



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 17, 2026 – 06:13 PM JST

PDB ID : 9XB8 / pdb_00009xb8
Title : ATP-dependent diazotase Mco01_40450
Authors : Ning, J.; Kawai, S.; Ohnishi, Y.; Katsuyama, Y.
Deposited on : 2025-10-23
Resolution : 3.40 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	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

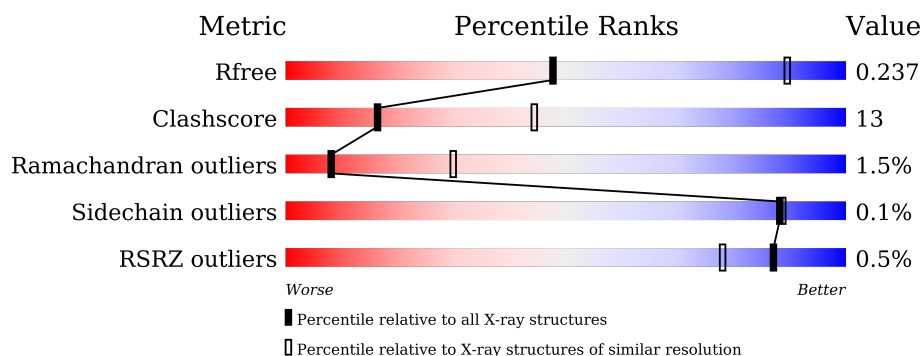
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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	1001 (3.44-3.36)
Clashscore	190562	1022 (3.44-3.36)
Ramachandran outliers	187476	1012 (3.44-3.36)
Sidechain outliers	187428	1012 (3.44-3.36)
RSRZ outliers	180081	1001 (3.44-3.36)

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	577	55% 19% • 25%
1	B	577	53% 21% 25%
1	C	577	% 51% 24% • 25%
1	D	577	% 52% 23% 25%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 13384 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 Fatty-acid-CoA ligase FadD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	433	Total	C	N	O	S	0	0	0
			3346	2122	590	624	10			
1	B	433	Total	C	N	O	S	0	0	0
			3346	2122	590	624	10			
1	C	433	Total	C	N	O	S	0	0	0
			3346	2122	590	624	10			
1	D	433	Total	C	N	O	S	0	0	0
			3346	2122	590	624	10			

