



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:12 AM GMT

PDB ID : 2PVP
Title : Crystal structure of D-Alanine-D-Alanine Ligase from Helicobacter pylori
Authors : Wu, D.; Zhang, L.; Jiang, H.; Shen, X.
Deposited on : 2007-05-10
Resolution : 2.40 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

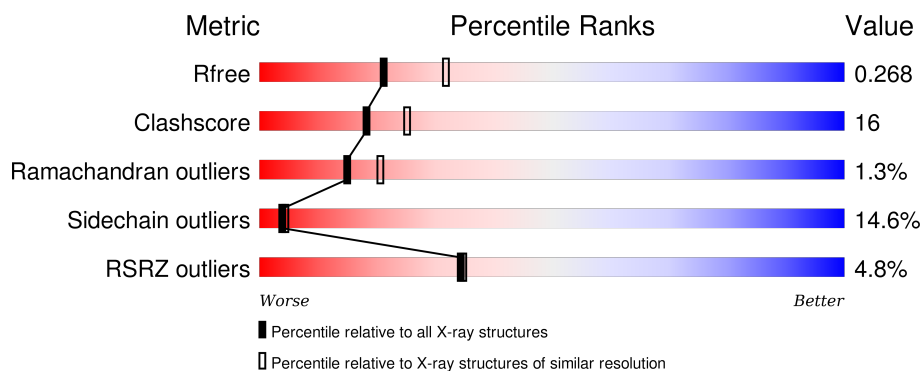
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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}	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	367	 5% 57% 24% 7% • 10%
1	B	367	 4% 59% 20% 7% • 14%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5286 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 D-alanine-D-alanine ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	329	Total	C	N	O	S	0	0	0
			2660	1741	422	490	7			
1	B	315	Total	C	N	O	S	0	0	0
			2531	1656	401	467	7			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	EXPRESSION TAG	UNP Q2N4T5
A	-18	GLY	-	EXPRESSION TAG	UNP Q2N4T5
A	-17	SER	-	EXPRESSION TAG	UNP Q2N4T5
A	-16	SER	-	EXPRESSION TAG	UNP Q2N4T5
A	-15	HIS	-	EXPRESSION TAG	UNP Q2N4T5
A	-14	HIS	-	EXPRESSION TAG	UNP Q2N4T5
A	-13	HIS	-	EXPRESSION TAG	UNP Q2N4T5
A	-12	HIS	-	EXPRESSION TAG	UNP Q2N4T5
A	-11	HIS	-	EXPRESSION TAG	UNP Q2N4T5
A	-10	HIS	-	EXPRESSION TAG	UNP Q2N4T5
A	-9	SER	-	EXPRESSION TAG	UNP Q2N4T5
A	-8	SER	-	EXPRESSION TAG	UNP Q2N4T5
A	-7	GLY	-	EXPRESSION TAG	UNP Q2N4T5
A	-6	LEU	-	EXPRESSION TAG	UNP Q2N4T5
A	-5	VAL	-	EXPRESSION TAG	UNP Q2N4T5
A	-4	PRO	-	EXPRESSION TAG	UNP Q2N4T5
A	-3	ARG	-	EXPRESSION TAG	UNP Q2N4T5
A	-2	GLY	-	EXPRESSION TAG	UNP Q2N4T5
A	-1	SER	-	EXPRESSION TAG	UNP Q2N4T5
A	0	HIS	-	EXPRESSION TAG	UNP Q2N4T5
B	-19	MET	-	EXPRESSION TAG	UNP Q2N4T5
B	-18	GLY	-	EXPRESSION TAG	UNP Q2N4T5
B	-17	SER	-	EXPRESSION TAG	UNP Q2N4T5
B	-16	SER	-	EXPRESSION TAG	UNP Q2N4T5
B	-15	HIS	-	EXPRESSION TAG	UNP Q2N4T5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-14	HIS	-	EXPRESSION TAG	UNP Q2N4T5
B	-13	HIS	-	EXPRESSION TAG	UNP Q2N4T5
B	-12	HIS	-	EXPRESSION TAG	UNP Q2N4T5
B	-11	HIS	-	EXPRESSION TAG	UNP Q2N4T5
B	-10	HIS	-	EXPRESSION TAG	UNP Q2N4T5
B	-9	SER	-	EXPRESSION TAG	UNP Q2N4T5
B	-8	SER	-	EXPRESSION TAG	UNP Q2N4T5
B	-7	GLY	-	EXPRESSION TAG	UNP Q2N4T5
B	-6	LEU	-	EXPRESSION TAG	UNP Q2N4T5
B	-5	VAL	-	EXPRESSION TAG	UNP Q2N4T5
B	-4	PRO	-	EXPRESSION TAG	UNP Q2N4T5
B	-3	ARG	-	EXPRESSION TAG	UNP Q2N4T5
B	-2	GLY	-	EXPRESSION TAG	UNP Q2N4T5
B	-1	SER	-	EXPRESSION TAG	UNP Q2N4T5
B	0	HIS	-	EXPRESSION TAG	UNP Q2N4T5

