



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 05:18 PM UTC

PDB ID : 8ZPC / pdb_00008zpc
Title : Acinetobacter baumannii Penicillin-Binding Protein 2
Authors : Jang, H.S.; Park, H.H.
Deposited on : 2024-05-29
Resolution : 3.31 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

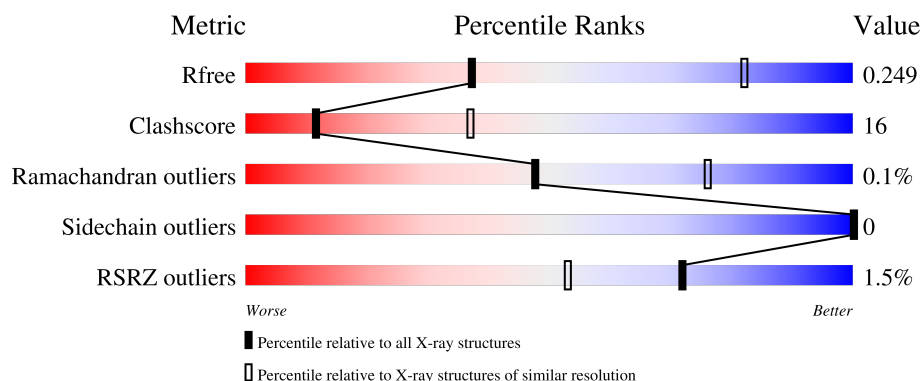
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.31 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	1153 (3.34-3.30)
Clashscore	190562	1193 (3.34-3.30)
Ramachandran outliers	187476	1172 (3.34-3.30)
Sidechain outliers	187428	1171 (3.34-3.30)
RSRZ outliers	180081	1153 (3.34-3.30)

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	631	 56% 26% 18%
1	B	631	 2% 56% 24% 19%

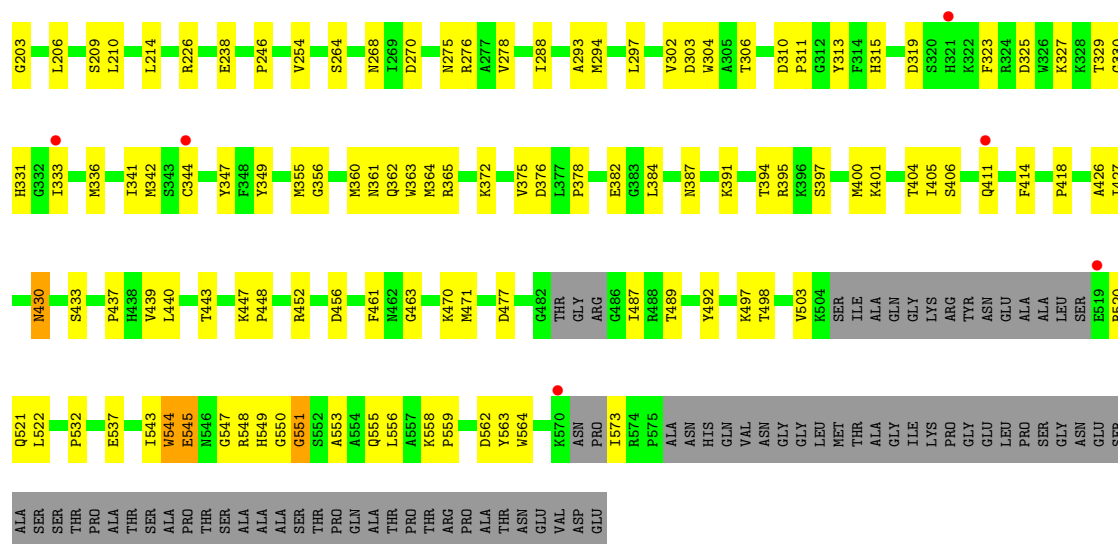
2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 8038 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 Peptidoglycan D,D-transpeptidase MrdA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	516	Total	C	N	O	S	0	0	0
			4055	2583	711	747	14			
1	B	509	Total	C	N	O	S	0	0	0
			3983	2539	697	733	14			



