



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 27, 2026 – 01:54 PM JST

PDB ID : 9UPH / pdb_00009uph
Title : Crystal structure of Imine Reductase Mutant(AHtanRedAm) from Actinoal-
loteichus hymeniacidonis in complex with NADPH
Authors : Gao, S.
Deposited on : 2025-04-28
Resolution : 2.80 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

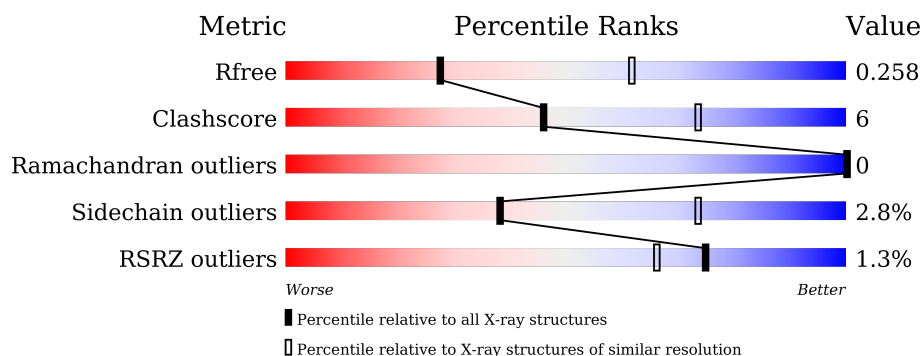
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	336	<div> <div>2%</div> <div>70% 15% . 15%</div> </div>
1	B	336	<div> <div>78% 7% . 14%</div> </div>
1	C	336	<div> <div>2%</div> <div>71% 12% . 16%</div> </div>
1	D	336	<div> <div>%</div> <div>71% 14% . 14%</div> </div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 8385 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 Beta-hydroxyacid dehydrogenase, 3-hydroxyisobutyrate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	285	Total	C	N	O	S	0	0	0
			2087	1313	363	404	7			
1	B	288	Total	C	N	O	S	0	0	0
			2115	1325	373	410	7			
1	C	282	Total	C	N	O	S	0	0	0
			2068	1299	360	402	7			
1	D	288	Total	C	N	O	S	0	0	0
			2115	1325	373	410	7			

There are 108 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP A0AAC9HQB1
A	2	GLY	-	expression tag	UNP A0AAC9HQB1
A	3	SER	-	expression tag	UNP A0AAC9HQB1
A	4	SER	-	expression tag	UNP A0AAC9HQB1
A	5	HIS	-	expression tag	UNP A0AAC9HQB1
A	6	HIS	-	expression tag	UNP A0AAC9HQB1
A	7	HIS	-	expression tag	UNP A0AAC9HQB1
A	8	HIS	-	expression tag	UNP A0AAC9HQB1
A	9	HIS	-	expression tag	UNP A0AAC9HQB1
A	10	HIS	-	expression tag	UNP A0AAC9HQB1
A	11	SER	-	expression tag	UNP A0AAC9HQB1
A	12	SER	-	expression tag	UNP A0AAC9HQB1
A	13	GLY	-	expression tag	UNP A0AAC9HQB1
A	14	LEU	-	expression tag	UNP A0AAC9HQB1
A	15	VAL	-	expression tag	UNP A0AAC9HQB1
A	16	PRO	-	expression tag	UNP A0AAC9HQB1
A	17	ARG	-	expression tag	UNP A0AAC9HQB1
A	18	GLY	-	expression tag	UNP A0AAC9HQB1
A	19	SER	-	expression tag	UNP A0AAC9HQB1
A	20	HIS	-	expression tag	UNP A0AAC9HQB1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	121	THR	ASN	conflict	UNP A0AAC9HQB1
A	207	ILE	PHE	conflict	UNP A0AAC9HQB1
A	234	LEU	TRP	conflict	UNP A0AAC9HQB1
A	238	ALA	MET	conflict	UNP A0AAC9HQB1
A	260	PHE	SER	conflict	UNP A0AAC9HQB1
A	264	HIS	MET	conflict	UNP A0AAC9HQB1
A	267	THR	ALA	conflict	UNP A0AAC9HQB1