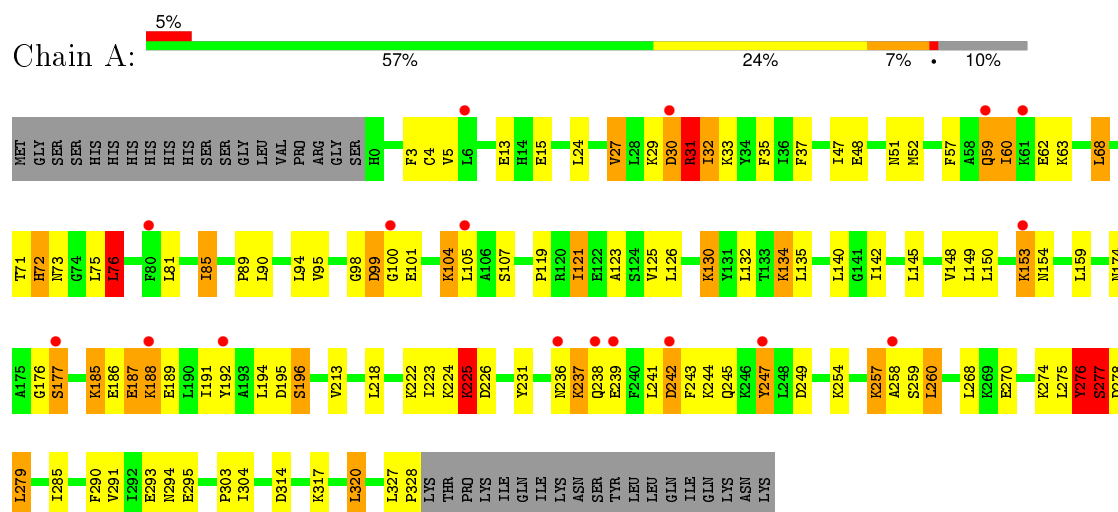
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	43	Total O 43 43	0	0
2	B	52	Total O 52 52	0	0

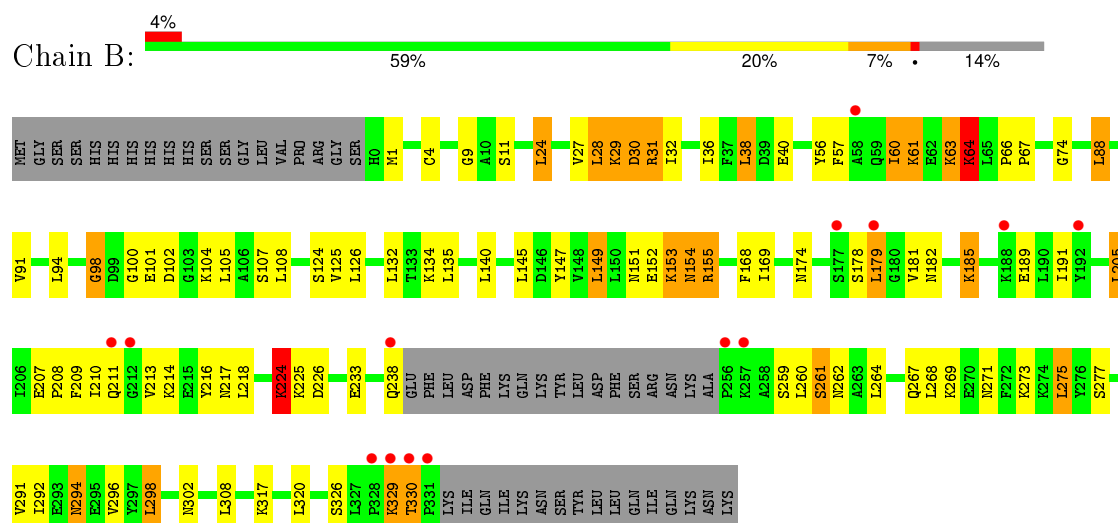
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: D-alanine-D-alanine ligase