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-15	MET	-	initiating methionine	UNP A0ABQ4G1Y4
A	-14	ASN	-	expression tag	UNP A0ABQ4G1Y4
A	-13	HIS	-	expression tag	UNP A0ABQ4G1Y4
A	-12	LYS	-	expression tag	UNP A0ABQ4G1Y4
A	-11	VAL	-	expression tag	UNP A0ABQ4G1Y4
A	-10	HIS	-	expression tag	UNP A0ABQ4G1Y4
A	-9	HIS	-	expression tag	UNP A0ABQ4G1Y4
A	-8	HIS	-	expression tag	UNP A0ABQ4G1Y4
A	-7	HIS	-	expression tag	UNP A0ABQ4G1Y4
A	-6	HIS	-	expression tag	UNP A0ABQ4G1Y4
A	-5	HIS	-	expression tag	UNP A0ABQ4G1Y4
A	-4	ILE	-	expression tag	UNP A0ABQ4G1Y4
A	-3	GLU	-	expression tag	UNP A0ABQ4G1Y4
A	-2	GLY	-	expression tag	UNP A0ABQ4G1Y4
A	-1	ARG	-	expression tag	UNP A0ABQ4G1Y4
A	0	HIS	-	expression tag	UNP A0ABQ4G1Y4
B	-15	MET	-	initiating methionine	UNP A0ABQ4G1Y4
B	-14	ASN	-	expression tag	UNP A0ABQ4G1Y4
B	-13	HIS	-	expression tag	UNP A0ABQ4G1Y4
B	-12	LYS	-	expression tag	UNP A0ABQ4G1Y4
B	-11	VAL	-	expression tag	UNP A0ABQ4G1Y4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-10	HIS	-	expression tag	UNP A0ABQ4G1Y4
B	-9	HIS	-	expression tag	UNP A0ABQ4G1Y4
B	-8	HIS	-	expression tag	UNP A0ABQ4G1Y4
B	-7	HIS	-	expression tag	UNP A0ABQ4G1Y4
B	-6	HIS	-	expression tag	UNP A0ABQ4G1Y4
B	-5	HIS	-	expression tag	UNP A0ABQ4G1Y4
B	-4	ILE	-	expression tag	UNP A0ABQ4G1Y4
B	-3	GLU	-	expression tag	UNP A0ABQ4G1Y4
B	-2	GLY	-	expression tag	UNP A0ABQ4G1Y4
B	-1	ARG	-	expression tag	UNP A0ABQ4G1Y4
B	0	HIS	-	expression tag	UNP A0ABQ4G1Y4
C	-15	MET	-	initiating methionine	UNP A0ABQ4G1Y4
C	-14	ASN	-	expression tag	UNP A0ABQ4G1Y4
C	-13	HIS	-	expression tag	UNP A0ABQ4G1Y4
C	-12	LYS	-	expression tag	UNP A0ABQ4G1Y4
C	-11	VAL	-	expression tag	UNP A0ABQ4G1Y4
C	-10	HIS	-	expression tag	UNP A0ABQ4G1Y4
C	-9	HIS	-	expression tag	UNP A0ABQ4G1Y4
C	-8	HIS	-	expression tag	UNP A0ABQ4G1Y4
C	-7	HIS	-	expression tag	UNP A0ABQ4G1Y4
C	-6	HIS	-	expression tag	UNP A0ABQ4G1Y4
C	-5	HIS	-	expression tag	UNP A0ABQ4G1Y4
C	-4	ILE	-	expression tag	UNP A0ABQ4G1Y4
C	-3	GLU	-	expression tag	UNP A0ABQ4G1Y4
C	-2	GLY	-	expression tag	UNP A0ABQ4G1Y4
C	-1	ARG	-	expression tag	UNP A0ABQ4G1Y4
C	0	HIS	-	expression tag	UNP A0ABQ4G1Y4
D	-15	MET	-	initiating methionine	UNP A0ABQ4G1Y4
D	-14	ASN	-	expression tag	UNP A0ABQ4G1Y4
D	-13	HIS	-	expression tag	UNP A0ABQ4G1Y4
D	-12	LYS	-	expression tag	UNP A0ABQ4G1Y4
D	-11	VAL	-	expression tag	UNP A0ABQ4G1Y4
D	-10	HIS	-	expression tag	UNP A0ABQ4G1Y4
D	-9	HIS	-	expression tag	UNP A0ABQ4G1Y4
D	-8	HIS	-	expression tag	UNP A0ABQ4G1Y4
D	-7	HIS	-	expression tag	UNP A0ABQ4G1Y4
D	-6	HIS	-	expression tag	UNP A0ABQ4G1Y4
D	-5	HIS	-	expression tag	UNP A0ABQ4G1Y4
D	-4	ILE	-	expression tag	UNP A0ABQ4G1Y4
D	-3	GLU	-	expression tag	UNP A0ABQ4G1Y4
D	-2	GLY	-	expression tag	UNP A0ABQ4G1Y4
D	-1	ARG	-	expression tag	UNP A0ABQ4G1Y4

