	expression tag	UNP P13029
H	419	SER	-	expression tag	UNP P13029
H	420	HIS	-	expression tag	UNP P13029
H	421	MET	-	expression tag	UNP P13029

- Molecule 1: Peroxidase/catalase HPI

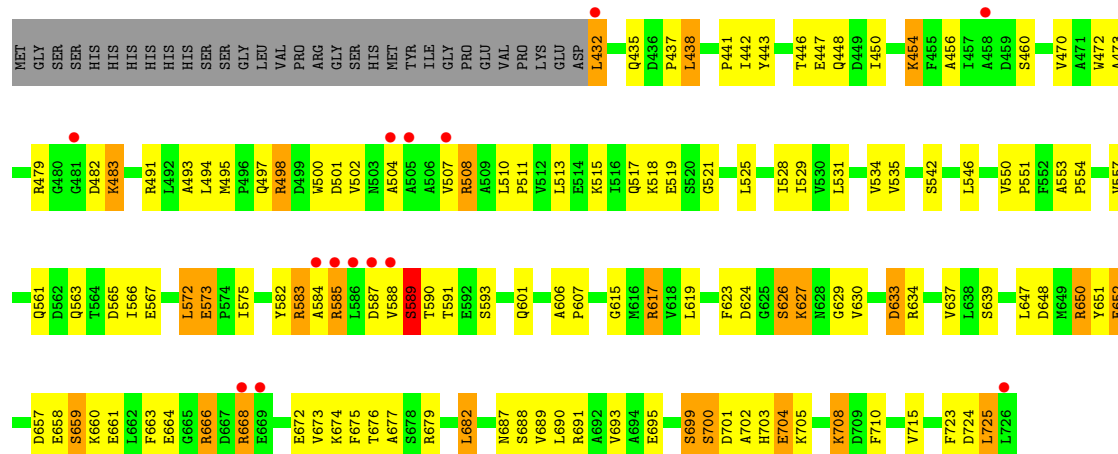




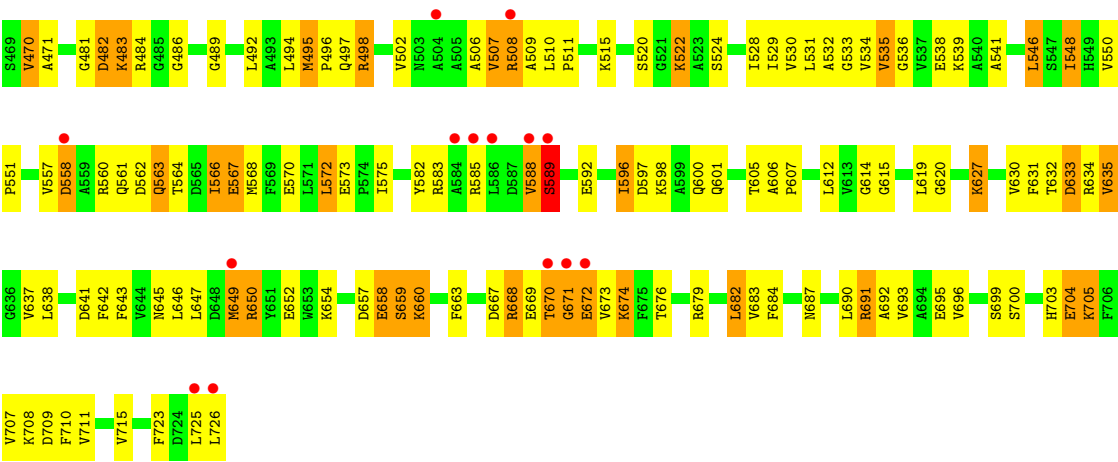
• Molecule 1: Peroxidase/catalase HPI



• Molecule 1: Peroxidase/catalase HPI



• Molecule 1: Peroxidase/catalase HPI



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	84.21Å 98.70Å 302.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.96 – 2.30 19.96 – 2.30	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.96-2.30) 91.2 (19.96-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.10 (at 2.30Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.233 , 0.327 0.251 , 0.316	Depositor DCC
R_{free} test set	10340 reflections (10.03%)	wwPDB-VP
Wilson B-factor (Å ²)	23.9	Xtriage
Anisotropy	0.090	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 28.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.37$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	18136	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 44.47 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.5185e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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	0.76	0/2307	1.09	5/3127 (0.2%)
1	B	0.76	0/2307	1.03	0/3127
1	C	0.80	0/2307	1.08	3/3127 (0.1%)
1	D	0.75	0/2307	1.05	4/3127 (0.1%)
1	E	0.74	0/2307	1.02	0/3127
1	F	0.68	0/2307	1.02	5/3127 (0.2%)
1	G	0.69	0/2307	1.02	3/3127 (0.1%)
1	H	0.71	1/2307 (0.0%)	1.00	1/3127 (0.0%)
All	All	0.74	1/18456 (0.0%)	1.04	21/25016 (0.1%)