• Molecule 1: D-alanine-D-alanine ligase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	70.97Å 89.02Å 121.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.40 32.78 – 2.40	Depositor EDS
% Data completeness (in resolution range)	97.5 (15.00-2.40) 97.6 (32.78-2.40)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.81 (at 2.39Å)	Xtriage
Refinement program	REFMAC5	Depositor
R, R_{free}	0.229 , 0.283 0.231 , 0.268	Depositor DCC
R_{free} test set	1514 reflections (5.32%)	DCC
Wilson B-factor (Å ²)	48.1	Xtriage
Anisotropy	0.637	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 44.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 30177 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5286	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.27% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	1.03	10/2720 (0.4%)	1.33	20/3667 (0.5%)
1	B	0.80	7/2587 (0.3%)	1.03	14/3489 (0.4%)
All	All	0.92	17/5307 (0.3%)	1.19	34/7156 (0.5%)

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	2
1	B	0	1
All	All	0	3

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	277	SER	CB-OG	26.23	1.76	1.42
1	A	27	VAL	CB-CG2	-17.43	1.16	1.52
1	B	178	SER	CB-OG	15.21	1.62	1.42
1	A	27	VAL	CB-CG1	13.47	1.81	1.52
1	B	30	ASP	CB-CG	-13.24	1.24	1.51
1	A	279	LEU	CB-CG	-12.96	1.15	1.52
1	B	225	LYS	CB-CG	-12.36	1.19	1.52
1	B	31	ARG	CB-CG	11.27	1.82	1.52
1	A	32	ILE	CB-CG1	-11.20	1.22	1.54
1	A	225	LYS	CB-CG	10.30	1.80	1.52
1	B	29	LYS	CA-CB	-9.74	1.32	1.53
1	A	278	ASP	CB-CG	9.18	1.71	1.51
1	A	226	ASP	CB-CG	-6.31	1.38	1.51
1	A	226	ASP	C-N	5.97	1.47	1.34
1	A	72	HIS	CB-CG	5.79	1.60	1.50
1	B	28	LEU	CB-CG	5.71	1.69	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	27	VAL	C-N	5.21	1.46	1.34