B	1	MET	-	initiating methionine	UNP A0AAC9HQB1
B	2	GLY	-	expression tag	UNP A0AAC9HQB1
B	3	SER	-	expression tag	UNP A0AAC9HQB1
B	4	SER	-	expression tag	UNP A0AAC9HQB1
B	5	HIS	-	expression tag	UNP A0AAC9HQB1
B	6	HIS	-	expression tag	UNP A0AAC9HQB1
B	7	HIS	-	expression tag	UNP A0AAC9HQB1
B	8	HIS	-	expression tag	UNP A0AAC9HQB1
B	9	HIS	-	expression tag	UNP A0AAC9HQB1
B	10	HIS	-	expression tag	UNP A0AAC9HQB1
B	11	SER	-	expression tag	UNP A0AAC9HQB1
B	12	SER	-	expression tag	UNP A0AAC9HQB1
B	13	GLY	-	expression tag	UNP A0AAC9HQB1
B	14	LEU	-	expression tag	UNP A0AAC9HQB1
B	15	VAL	-	expression tag	UNP A0AAC9HQB1
B	16	PRO	-	expression tag	UNP A0AAC9HQB1
B	17	ARG	-	expression tag	UNP A0AAC9HQB1
B	18	GLY	-	expression tag	UNP A0AAC9HQB1
B	19	SER	-	expression tag	UNP A0AAC9HQB1
B	20	HIS	-	expression tag	UNP A0AAC9HQB1
B	121	THR	ASN	conflict	UNP A0AAC9HQB1
B	207	ILE	PHE	conflict	UNP A0AAC9HQB1
B	234	LEU	TRP	conflict	UNP A0AAC9HQB1
B	238	ALA	MET	conflict	UNP A0AAC9HQB1
B	260	PHE	SER	conflict	UNP A0AAC9HQB1
B	264	HIS	MET	conflict	UNP A0AAC9HQB1
B	267	THR	ALA	conflict	UNP A0AAC9HQB1
C	1	MET	-	initiating methionine	UNP A0AAC9HQB1
C	2	GLY	-	expression tag	UNP A0AAC9HQB1
C	3	SER	-	expression tag	UNP A0AAC9HQB1
C	4	SER	-	expression tag	UNP A0AAC9HQB1
C	5	HIS	-	expression tag	UNP A0AAC9HQB1
C	6	HIS	-	expression tag	UNP A0AAC9HQB1
C	7	HIS	-	expression tag	UNP A0AAC9HQB1
C	8	HIS	-	expression tag	UNP A0AAC9HQB1

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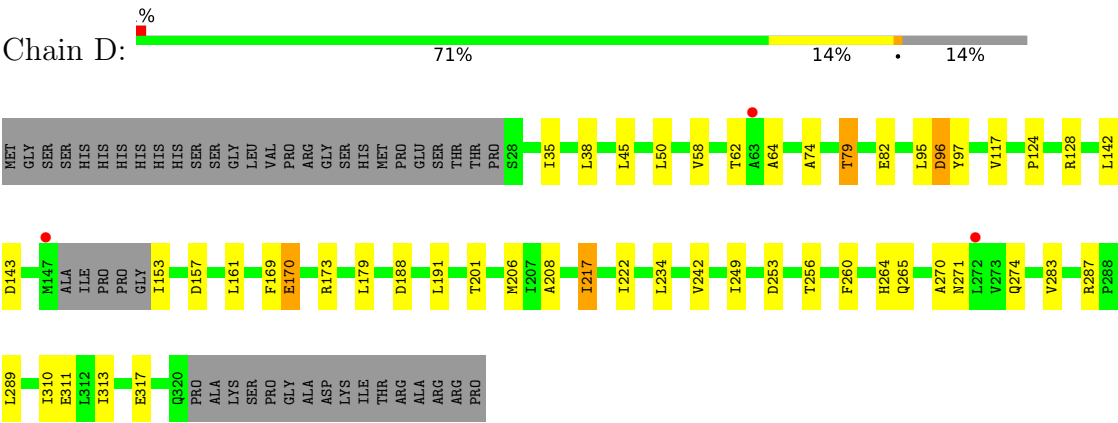
Chain	Residue	Modelled	Actual	Comment	Reference
C	9	HIS	-	expression tag	UNP A0AAC9HQB1
C	10	HIS	-	expression tag	UNP A0AAC9HQB1
C	11	SER	-	expression tag	UNP A0AAC9HQB1
C	12	SER	-	expression tag	UNP A0AAC9HQB1
C	13	GLY	-	expression tag	UNP A0AAC9HQB1
C	14	LEU	-	expression tag	UNP A0AAC9HQB1
C	15	VAL	-	expression tag	UNP A0AAC9HQB1
C	16	PRO	-	expression tag	UNP A0AAC9HQB1
C	17	ARG	-	expression tag	UNP A0AAC9HQB1
C	18	GLY	-	expression tag	UNP A0AAC9HQB1
C	19	SER	-	expression tag	UNP A0AAC9HQB1
C	20	HIS	-	expression tag	UNP A0AAC9HQB1
C	121	THR	ASN	conflict	UNP A0AAC9HQB1
C	207	ILE	PHE	conflict	UNP A0AAC9HQB1
C	234	LEU	TRP	conflict	UNP A0AAC9HQB1
C	238	ALA	MET	conflict	UNP A0AAC9HQB1
C	260	PHE	SER	conflict	UNP A0AAC9HQB1