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	1
1	B	0	1
1	F	0	2
1	G	0	1
1	H	0	1
All	All	0	6

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	495	MET	SD-CE	6.11	1.94	1.79

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	506	ALA	N-CA-C	-8.67	104.74	114.62
1	A	502	VAL	CB-CA-C	-7.60	100.96	112.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	433	ILE	N-CA-C	7.31	117.40	110.53
1	D	642	PHE	N-CA-C	-7.13	103.44	111.07
1	C	642	PHE	N-CA-C	-7.06	103.66	111.36

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	623	PHE	Peptide
1	B	724	ASP	Peptide
1	F	443	TYR	Peptide
1	F	724	ASP	Peptide
1	G	574	PRO	Peptide

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	2267	0	2255	131	0
1	B	2267	0	2255	98	0
1	C	2267	0	2255	128	0
1	D	2267	0	2255	134	1
1	E	2267	0	2255	153	0
1	F	2267	0	2255	187	0
1	G	2267	0	2255	167	0
1	H	2267	0	2255	163	1
All	All	18136	0	18040	1133	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 31.

The worst 5 of 1133 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:E:437:PRO:C	1:E:438:LEU:HD22	1.22	1.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:502:VAL:CG2	1:E:582:TYR:CE2	2.09	1.34
1:E:502:VAL:HG22	1:E:582:TYR:CE2	1.67	1.28
1:F:624:ASP:OD2	1:F:626:SER:HB2	1.26	1.28
1:H:502:VAL:CG2	1:H:582:TYR:CE2	2.18	1.26

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:590:THR:OG1	1:H:567:GLU:OE2[3_755]	2.08	0.12

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	293/326 (90%)	276 (94%)	15 (5%)	2 (1%)	18	23
1	B	293/326 (90%)	269 (92%)	23 (8%)	1 (0%)	36	46
1	C	293/326 (90%)	277 (94%)	16 (6%)	0	100	100
1	D	293/326 (90%)	274 (94%)	18 (6%)	1 (0%)	36	46
1	E	293/326 (90%)	271 (92%)	19 (6%)	3 (1%)	12	15
1	F	293/326 (90%)	260 (89%)	23 (8%)	10 (3%)	3	2
1	G	293/326 (90%)	267 (91%)	21 (7%)	5 (2%)	7	7
1	H	293/326 (90%)	271 (92%)	19 (6%)	3 (1%)	12	15
All	All	2344/2608 (90%)	2165 (92%)	154 (7%)	25 (1%)	11	13

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	700	SER

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Mol	Chain	Res	Type
1	E	589	SER
1	F	586	LEU
1	F	671	GLY
1	F	705	LYS

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	238/265 (90%)	200 (84%)	38 (16%)	2	2
1	B	238/265 (90%)	204 (86%)	34 (14%)	3	3
1	C	238/265 (90%)	207 (87%)	31 (13%)	4	4
1	D	238/265 (90%)	198 (83%)	40 (17%)	2	2
1	E	238/265 (90%)	202 (85%)	36 (15%)	3	3
1	F	238/265 (90%)	187 (79%)	51 (21%)	1	1
1	G	238/265 (90%)	199 (84%)	39 (16%)	2	2
1	H	238/265 (90%)	188 (79%)	50 (21%)	1	1
All	All	1904/2120 (90%)	1585 (83%)	319 (17%)	2	2

5 of 319 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	450	ILE
1	H	548	ILE
1	G	518	LYS
1	G	674	LYS
1	H	633	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	687	ASN

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Mol	Chain	Res	Type
1	G	703	HIS
1	H	645	ASN
1	C	687	ASN
1	C	601	GLN

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	295/326 (90%)	0.20	6 (2%) 65 66	9, 22, 41, 64	0
1	B	295/326 (90%)	0.18	3 (1%) 79 80	12, 21, 41, 70	0
1	C	295/326 (90%)	0.03	5 (1%) 69 70	7, 19, 39, 55	0
1	D	295/326 (90%)	0.08	4 (1%) 73 75	9, 20, 41, 51	0
1	E	295/326 (90%)	0.30	14 (4%) 36 38	7, 23, 49, 73	0
1	F	295/326 (90%)	0.61	24 (8%) 18 19	12, 30, 56, 76	0
1	G	295/326 (90%)	0.35	11 (3%) 45 48	10, 25, 51, 81	0
1	H	295/326 (90%)	0.43	16 (5%) 31 33	10, 27, 54, 71	0
All	All	2360/2608 (90%)	0.27	83 (3%) 47 49	7, 23, 47, 81	0

The worst 5 of 83 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	726	LEU	8.0
1	F	726	LEU	7.5
1	A	726	LEU	6.5
1	G	726	LEU	5.4
1	A	432	LEU	5.2

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.