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	276	TYR	CB-CG-CD1	-41.08	96.35	121.00
1	A	276	TYR	CB-CG-CD2	32.89	140.73	121.00
1	B	30	ASP	CB-CG-OD1	21.71	137.84	118.30
1	B	30	ASP	CB-CG-OD2	-20.40	99.94	118.30
1	A	278	ASP	CB-CG-OD1	16.42	133.08	118.30
1	B	28	LEU	CB-CG-CD2	16.32	138.75	111.00
1	B	30	ASP	CA-CB-CG	13.12	142.26	113.40
1	A	27	VAL	CA-CB-CG1	-12.81	91.69	110.90
1	A	31	ARG	CB-CG-CD	12.67	144.53	111.60
1	A	278	ASP	CB-CG-OD2	-12.65	106.91	118.30
1	A	260	LEU	CB-CG-CD2	-12.24	90.19	111.00
1	A	27	VAL	CA-CB-CG2	11.63	128.34	110.90
1	A	225	LYS	CA-CB-CG	-8.71	94.23	113.40
1	B	224	LYS	CB-CA-C	8.54	127.48	110.40
1	B	225	LYS	CA-CB-CG	8.04	131.09	113.40
1	A	99	ASP	CB-CA-C	-7.64	95.13	110.40
1	A	279	LEU	CA-CB-CG	7.58	132.73	115.30
1	B	28	LEU	CA-CB-CG	-7.56	97.92	115.30
1	B	28	LEU	CB-CG-CD1	-7.16	98.83	111.00
1	A	278	ASP	CA-CB-CG	-7.07	97.84	113.40
1	A	32	ILE	CA-CB-CG2	-6.93	97.05	110.90
1	A	257	LYS	O-C-N	-6.87	111.71	122.70
1	B	31	ARG	CA-CB-CG	-6.85	98.33	113.40
1	B	29	LYS	CB-CA-C	6.58	123.56	110.40
1	B	27	VAL	O-C-N	6.54	133.16	122.70
1	A	76	LEU	CA-CB-CG	5.91	128.89	115.30
1	A	277	SER	N-CA-C	5.84	126.76	111.00
1	B	225	LYS	O-C-N	-5.74	113.52	122.70
1	A	242	ASP	CB-CG-OD2	5.61	123.34	118.30
1	A	30	ASP	CB-CG-OD2	5.25	123.03	118.30
1	A	99	ASP	N-CA-C	5.15	124.89	111.00
1	A	276	TYR	O-C-N	5.09	130.85	122.70
1	B	27	VAL	CA-C-N	-5.08	106.03	117.20
1	B	108	LEU	CA-CB-CG	5.00	126.80	115.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	276	TYR	Sidechain
1	A	30	ASP	Peptide
1	B	63	LYS	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	2660	0	2678	107	1
1	B	2531	0	2558	59	1
2	A	43	0	0	3	0
2	B	52	0	0	4	0
All	All	5286	0	5236	163	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 16.