C	264	HIS	MET	conflict	UNP A0AAC9HQB1
C	267	THR	ALA	conflict	UNP A0AAC9HQB1
D	1	MET	-	initiating methionine	UNP A0AAC9HQB1
D	2	GLY	-	expression tag	UNP A0AAC9HQB1
D	3	SER	-	expression tag	UNP A0AAC9HQB1
D	4	SER	-	expression tag	UNP A0AAC9HQB1
D	5	HIS	-	expression tag	UNP A0AAC9HQB1
D	6	HIS	-	expression tag	UNP A0AAC9HQB1
D	7	HIS	-	expression tag	UNP A0AAC9HQB1
D	8	HIS	-	expression tag	UNP A0AAC9HQB1
D	9	HIS	-	expression tag	UNP A0AAC9HQB1
D	10	HIS	-	expression tag	UNP A0AAC9HQB1
D	11	SER	-	expression tag	UNP A0AAC9HQB1
D	12	SER	-	expression tag	UNP A0AAC9HQB1
D	13	GLY	-	expression tag	UNP A0AAC9HQB1
D	14	LEU	-	expression tag	UNP A0AAC9HQB1
D	15	VAL	-	expression tag	UNP A0AAC9HQB1
D	16	PRO	-	expression tag	UNP A0AAC9HQB1
D	17	ARG	-	expression tag	UNP A0AAC9HQB1
D	18	GLY	-	expression tag	UNP A0AAC9HQB1
D	19	SER	-	expression tag	UNP A0AAC9HQB1
D	20	HIS	-	expression tag	UNP A0AAC9HQB1
D	121	THR	ASN	conflict	UNP A0AAC9HQB1
D	207	ILE	PHE	conflict	UNP A0AAC9HQB1
D	234	LEU	TRP	conflict	UNP A0AAC9HQB1

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Chain	Residue	Modelled	Actual	Comment	Reference
D	238	ALA	MET	conflict	UNP A0AAC9HQB1
D	260	PHE	SER	conflict	UNP A0AAC9HQB1
D	264	HIS	MET	conflict	UNP A0AAC9HQB1
D	267	THR	ALA	conflict	UNP A0AAC9HQB1

● Molecule 1: Beta-hydroxyacid dehydrogenase, 3-hydroxyisobutyrate dehydrogenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	66.22Å 104.94Å 94.21Å 90.00° 94.49° 90.00°	Depositor
Resolution (Å)	33.01 – 2.80 33.01 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.8 (33.01-2.80) 99.7 (33.01-2.80)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.02 (at 2.81Å)	Xtriage
Refinement program	PHENIX 1.15.1_3469	Depositor
R, R_{free}	0.204 , 0.261 0.206 , 0.258	Depositor DCC
R_{free} test set	1550 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	61.6	Xtriage
Anisotropy	0.450	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 48.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8385	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.19% 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	0.16	0/2128	0.36	0/2906
1	B	0.16	0/2154	0.33	0/2939
1	C	0.15	0/2106	0.33	0/2873
1	D	0.15	0/2154	0.34	0/2939
All	All	0.15	0/8542	0.34	0/11657

There are no bond length outliers.