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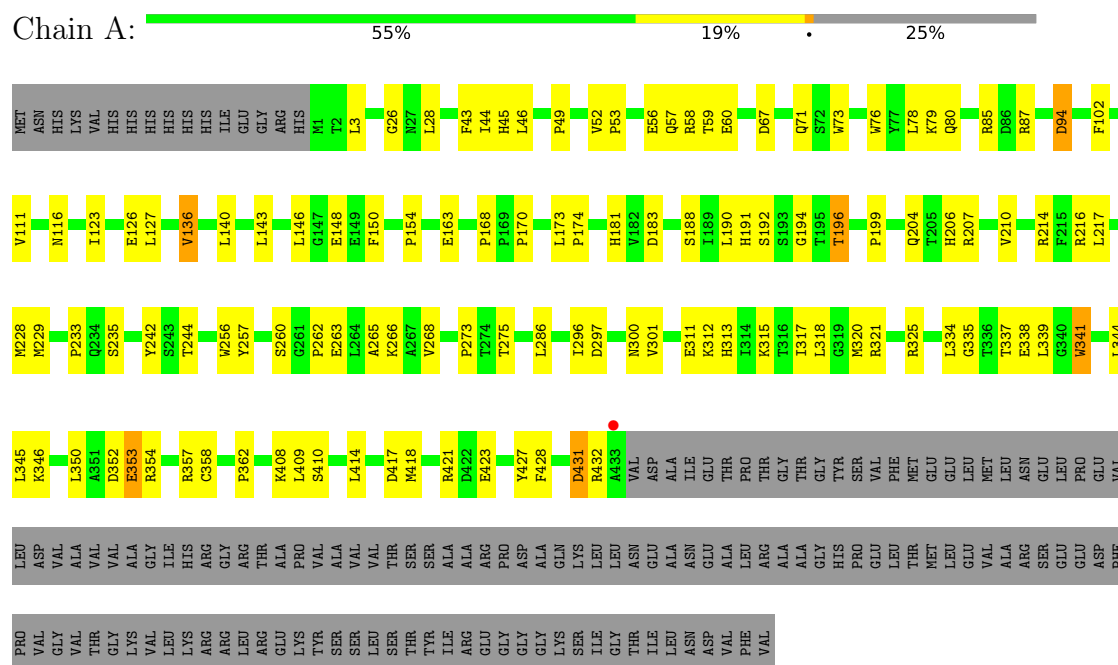
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Chain	Residue	Modelled	Actual	Comment	Reference
D	0	HIS	-	expression tag	UNP A0ABQ4G1Y4

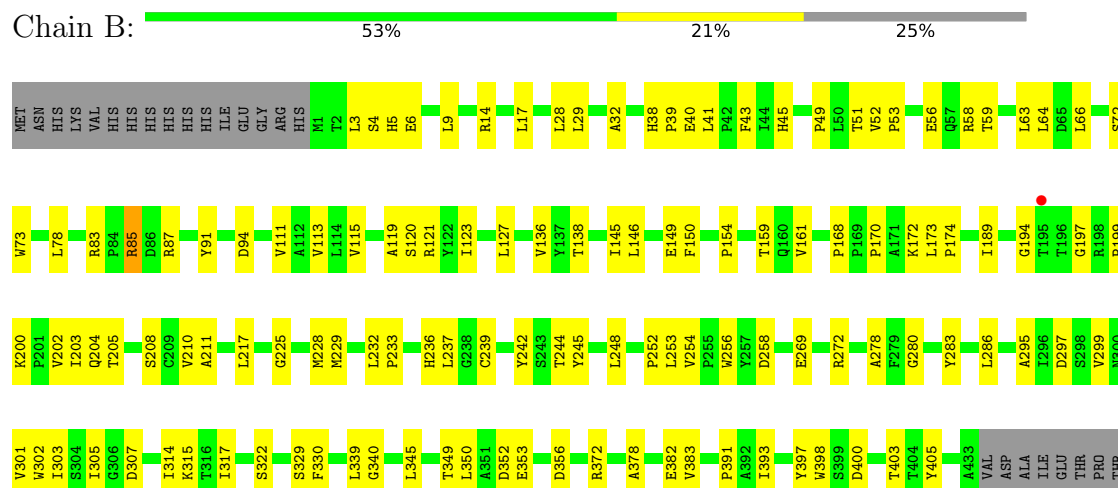
3 Residue-property plots

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: Fatty-acid-CoA ligase FadD



• Molecule 1: Fatty-acid-CoA ligase FadD



GLY	THR	ALA	ALA	GLY	HIS	TYR	SER	VAL	PHE	MET	GLU	LEU	MET	LEU	ASN	GLU	LEU	ASP	GLU	VAL	LEU	VAL	ALA	VAL	GLY	ILE	HIS	ARG	GLY	ARG	THR	ALA	PRO	GLY	GLY	ALA	GLN	LYS	LEU	LEU	ASN	GLU	ALA	PHE	VAL	VAL
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