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	121.44Å 151.53Å 177.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.38 – 3.31 47.38 – 3.31	Depositor EDS
% Data completeness (in resolution range)	99.2 (47.38-3.31) 99.1 (47.38-3.31)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.22 (at 3.33Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.195 , 0.248 0.197 , 0.249	Depositor DCC
R_{free} test set	1213 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	48.5	Xtriage
Anisotropy	0.947	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 47.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	8038	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.87% 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	0.51	0/4150	0.76	5/5622 (0.1%)
1	B	0.46	0/4077	0.76	7/5526 (0.1%)
All	All	0.49	0/8227	0.76	12/11148 (0.1%)

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	544	TRP	CA-CB-CG	7.32	127.51	113.60
1	A	456	ASP	N-CA-C	6.18	118.10	111.36
1	A	142	ILE	CA-C-N	-5.98	114.27	122.16
1	A	142	ILE	C-N-CA	-5.98	114.27	122.16
1	B	550	GLY	N-CA-C	-5.98	103.41	111.54
1	B	545	GLU	N-CA-C	-5.97	101.44	110.28
1	B	551	GLY	N-CA-C	-5.31	100.59	113.18
1	A	302	VAL	CA-C-N	5.19	132.33	123.05
1	A	302	VAL	C-N-CA	5.19	132.33	123.05
1	B	456	ASP	N-CA-C	5.18	116.61	111.07
1	B	544	TRP	CB-CA-C	-5.04	101.81	110.22
1	B	430	ASN	N-CA-CB	-5.01	102.78	110.44

There are no chirality outliers.

There are no planarity outliers.