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	2087	0	2041	34	0
1	B	2115	0	2069	19	0
1	C	2068	0	2019	27	0
1	D	2115	0	2069	36	0
All	All	8385	0	8198	96	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (96) 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:149:ILE:HG13	1:A:151:PRO:HD2	1.72	0.71
1:A:230:MET:HE1	1:D:161:LEU:HD21	1.73	0.71
1:D:142:LEU:HD11	1:D:169:PHE:HA	1.74	0.68
1:A:119:LEU:HD13	1:A:146:ILE:HD11	1.78	0.66
1:A:121:THR:HG22	1:D:271:ASN:HD21	1.60	0.65
1:B:208:ALA:HB2	1:C:289:LEU:HD22	1.79	0.64
1:C:123:THR:HG22	1:C:125:LYS:H	1.64	0.62
1:A:289:LEU:HD22	1:D:208:ALA:HB2	1.80	0.62
1:A:314:ARG:NH1	1:A:318:ARG:O	2.33	0.62
1:A:87:SER:O	1:A:114:ARG:NH1	2.33	0.62
1:B:258:VAL:HG11	1:B:305:ASP:HB2	1.81	0.62
1:A:208:ALA:HB2	1:D:289:LEU:HD22	1.83	0.60
1:A:217:ILE:HG23	1:A:222:ILE:HB	1.82	0.60
1:B:261:ASN:HB2	1:B:302:GLY:O	2.02	0.59
1:C:45:LEU:HD22	1:C:179:LEU:HD13	1.83	0.58
1:B:50:LEU:HD11	1:B:74:ALA:HB2	1.86	0.58
1:C:262:LEU:HD13	1:C:306:VAL:HA	1.84	0.57
1:A:249:ILE:HD12	1:A:310:ILE:HG21	1.85	0.57
1:D:62:THR:HG22	1:D:64:ALA:H	1.70	0.56
1:C:35:ILE:HD11	1:C:49:PHE:HD2	1.70	0.56
1:A:188:ASP:HB3	1:A:191:LEU:HG	1.88	0.56
1:B:186:GLY:HA3	1:B:191:LEU:HD12	1.87	0.56
1:A:285:LEU:HD11	1:D:313:ILE:HG21	1.88	0.55
1:D:97:TYR:OH	1:D:143:ASP:OD2	2.23	0.55
1:C:119:LEU:HD13	1:C:146:ILE:HD11	1.90	0.53
1:D:170:GLU:HG2	1:D:170:GLU:O	2.09	0.53
1:A:296:GLN:HE21	1:A:312:LEU:HD21	1.73	0.52
1:D:35:ILE:HB	1:D:58:VAL:HG12	1.91	0.52
1:D:96:ASP:N	1:D:96:ASP:OD1	2.42	0.52
1:D:270:ALA:O	1:D:274:GLN:NE2	2.43	0.52
1:D:283:VAL:O	1:D:287:ARG:HG3	2.09	0.52
1:B:43:THR:HG23	1:B:69:LEU:HD21	1.91	0.52
1:D:117:VAL:HG22	1:D:142:LEU:HB2	1.92	0.52
1:D:38:LEU:HD11	1:D:58:VAL:HB	1.92	0.51
1:C:217:ILE:HG13	1:C:227:LEU:HD22	1.92	0.51
1:B:285:LEU:HD21	1:C:292:LEU:HD12	1.93	0.51
1:A:287:ARG:O	1:A:291:GLU:HG2	2.09	0.51
1:B:38:LEU:HD12	1:B:60:ASN:HB2	1.93	0.51
1:C:39:GLY:O	1:C:43:THR:N	2.34	0.50
1:D:217:ILE:HG23	1:D:222:ILE:HB	1.93	0.50
1:A:296:GLN:OE1	1:A:308:SER:OG	2.30	0.49