● Molecule 1: Fatty-acid-CoA ligase Fadd



SER	VAL	S401	T274	T159	L63
LEU	VAL	D402	T274	T159	L64
THR	THR	T403	P168	P168	D65
SER	SER	S406	M277	P169	L66
TYR	SER	R406	A278	P170	D67
ILE	ALA	S407	F279	P174	E68
ARG	ALA	K408	G280	P174	L69
ALA	ARG	K408	G280	P174	V70
PRO	ASP	Y420	Y283	Q175	S72
GLY	GLY	Y420	Y283	E176	Q71
GLY	ASP	Y420	Y283	A177	W73
GLY	ALA	Q429	A289	R178	S74
GLY	ALA	Q429	A289	R178	W75
LYS	GLN	V430	D290	H181	V76
SER	LYS	D431	L291	H181	V77
ILE	LEU	R432	G294	V182	L78
GLY	LEU	A433	G294	D183	K79
THR	ASN	VAL	A295	E184	
ILE	GLU	ASP	T296	D185	R85
LEU	ALA	ALA	D297	P186	
ASN	ASN	ILE	N300	V187	Y91
ASP	GLU	GLU	N300	S188	
VAL	VAL	THR			
PHE	LEU	THR	I305	T195	E12
VAL	ARG	THR	G306		
	ALA	GLY	D307	K200	L17
	ALA	THR		P201	H101
	GLY	GLY	I314	V202	F102
	HIS	TYR	K315	I203	D20
	PRO	SER		Q204	
	GLU	VAL	G319	T205	L23
LEU	LEU	PHE	M320	H206	Q24
THR	MET	GLU	R321	R207	G25
MET	GLU	GLU	E338	R214	G26
LEU	LEU	LEU		F215	N27
LEU	GLU	LEU		R216	L28
VAL	VAL	MET	L344		L29
ALA	ALA	LEU	L345		T30
ARG	ASN	ASN	A226		K31
GLY	GLU	GLU	R348	I227	H38
SER	GLU	LEU	T349	M228	P39
GLU	GLU	PRO	L350	M229	E40
ASP	GLU	GLU		T230	L41
PHE	VAL	VAL	R354	A231	P42
PRO	LEU	LEU	N355	L232	F43
VAL	ASP	ASP	D356	P233	V136
GLY	VAL	VAL	R357	I44	
VAL	VAL	ALA	C358	Y242	H142
THR	VAL	VAL	V359	S243	L46
GLY	VAL	VAL	G360	T244	I145
LYS	ALA	ALA	K361	Y245	L146
LEU	ILE	ILE	P362	E148	G147
LYS	ARG	HIS	V363	L248	E149
ARG	ARG	ARG	G364		P53
ARG	GLY	GLY	V365	P255	S54
	ARG	GLY	N381	W256	G55
	LEU	ARG		Y257	L152
	THR	THR		D258	L153
	GLU	ALA	Y397	T260	P58
LYS	LYS	PRO	W398	S260	T59
	VAL	VAL	S399	L157	E60
SER	ALA	ALA	D400	R157	L61
				H152	S62

● Molecule 1: Fatty-acid-CoA ligase Fadd



MET	ASN	HIS	LYS	VAL	HIS	HIS	HIS	HIS	ILE	GLU	ARG	HIS	R1	T2	L3	S4	H5	L9	T10	Q13	R14	L17	G24	G25	G26	L29	H38	P39	E40	L41	P42	F43	I44	H45	T51	V52	P53	E56	S62	L63	L64	D65	W73	R83						
D86	R87	V88	A89	L92	H93	D94	V111	A112	V113	M116	S117	S120	I123	T127	G135	V136	Y137	L140	L146	F150	G158	W158	E163	P166	A167	P168	P169	P170	H181	E184	S188	I189	L190	G194	T195	T196	G197	R198	P199	V202	T203	C204								
T205	H206	V210	A211	G212	P213	L217	H220	Q223	P224	G225	A226	I227	M228	N229	T230	A231	P233	L237	G238	C239	S243	T244	Z245	A246	V247	L248	G249	P252	P255	D258	E269	R272	P273	T274	T275	V276	M277	A278	Y283	L286	A289	D290	L291							
I296	V301	W302	I303	S304	I305	G306	D307	A308	V309	H310	E311	K312	H313	I314	I317	L318	M320	A326	P327	F330	G335	T336	T337	E338	L339	G340	V343	R348	T349	D352	R357	V363	V370	L371	R372	T376	A392	W398	S401	Y405	I408									
A419	Y420	R421	N426	Y427	F428	A433	VAL	ASP	ALA	ILE	GLU	THR	PRO	THR	GLY	THR	GLY	SER	VAL	PHE	GLU	LEU	MET	GLY	PRO	GLY	VAL	LEU	ASP	VAL	ALA	VAL	VAL	ALA	GLY	ILE	HIS	ARG	GLY	ARG	THR	ALA	PRO	VAL	ALA	VAL	THR	SER	SER	ALA