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	4055	0	4028	140	1
1	B	3983	0	3927	125	0
All	All	8038	0	7955	256	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 (256) 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:169:SER:HB3	1:B:378:PRO:HD3	1.45	0.96
1:A:169:SER:HB3	1:A:378:PRO:HD3	1.49	0.94
1:B:294:MET:HE1	1:B:471:MET:HG2	1.52	0.92
1:A:143:ASN:ND2	1:A:146:GLU:OE2	2.05	0.90
1:A:294:MET:HB3	1:A:363:TRP:HH2	1.38	0.89
1:A:362:GLN:HG3	1:B:448:PRO:HD2	1.57	0.85
1:A:294:MET:HE1	1:A:471:MET:HG2	1.58	0.84
1:A:355:MET:HE3	1:A:360:MET:HG3	1.60	0.82
1:A:331:HIS:CD2	1:A:344:CYS:SG	2.73	0.82
1:A:310:ASP:OD2	1:A:331:HIS:HD2	1.61	0.81
1:A:294:MET:HB3	1:A:363:TRP:CH2	2.17	0.80
1:B:341:ILE:HD11	1:B:477:ASP:HB3	1.63	0.80
1:B:270:ASP:OD1	1:B:520:ARG:NH2	2.16	0.79
1:B:355:MET:HE3	1:B:360:MET:HG3	1.66	0.77
1:A:50:LEU:HD11	1:A:55:VAL:HG21	1.66	0.77
1:B:310:ASP:OD2	1:B:331:HIS:HD2	1.67	0.76
1:B:418:PRO:HG3	1:B:543:ILE:HD12	1.69	0.75
1:A:82:ARG:NH2	1:A:158:THR:O	2.19	0.75
1:A:361:ASN:OD1	1:A:365:ARG:NH1	2.20	0.75
1:A:177:THR:HB	1:A:201:THR:HB	1.68	0.74
1:A:341:ILE:HG22	1:A:342:MET:HG2	1.69	0.74
1:A:50:LEU:HB2	1:A:94:ILE:HD11	1.68	0.74
1:B:532:PRO:HD2	1:B:537:GLU:HG3	1.70	0.73
1:A:434:HIS:O	1:A:456:ASP:OD1	2.06	0.73
1:B:78:ARG:O	1:B:82:ARG:HG3	1.87	0.73
1:A:418:PRO:HG3	1:A:543:ILE:HD12	1.70	0.71
1:B:487:ILE:HD11	1:B:555:GLN:HA	1.71	0.70
1:A:400:MET:HB2	1:A:403:GLU:HG3	1.73	0.70
1:B:91:ARG:NH2	1:B:119:GLU:OE1	2.27	0.68
1:A:82:ARG:HD3	1:A:147:LEU:HD21	1.75	0.68
1:A:27:ALA:HB3	1:A:202:ARG:HG3	1.76	0.67
1:B:38:LEU:HD21	1:B:41:ASP:HB3	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:489:THR:HB	1:A:558:LYS:HE3	1.77	0.67
1:B:121:GLN:OE1	1:B:159:ASN:ND2	2.29	0.66
1:B:361:ASN:OD1	1:B:365:ARG:NH1	2.29	0.65
1:B:522:LEU:HD13	1:B:548:ARG:HG3	1.76	0.65
1:A:368:GLY:HA3	1:A:423:MET:HE3	1.77	0.65
1:B:315:HIS:NE2	1:B:319:ASP:O	2.30	0.65
1:B:558:LYS:NZ	1:B:562:ASP:OD2	2.29	0.65
1:B:276:ARG:NE	1:B:545:GLU:OE1	2.28	0.65
1:B:165:GLY:H	1:B:378:PRO:HG2	1.62	0.64
1:B:82:ARG:NH2	1:B:141:ARG:HG2	2.12	0.64
1:A:325:ASP:OD2	1:A:331:HIS:CD2	2.51	0.63
1:A:310:ASP:OD2	1:A:331:HIS:CD2	2.50	0.63
1:A:352:ALA:HB2	1:A:408:SER:HB3	1.80	0.63
1:A:152:LYS:HB3	1:A:154:LEU:H	1.64	0.63
1:B:331:HIS:CD2	1:B:344:CYS:SG	2.92	0.62
1:B:349:TYR:CD1	1:B:405:ILE:HG23	2.34	0.62
1:B:21:LEU:HA	1:B:181:GLU:HG3	1.81	0.62
1:B:294:MET:HE1	1:B:471:MET:CG	2.27	0.62
1:B:99:THR:HG22	1:B:102:ASN:ND2	2.16	0.61
1:B:341:ILE:HG22	1:B:342:MET:HG2	1.82	0.60
1:A:302:VAL:HG12	1:A:306:THR:HG21	1.82	0.60
1:B:544:TRP:HE1	1:B:556:LEU:HG	1.66	0.60
1:B:140:GLY:HA3	1:B:163:LYS:HE2	1.83	0.60
1:A:50:LEU:HD13	1:A:116:VAL:HG22	1.84	0.59