1:D:317:GLU:OE1	1:D:317:GLU:N	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:50:LEU:HD11	1:D:74:ALA:HB2	1.95	0.48
1:A:84:ILE:HD13	1:A:111:LEU:HG	1.95	0.48
1:B:206:MET:HE2	1:C:206:MET:HG3	1.95	0.48
1:D:170:GLU:HA	1:D:173:ARG:HB2	1.96	0.48
1:C:103:THR:HG22	1:C:104:LEU:HD23	1.95	0.48
1:A:204:TYR:OH	1:D:265:GLN:HB3	2.14	0.47
1:B:217:ILE:HG13	1:B:227:LEU:HD22	1.95	0.47
1:D:124:PRO:O	1:D:128:ARG:HG3	2.13	0.47
1:C:43:THR:HG22	1:C:47:ASN:HD21	1.79	0.47
1:A:245:TYR:O	1:A:249:ILE:HG12	2.15	0.46
1:C:51:ASP:OD1	1:C:72:ARG:NH2	2.47	0.46
1:A:50:LEU:HD13	1:A:72:ARG:HB3	1.97	0.46
1:B:200:LEU:HD23	1:B:200:LEU:HA	1.76	0.46
1:B:262:LEU:HD11	1:B:293:MET:HG2	1.97	0.46
1:C:206:MET:HE2	1:C:206:MET:HB3	1.79	0.46
1:D:45:LEU:HD22	1:D:179:LEU:HD22	1.97	0.46
1:D:249:ILE:HG12	1:D:310:ILE:HG21	1.98	0.46
1:A:41:MET:HE1	1:D:260:PHE:CZ	2.51	0.46
1:B:217:ILE:HG23	1:B:222:ILE:HB	1.97	0.46
1:A:79:THR:HG22	1:A:81:THR:H	1.81	0.45
1:C:311:GLU:OE2	1:C:320:GLN:HG2	2.16	0.45
1:C:255:GLU:HA	1:C:304:GLY:HA2	1.97	0.45
1:D:153:ILE:HD13	1:D:153:ILE:HA	1.83	0.45
1:A:286:LEU:HD11	1:D:201:THR:HG23	1.97	0.45
1:D:188:ASP:HB3	1:D:191:LEU:HG	1.98	0.45
1:B:262:LEU:HD13	1:B:306:VAL:HA	1.99	0.45
1:A:199:LEU:HB3	1:D:234:LEU:HD22	1.98	0.45
1:A:210:ILE:HD13	1:D:242:VAL:HG22	1.99	0.44
1:C:269:PHE:CD1	1:C:290:PHE:HB2	2.52	0.44
1:B:38:LEU:HB2	1:B:60:ASN:HB2	1.99	0.44
1:A:203:MET:HE2	1:A:203:MET:HB3	1.87	0.44
1:C:153:ILE:HD12	1:C:153:ILE:HA	1.89	0.44
1:B:217:ILE:HD13	1:B:217:ILE:HA	1.86	0.43
1:D:253:ASP:OD2	1:D:256:THR:OG1	2.31	0.43
1:A:38:LEU:HD23	1:A:38:LEU:HA	1.74	0.43
1:A:149:ILE:HD12	1:A:150:PRO:HD2	1.99	0.43
1:C:41:MET:O	1:C:45:LEU:HG	2.18	0.43
1:C:101:HIS:CE1	1:C:102:GLU:HG3	2.53	0.43
1:C:212:GLN:HB2	1:C:285:LEU:HD12	2.01	0.43
1:A:40:ALA:HB3	1:D:264:HIS:HE1	1.85	0.42
1:A:34:THR:HA	1:A:57:THR:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:238:ALA:HB1	1:D:206:MET:HE1	2.02	0.41
1:B:206:MET:HE3	1:C:235:LEU:HD22	2.01	0.41
1:C:87:SER:O	1:C:114:ARG:NH1	2.53	0.41
1:A:261:ASN:HB3	1:A:302:GLY:O	2.20	0.41
1:C:43:THR:HG22	1:C:47:ASN:ND2	2.34	0.41