All (163) 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:B:31:ARG:CG	1:B:31:ARG:CB	1.83	1.56
1:A:225:LYS:CG	1:A:225:LYS:CB	1.80	1.54
1:A:27:VAL:CB	1:A:27:VAL:CG1	1.81	1.54
1:A:231:TYR:CE1	1:A:242:ASP:OD1	1.81	1.32
1:A:277:SER:OG	1:A:277:SER:CB	1.76	1.32
1:A:244:LYS:NZ	1:A:259:SER:OG	1.74	1.20
1:B:179:LEU:CD1	2:B:386:HOH:O	1.97	1.11
1:B:64:LYS:HG3	1:B:64:LYS:O	1.45	1.07
1:A:35:PHE:HB3	1:A:52:MET:HE3	1.32	1.05
1:A:231:TYR:CD1	1:A:242:ASP:HB2	1.92	1.05
1:A:27:VAL:CG1	1:A:27:VAL:CA	2.41	0.99
1:A:225:LYS:CA	1:A:225:LYS:CG	2.44	0.94
1:A:231:TYR:CE1	1:A:242:ASP:HB2	2.02	0.94
1:A:35:PHE:HB3	1:A:52:MET:CE	1.99	0.92
1:A:32:ILE:HG22	1:A:32:ILE:O	1.68	0.92
1:B:179:LEU:HD13	2:B:386:HOH:O	1.64	0.91
1:A:27:VAL:CG2	1:A:27:VAL:CG1	2.46	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:231:TYR:CD1	1:A:242:ASP:CB	2.57	0.88
1:A:123:ALA:HB2	1:A:279:LEU:O	1.73	0.87
1:A:231:TYR:CD1	1:A:242:ASP:OD1	2.28	0.86
1:A:225:LYS:CB	1:A:225:LYS:CD	2.54	0.85
1:A:241:LEU:HD22	1:A:258:ALA:O	1.77	0.84
1:B:31:ARG:CG	1:B:31:ARG:CA	2.55	0.84
1:A:231:TYR:HD1	1:A:242:ASP:HB2	1.45	0.82
1:A:231:TYR:CE1	1:A:242:ASP:CB	2.65	0.80
1:B:64:LYS:CG	1:B:64:LYS:O	2.30	0.80
1:A:231:TYR:CE1	1:A:242:ASP:CG	2.55	0.79
1:B:179:LEU:HD11	2:B:386:HOH:O	1.72	0.79
1:B:213:VAL:HG21	1:B:292:ILE:HG12	1.64	0.79
1:A:98:GLY:O	1:A:99:ASP:HB2	1.84	0.77
1:A:4:CYS:SG	1:A:89:PRO:HD2	2.25	0.76
1:B:4:CYS:SG	1:B:36:ILE:CD1	2.74	0.76
1:B:28:LEU:HB2	1:B:32:ILE:HD11	1.69	0.76
1:A:239:GLU:OE2	2:A:376:HOH:O	2.04	0.75
1:A:247:TYR:HD1	1:A:247:TYR:H	1.37	0.73
1:A:35:PHE:CB	1:A:52:MET:HE3	2.15	0.72
1:B:329:LYS:C	1:B:330:THR:HG22	2.09	0.72
1:A:35:PHE:CB	1:A:52:MET:CE	2.67	0.72
1:A:222:LYS:NZ	1:A:277:SER:O	2.24	0.70
1:B:9:GLY:HA2	1:B:38:LEU:HD13	1.74	0.70
1:A:231:TYR:CD1	1:A:242:ASP:CG	2.65	0.69
1:B:260:LEU:HD22	1:B:264:LEU:HD23	1.75	0.68
1:A:231:TYR:HD1	1:A:242:ASP:CB	2.03	0.68
1:A:121:ILE:N	1:A:121:ILE:HD12	2.09	0.68
1:B:4:CYS:SG	1:B:36:ILE:HD11	2.33	0.67
1:B:74:GLY:HA2	1:B:88:LEU:HG	1.77	0.67
1:B:4:CYS:SG	1:B:36:ILE:HD12	2.33	0.66
1:A:276:TYR:O	1:A:276:TYR:CD2	2.49	0.66
1:A:32:ILE:HG21	1:A:35:PHE:CE1	2.32	0.64
1:A:225:LYS:HA	1:A:225:LYS:CG	2.28	0.64
1:A:285:ILE:HG22	1:A:303:PRO:HA	1.80	0.64
1:B:40:GLU:H	1:B:40:GLU:CD	2.02	0.63
1:A:270:GLU:O	1:A:274:LYS:HG2	1.99	0.62
1:A:153:LYS:O	1:A:153:LYS:HG2	2.01	0.60