1:A:376:ASP:OD1	1:A:376:ASP:N	2.35	0.59
1:A:251:ASN:O	1:A:254:VAL:HG12	2.03	0.58
1:B:327:LYS:HZ3	1:B:329:THR:HB	1.69	0.58
1:A:363:TRP:HD1	1:B:448:PRO:CG	2.17	0.57
1:B:165:GLY:N	1:B:378:PRO:HG2	2.19	0.57
1:B:155:TYR:HD1	1:B:158:THR:HG21	1.69	0.57
1:A:469:VAL:HG13	1:A:472:ARG:HH21	1.69	0.57
1:A:550:GLY:O	1:A:553:ALA:N	2.37	0.56
1:A:356:GLY:O	1:A:360:MET:HB2	2.05	0.56
1:A:364:MET:HE2	1:A:364:MET:HA	1.86	0.56
1:A:469:VAL:HG13	1:A:472:ARG:NH2	2.21	0.56
1:A:325:ASP:OD2	1:A:344:CYS:SG	2.64	0.56
1:A:50:LEU:HD11	1:A:55:VAL:CG2	2.36	0.55
1:B:96:LEU:HD23	1:B:121:GLN:HE22	1.71	0.55
1:A:448:PRO:HD2	1:B:362:GLN:HB3	1.89	0.55
1:B:551:GLY:O	1:B:555:GLN:HG3	2.07	0.55
1:A:165:GLY:H	1:A:378:PRO:HG2	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:542:VAL:HG23	1:A:553:ALA:HB1	1.88	0.54
1:A:49:THR:HB	1:A:91:ARG:HB2	1.90	0.54
1:A:56:GLU:CD	1:A:56:GLU:H	2.16	0.54
1:B:310:ASP:OD2	1:B:331:HIS:CD2	2.55	0.54
1:A:440:LEU:HD11	1:A:443:THR:HG22	1.88	0.54
1:B:327:LYS:NZ	1:B:330:GLY:O	2.38	0.54
1:B:387:ASN:OD1	1:B:387:ASN:N	2.41	0.54
1:A:456:ASP:OD1	1:A:456:ASP:N	2.35	0.54
1:B:333:ILE:HD12	1:B:333:ILE:O	2.08	0.54
1:B:144:ASP:CB	1:B:147:LEU:HG	2.38	0.53
1:B:141:ARG:O	1:B:163:LYS:NZ	2.37	0.53
1:B:304:TRP:CD1	1:B:470:LYS:HD2	2.44	0.53
1:A:310:ASP:OD2	1:A:344:CYS:SG	2.67	0.52
1:B:384:LEU:O	1:B:414:PHE:HA	2.10	0.52
1:A:170:TYR:CE1	1:A:440:LEU:HD22	2.43	0.52
1:A:325:ASP:OD2	1:A:331:HIS:HD2	1.92	0.52
1:A:226:ARG:NH1	1:A:546:ASN:OD1	2.43	0.51
1:B:99:THR:HG23	1:B:102:ASN:H	1.75	0.51
1:B:144:ASP:HB3	1:B:147:LEU:HG	1.93	0.51
1:A:236:THR:HB	1:A:238:GLU:HG3	1.93	0.51
1:B:226:ARG:HH22	1:B:520:ARG:HG2	1.75	0.51
1:B:136:ILE:HA	1:B:166:VAL:HB	1.93	0.51
1:B:427:ILE:HA	1:B:430:ASN:HD22	1.75	0.51
1:A:50:LEU:HD23	1:A:79:PHE:CZ	2.46	0.51
1:A:291:MET:O	1:A:363:TRP:HZ3	1.93	0.51
1:B:209:SER:HB2	1:B:238:GLU:HB3	1.92	0.51
1:A:50:LEU:HD23	1:A:79:PHE:HZ	1.75	0.51
1:B:364:MET:HE2	1:B:364:MET:HA	1.93	0.51
1:A:69:LEU:O	1:A:102:ASN:ND2	2.44	0.51
1:A:206:LEU:HG	1:A:440:LEU:HD13	1.93	0.50
1:A:356:GLY:C	1:A:360:MET:HE3	2.36	0.50
1:A:294:MET:HE1	1:A:471:MET:CG	2.34	0.50
1:A:461:PHE:CE2	1:A:463:GLY:HA3	2.46	0.50
1:B:310:ASP:OD2	1:B:344:CYS:SG	2.70	0.50
1:A:154:LEU:HB3	1:A:155:TYR:HD1	1.76	0.50
1:A:363:TRP:HD1	1:B:448:PRO:HB3	1.77	0.50
1:B:62:ILE:HD13	1:B:76:VAL:HG11	1.93	0.50
1:A:96:LEU:HD21	1:A:159:ASN:HB3	1.93	0.50
1:B:426:ALA:O	1:B:430:ASN:HB3	2.12	0.50
1:B:311:PRO:HB2	1:B:313:TYR:CE1	2.47	0.49
1:B:302:VAL:HG13	1:B:306:THR:HB	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:542:VAL:CG2	1:A:553:ALA:HB1	2.42	0.49
1:B:323:PHE:CD1	1:B:405:ILE:HG21	2.48	0.49
1:A:165:GLY:N	1:A:378:PRO:HG2	2.28	0.49