1:C:262:LEU:HD11	1:C:293:MET:HG2	2.01	0.41
1:A:148:ALA:HA	1:D:260:PHE:CD2	2.56	0.41
1:B:161:LEU:HD21	1:C:230:MET:HE1	2.02	0.41
1:A:206:MET:HG3	1:D:206:MET:HB2	2.03	0.41
1:B:165:PRO:HD3	1:B:189:HIS:NE2	2.36	0.41
1:D:79:THR:HG23	1:D:82:GLU:HB2	2.02	0.41
1:A:149:ILE:HD13	1:D:234:LEU:HD11	2.03	0.40
1:C:310:ILE:HA	1:C:313:ILE:HG12	2.03	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	281/336 (84%)	277 (99%)	4 (1%)	0	100	100
1	B	284/336 (84%)	280 (99%)	4 (1%)	0	100	100
1	C	276/336 (82%)	270 (98%)	6 (2%)	0	100	100
1	D	284/336 (84%)	279 (98%)	5 (2%)	0	100	100
All	All	1125/1344 (84%)	1106 (98%)	19 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	208/249 (84%)	202 (97%)	6 (3%)	37	73
1	B	210/249 (84%)	205 (98%)	5 (2%)	43	77
1	C	206/249 (83%)	201 (98%)	5 (2%)	43	77
1	D	210/249 (84%)	203 (97%)	7 (3%)	33	69
All	All	834/996 (84%)	811 (97%)	23 (3%)	38	73

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	38	LEU
1	A	76	HIS
1	A	104	LEU
1	A	201	THR
1	A	216	LEU
1	A	217	ILE
1	B	166	LEU
1	B	200	LEU
1	B	201	THR
1	B	206	MET
1	B	217	ILE
1	C	153	ILE
1	C	157	ASP
1	C	217	ILE
1	C	234	LEU
1	C	266	SER
1	D	79	THR
1	D	95	LEU
1	D	96	ASP
1	D	157	ASP
1	D	170	GLU
1	D	217	ILE
1	D	311	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	76	HIS
1	A	244	HIS
1	A	296	GLN
1	B	248	GLN
1	C	101	HIS
1	C	137	HIS
1	C	248	GLN
1	D	172	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	285/336 (84%)	-0.11	6 (2%) 63 54	30, 62, 104, 155	0
1	B	288/336 (85%)	-0.26	0 100 100	31, 57, 98, 125	0
1	C	282/336 (83%)	0.01	6 (2%) 63 54	31, 64, 120, 169	0
1	D	288/336 (85%)	-0.13	3 (1%) 79 72	35, 58, 113, 158	0
All	All	1143/1344 (85%)	-0.12	15 (1%) 75 66	30, 60, 112, 169	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	148	ALA	3.8
1	C	67	THR	3.6
1	C	40	ALA	3.2
1	A	149	ILE	3.2
1	A	148	ALA	2.9
1	A	259	VAL	2.7
1	A	150	PRO	2.6
1	D	272	LEU	2.6
1	D	63	ALA	2.5
1	D	147	MET	2.4
1	A	151	PRO	2.2
1	A	68	ALA	2.2
1	C	28	SER	2.2
1	C	257	GLY	2.1
1	C	153	ILE	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.