[illegible]

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	61.19Å 163.99Å 107.69Å 90.00° 99.71° 90.00°	Depositor
Resolution (Å)	49.01 – 3.40 49.01 – 3.40	Depositor EDS
% Data completeness (in resolution range)	93.4 (49.01-3.40) 93.4 (49.01-3.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.79 (at 3.40Å)	Xtriage
Refinement program	PHENIX 1.21_5207	Depositor
R, R_{free}	0.154 , 0.237 0.154 , 0.237	Depositor DCC
R_{free} test set	1856 reflections (6.45%)	wwPDB-VP
Wilson B-factor (Å ²)	47.2	Xtriage
Anisotropy	0.244	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 33.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	13384	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 2.98% 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	0.42	1/3432 (0.0%)	0.59	0/4684
1	B	0.42	1/3432 (0.0%)	0.61	1/4684 (0.0%)
1	C	0.40	0/3432	0.61	0/4684
1	D	0.41	1/3432 (0.0%)	0.59	0/4684
All	All	0.41	3/13728 (0.0%)	0.60	1/18736 (0.0%)

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	B	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	197	GLY	C-N	7.04	1.48	1.33
1	D	196	THR	CA-C	6.50	1.61	1.52
1	A	196	THR	CA-C	6.08	1.60	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	210	VAL	N-CA-C	-5.48	108.51	113.71

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	85	ARG	Sidechain

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	3346	0	3301	81	1
1	B	3346	0	3301	83	1
1	C	3346	0	3301	95	0
1	D	3346	0	3301	97	0
All	All	13384	0	13204	346	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 13.

The worst 5 of 346 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:3:LEU:HD11	1:A:45:HIS:HB2	1.52	0.92
1:D:3:LEU:HD11	1:D:45:HIS:HB2	1.52	0.90
1:B:28:LEU:HD11	1:B:244:THR:HG23	1.54	0.89
1:D:309:VAL:HG13	1:D:314:ILE:HD11	1.56	0.87
1:D:232:LEU:HD22	1:D:305:ILE:HD11	1.55	0.86

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:A:85:ARG:NH1	1:B:405:TYR:O[1_655]	2.16	0.04

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	431/577 (75%)	394 (91%)	28 (6%)	9 (2%)	5	24
1	B	431/577 (75%)	395 (92%)	33 (8%)	3 (1%)	18	47
1	C	431/577 (75%)	400 (93%)	23 (5%)	8 (2%)	6	26
1	D	431/577 (75%)	393 (91%)	33 (8%)	5 (1%)	10	35
All	All	1724/2308 (75%)	1582 (92%)	117 (7%)	25 (2%)	8	30

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	353	GLU
1	A	431	ASP
1	C	154	PRO
1	C	320	MET
1	A	206	HIS

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	352/471 (75%)	351 (100%)	1 (0%)	86	84
1	B	352/471 (75%)	352 (100%)	0	100	100
1	C	352/471 (75%)	351 (100%)	1 (0%)	86	84
1	D	352/471 (75%)	352 (100%)	0	100	100
All	All	1408/1884 (75%)	1406 (100%)	2 (0%)	88	89

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	136	VAL
1	C	195	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	310	HIS
1	D	36	ASN
1	B	130	GLN
1	B	107	GLN
1	B	142	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 [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	433/577 (75%)	-0.44	1 (0%) 91 87	16, 36, 81, 99	0
1	B	433/577 (75%)	-0.52	1 (0%) 91 87	17, 35, 66, 98	0
1	C	433/577 (75%)	-0.46	3 (0%) 84 73	15, 36, 71, 110	0
1	D	433/577 (75%)	-0.36	4 (0%) 81 68	18, 38, 86, 121	0
All	All	1732/2308 (75%)	-0.44	9 (0%) 87 78	15, 36, 78, 121	0

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	196	THR	3.8
1	D	195	THR	3.5
1	D	2	THR	3.4
1	C	176	GLU	3.2
1	C	4	SER	2.6

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.