1:A:231:TYR:CZ	1:A:242:ASP:OD1	2.50	0.60
1:A:191:ILE:HD12	1:A:191:ILE:H	1.67	0.60
1:A:37:PHE:HB2	1:A:47:ILE:HD13	1.84	0.60
1:A:48:GLU:HB2	1:A:51:ASN:HD22	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:224:LYS:HD2	1:B:326:SER:HB2	1.84	0.59
1:A:31:ARG:NH1	1:A:317:LYS:CD	2.66	0.59
1:A:37:PHE:HB3	1:A:47:ILE:HD11	1.85	0.59
1:A:27:VAL:HA	1:A:27:VAL:CG1	2.33	0.58
1:A:31:ARG:NH1	1:A:317:LYS:HD2	2.19	0.58
1:A:192:TYR:O	1:A:196:SER:HB3	2.03	0.58
1:A:125:VAL:HG21	1:B:125:VAL:HG21	1.86	0.58
1:B:31:ARG:HG3	1:B:317:LYS:NZ	2.19	0.57
1:A:95:VAL:O	1:A:100:GLY:HA3	2.04	0.57
1:B:28:LEU:HB2	1:B:32:ILE:CD1	2.34	0.57
1:B:56:TYR:CE1	1:B:63:LYS:HE2	2.39	0.57
1:A:291:VAL:HA	1:A:295:GLU:O	2.05	0.57
1:B:329:LYS:C	1:B:330:THR:CG2	2.73	0.56
1:B:216:TYR:CZ	1:B:260:LEU:HD21	2.40	0.56
1:B:214:LYS:HB2	1:B:291:VAL:HB	1.87	0.56
1:B:31:ARG:CB	1:B:31:ARG:CD	2.80	0.56
1:A:32:ILE:HG21	1:A:35:PHE:CZ	2.41	0.56
1:B:275:LEU:HD21	1:B:298:LEU:HG	1.89	0.55
1:A:13:GLU:OE1	1:A:177:SER:HB2	2.08	0.54
1:A:24:LEU:HA	1:A:27:VAL:HG22	1.89	0.54
1:A:48:GLU:HB2	1:A:51:ASN:ND2	2.22	0.54
1:A:121:ILE:CD1	1:A:121:ILE:N	2.71	0.54
1:A:225:LYS:HD3	1:A:225:LYS:CB	2.35	0.53
1:A:72:HIS:H	1:A:72:HIS:CD2	2.24	0.53
1:A:57:PHE:HA	1:A:60:ILE:HB	1.91	0.53
1:B:217:ASN:HB2	1:B:233:GLU:HB3	1.90	0.53
1:A:159:LEU:HD11	1:A:187:GLU:HB2	1.90	0.53
1:A:37:PHE:HB2	1:A:47:ILE:CD1	2.38	0.53
1:A:231:TYR:HE1	1:A:242:ASP:HB2	1.67	0.52
1:A:231:TYR:HE1	1:A:242:ASP:CB	2.20	0.52
1:A:121:ILE:CD1	1:A:121:ILE:H	2.22	0.52
1:A:237:LYS:O	1:A:238:GLN:HB2	2.09	0.52
1:B:169:ILE:HD11	1:B:181:VAL:HG12	1.90	0.52
1:A:37:PHE:CB	1:A:47:ILE:HD11	2.40	0.52
1:A:35:PHE:CB	1:A:52:MET:HE2	2.39	0.52
1:B:24:LEU:HG	1:B:94:LEU:HD11	1.91	0.51
1:A:5:VAL:HG13	1:A:94:LEU:HD12	1.93	0.51
1:A:31:ARG:NH1	1:A:317:LYS:HD3	2.26	0.51
1:B:149:LEU:HD23	1:B:205:LEU:HD13	1.92	0.51
1:B:98:GLY:O	1:B:102:ASP:CG	2.49	0.50
1:A:130:LYS:HE3	1:A:174:ASN:HA	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:37:PHE:CB	1:A:47:ILE:CD1	2.89	0.50
1:A:72:HIS:O	1:A:73:ASN:HB2	2.11	0.50
1:A:134:LYS:HD2	2:A:360:HOH:O	2.12	0.49
1:B:61:LYS:C	1:B:63:LYS:H	2.15	0.49
1:B:154:ASN:HD22	1:B:154:ASN:C	2.15	0.49
1:A:121:ILE:H	1:A:121:ILE:HD12	1.75	0.49
1:A:213:VAL:HG21	1:A:290:PHE:HB3	1.93	0.49
1:A:186:GLU:O	1:A:188:LYS:N	2.46	0.48
1:B:134:LYS:HD3	1:B:147:TYR:CD2	2.49	0.47
1:B:168:PHE:HB2	1:B:207:GLU:O	2.14	0.47
1:A:98:GLY:O	1:A:99:ASP:CB	2.58	0.47
1:A:187:GLU:O	1:A:187:GLU:CG	2.62	0.47
1:B:269:LYS:O	1:B:273:LYS:HG3	2.14	0.47
1:B:151:ASN:H	1:B:154:ASN:HD21	1.63	0.47
1:A:99:ASP:O	1:A:105:LEU:HD12	2.15	0.47
1:A:185:LYS:N	1:A:189:GLU:OE2	2.33	0.46
1:B:291:VAL:CG1	1:B:294:ASN:HA	2.45	0.46
1:A:247:TYR:CD1	1:A:247:TYR:N	2.82	0.46
1:A:119:PRO:HG3	1:A:303:PRO:HB2	1.97	0.46
1:B:57:PHE:CD2	1:B:60:ILE:HG13	2.51	0.46
1:A:71:THR:HG21	1:A:85:ILE:HD11	1.98	0.45
1:B:330:THR:OG1	1:B:330:THR:O	2.30	0.45
1:A:223:ILE:O	1:A:224:LYS:HB2	2.17	0.44
1:B:271:ASN:HD22	1:B:296:VAL:HG11	1.81	0.44
1:B:261:SER:HB2	1:B:264:LEU:H	1.82	0.44
1:A:32:ILE:CG2	1:A:35:PHE:CE1	2.98	0.44
1:B:185:LYS:HG2	1:B:189:GLU:OE2	2.17	0.44
1:A:89:PRO:O	1:A:90:LEU:C	2.55	0.44
1:B:154:ASN:HD22	1:B:155:ARG:N	2.16	0.44
1:A:59:GLN:O	1:A:62:GLU:HG2	2.16	0.44
1:A:225:LYS:HG3	1:A:225:LYS:CA	2.44	0.44
1:A:104:LYS:HA	1:B:107:SER:HB3	1.99	0.44
1:A:242:ASP:OD2	1:A:243:PHE:N	2.39	0.44
1:A:68:LEU:HD23	1:A:75:LEU:HD13	2.00	0.43
1:A:293:GLU:O	1:A:294:ASN:HB2	2.17	0.43
1:B:291:VAL:HG13	1:B:294:ASN:HA	2.00	0.43
1:B:174:ASN:O	1:B:174:ASN:OD1	2.37	0.43
1:B:66:PRO:HA	1:B:67:PRO:HD3	1.80	0.43
1:A:3:PHE:CZ	1:A:320:LEU:HD13	2.53	0.43
1:A:188:LYS:HA	1:A:188:LYS:HD2	1.64	0.43
1:A:99:ASP:O	1:A:105:LEU:CG	2.67	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:207:GLU:HB3	1:B:208:PRO:HD2	2.01	0.43
1:A:99:ASP:O	1:A:105:LEU:HG	2.19	0.42
1:B:11:SER:HB2	1:B:98:GLY:HA3	2.02	0.42
1:B:74:GLY:HA2	1:B:88:LEU:CG	2.47	0.42
1:A:213:VAL:CG2	1:A:290:PHE:HB3	2.50	0.42
1:A:254:LYS:HG2	2:A:387:HOH:O	2.18	0.42
1:A:148:VAL:HG12	1:A:150:LEU:CD2	2.49	0.42
1:A:327:LEU:HA	1:A:328:PRO:HD3	1.92	0.42
1:B:329:LYS:HG2	1:B:330:THR:N	2.35	0.42
1:A:225:LYS:HD3	1:A:225:LYS:HB2	2.02	0.41
1:B:31:ARG:CA	1:B:31:ARG:HG2	2.48	0.41
1:A:153:LYS:O	1:A:153:LYS:CG	2.68	0.41
1:B:210:ILE:HG22	2:B:399:HOH:O	2.20	0.41
1:A:31:ARG:HH12	1:A:317:LYS:CD	2.32	0.41
1:A:101:GLU:CG	1:A:304:ILE:HD12	2.50	0.41
1:A:107:SER:HB3	1:B:104:LYS:HA	2.03	0.41
1:A:142:ILE:HD11	1:A:274:LYS:HG3	2.03	0.41
1:A:191:ILE:HD12	1:A:191:ILE:N	2.33	0.41
1:A:31:ARG:HH12	1:A:317:LYS:HD2	1.86	0.41
1:B:209:PHE:CE2	1:B:211:GLN:HB3	2.57	0.40
1:B:101:GLU:O	1:B:124:SER:HB3	2.20	0.40
1:A:76:LEU:HD22	1:A:85:ILE:CD1	2.52	0.40
1:B:100:GLY:HA2	1:B:105:LEU:HD12	2.02	0.40

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:249:ASP:OD1	1:B:261:SER:OG[1_655]	1.93	0.27

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	327/367 (89%)	307 (94%)	17 (5%)	3 (1%)	21	30
1	B	311/367 (85%)	293 (94%)	13 (4%)	5 (2%)	12	16
All	All	638/734 (87%)	600 (94%)	30 (5%)	8 (1%)	15	21

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	277	SER
1	A	154	ASN
1	B	64	LYS
1	B	98	GLY
1	B	153	LYS
1	B	277	SER
1	B	155	ARG
1	A	176	GLY

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	291/326 (89%)	249 (86%)	42 (14%)	4	4
1	B	278/326 (85%)	237 (85%)	41 (15%)	4	4
All	All	569/652 (87%)	486 (85%)	83 (15%)	4	4

All (83) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	GLU
1	A	29	LYS
1	A	31	ARG
1	A	33	LYS
1	A	59	GLN
1	A	60	ILE
1	A	63	LYS
1	A	68	LEU

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Mol	Chain	Res	Type
1	A	76	LEU
1	A	81	LEU
1	A	85	ILE
1	A	104	LYS
1	A	121	ILE
1	A	126	LEU
1	A	130	LYS
1	A	132	LEU
1	A	134	LYS
1	A	135	LEU
1	A	140	LEU
1	A	145	LEU
1	A	149	LEU
1	A	153	LYS
1	A	177	SER
1	A	185	LYS
1	A	187	GLU
1	A	188	LYS
1	A	194	LEU
1	A	195	ASP
1	A	196	SER
1	A	218	LEU
1	A	225	LYS
1	A	236	ASN
1	A	237	LYS
1	A	245	GLN
1	A	247	TYR
1	A	257	LYS
1	A	260	LEU
1	A	268	LEU
1	A	275	LEU
1	A	276	TYR
1	A	314	ASP
1	A	320	LEU
1	B	1	MET
1	B	24	LEU
1	B	29	LYS
1	B	30	ASP
1	B	38	LEU
1	B	60	ILE
1	B	61	LYS
1	B	64	LYS

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Mol	Chain	Res	Type
1	B	88	LEU
1	B	91	VAL
1	B	126	LEU
1	B	132	LEU
1	B	135	LEU
1	B	140	LEU
1	B	145	LEU
1	B	149	LEU
1	B	152	GLU
1	B	153	LYS
1	B	154	ASN
1	B	179	LEU
1	B	182	ASN
1	B	185	LYS
1	B	191	ILE
1	B	205	LEU
1	B	218	LEU
1	B	224	LYS
1	B	226	ASP
1	B	238	GLN
1	B	259	SER
1	B	261	SER
1	B	262	ASN
1	B	267	GLN
1	B	268	LEU
1	B	275	LEU
1	B	294	ASN
1	B	298	LEU
1	B	302	ASN
1	B	308	LEU
1	B	320	LEU
1	B	329	LYS
1	B	330	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	51	ASN
1	A	72	HIS
1	A	163	ASN
1	A	211	GLN
1	A	262	ASN

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Mol	Chain	Res	Type
1	A	271	ASN
1	A	322	ASN
1	A	325	GLN
1	B	154	ASN
1	B	163	ASN
1	B	165	ASN
1	B	174	ASN
1	B	236	ASN
1	B	294	ASN
1	B	302	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 carbohydrates 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	329/367 (89%)	0.26	17 (5%) 31 31	20, 51, 82, 102	0
1	B	315/367 (85%)	0.26	14 (4%) 38 39	20, 58, 86, 118	0
All	All	644/734 (87%)	0.26	31 (4%) 34 35	20, 54, 85, 118	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	258	ALA	9.4
1	B	331	PRO	7.2
1	B	328	PRO	5.9
1	B	330	THR	5.6
1	B	177	SER	4.9
1	A	236	ASN	4.7
1	A	247	TYR	4.7
1	B	192	TYR	3.9
1	B	211	GLN	3.7
1	A	59	GLN	3.5
1	B	238	GLN	3.5
1	A	238	GLN	3.3
1	A	239	GLU	3.2
1	B	329	LYS	3.1
1	A	192	TYR	3.0
1	A	242	ASP	2.9
1	B	256	PRO	2.8
1	B	212	GLY	2.7
1	B	58	ALA	2.7
1	A	100	GLY	2.6
1	A	30	ASP	2.5
1	A	6	LEU	2.5
1	A	188	LYS	2.4
1	A	177	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	80	PHE	2.2
1	A	105	LEU	2.2
1	B	257	LYS	2.1
1	A	153	LYS	2.1
1	B	188	LYS	2.1
1	A	61	LYS	2.0
1	B	179	LEU	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 carbohydrates 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.