1:A:268:ASN:HB3	1:A:272:PRO:HD3	1.95	0.49
1:B:210:LEU:HD12	1:B:210:LEU:N	2.27	0.49
1:B:214:LEU:HD13	1:B:564:TRP:HB2	1.95	0.49
1:B:544:TRP:NE1	1:B:556:LEU:HG	2.28	0.49
1:B:544:TRP:CD1	1:B:553:ALA:HA	2.48	0.48
1:A:349:TYR:CD1	1:A:405:ILE:HG23	2.48	0.48
1:B:139:VAL:O	1:B:254:VAL:HA	2.14	0.48
1:A:247:SER:O	1:A:272:PRO:HB3	2.14	0.48
1:A:375:VAL:HA	1:A:437:PRO:O	2.13	0.48
1:A:44:PRO:HA	1:A:121:GLN:O	2.13	0.48
1:A:258:ASN:HB2	1:A:261:ASP:H	1.78	0.48
1:B:69:LEU:HD22	1:B:98:LEU:HD22	1.96	0.48
1:B:497:LYS:HG3	1:B:498:THR:N	2.29	0.48
1:A:306:THR:O	1:A:335:ASN:HA	2.14	0.48
1:A:489:THR:HG23	1:A:492:TYR:O	2.14	0.48
1:B:461:PHE:CE2	1:B:463:GLY:HA3	2.49	0.47
1:A:291:MET:O	1:A:363:TRP:CZ3	2.68	0.47
1:A:489:THR:HB	1:A:558:LYS:CE	2.44	0.47
1:B:226:ARG:NH2	1:B:520:ARG:HG2	2.30	0.47
1:A:75:ASP:OD1	1:A:141:ARG:NH1	2.47	0.47
1:A:233:ASP:HB2	1:A:240:LEU:HD21	1.96	0.47
1:B:303:ASP:OD2	1:B:304:TRP:N	2.48	0.47
1:A:139:VAL:O	1:A:254:VAL:HA	2.14	0.47
1:B:406:SER:HB3	1:B:411:GLN:O	2.15	0.47
1:B:140:GLY:H	1:B:163:LYS:HG2	1.80	0.47
1:B:325:ASP:OD2	1:B:331:HIS:CD2	2.67	0.47
1:A:360:MET:HE1	1:A:404:THR:HG23	1.97	0.47
1:B:246:PRO:HG3	1:B:270:ASP:HB3	1.97	0.47
1:A:294:MET:HB2	1:A:294:MET:HE2	1.44	0.47
1:A:365:ARG:HE	1:A:371:GLN:NE2	2.13	0.47
1:B:302:VAL:HG11	1:B:347:TYR:OH	2.15	0.47
1:B:363:TRP:HD1	1:B:364:MET:HE3	1.80	0.47
1:A:363:TRP:HD1	1:B:448:PRO:CB	2.29	0.46
1:A:262:TYR:OH	1:A:266:ARG:HD3	2.15	0.46
1:A:281:VAL:HG21	1:A:383:GLY:HA2	1.98	0.46
1:B:206:LEU:HG	1:B:440:LEU:HD13	1.97	0.46
1:A:310:ASP:OD2	1:A:325:ASP:OD2	2.34	0.46
1:A:562:ASP:O	1:A:566:LEU:HB2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:360:MET:HB2	1:B:360:MET:HE3	1.68	0.46
1:B:360:MET:HE1	1:B:404:THR:HG23	1.98	0.46
1:A:331:HIS:HB3	1:A:342:MET:CE	2.46	0.46
1:A:361:ASN:O	1:A:365:ARG:HG3	2.15	0.46
1:A:532:PRO:CD	1:A:537:GLU:HG3	2.46	0.46
1:B:82:ARG:HH22	1:B:141:ARG:HG2	1.81	0.46
1:B:121:GLN:HG2	1:B:122:MET:N	2.30	0.46
1:A:345:ASP:HB3	1:A:349:TYR:CZ	2.51	0.46
1:A:21:LEU:HD23	1:A:21:LEU:HA	1.76	0.45
1:A:173:LEU:HD22	1:A:204:ASN:HB2	1.98	0.45
1:B:394:THR:HG22	1:B:395:ARG:HG3	1.98	0.45
1:B:573:ILE:HD13	1:B:573:ILE:HG21	1.75	0.45
1:A:549:HIS:ND1	1:A:549:HIS:N	2.63	0.45
1:A:549:HIS:O	1:A:552:SER:HB2	2.16	0.45
1:A:303:ASP:HB3	1:A:305:ALA:H	1.82	0.45
1:A:352:ALA:CB	1:A:408:SER:HB3	2.44	0.45
1:A:391:LYS:NZ	1:A:397:SER:HB2	2.32	0.45
1:A:303:ASP:HB2	1:A:306:THR:OG1	2.17	0.44
1:A:456:ASP:HB2	1:B:452:ARG:HG3	1.98	0.44
1:B:49:THR:HG21	1:B:119:GLU:OE2	2.17	0.44
1:A:124:ARG:NE	1:A:167:GLU:OE2	2.51	0.44
1:B:154:LEU:O	1:B:178:PRO:HG3	2.17	0.44
1:B:563:TYR:CE2	1:B:573:ILE:HG13	2.53	0.44
1:A:387:ASN:OD1	1:A:387:ASN:N	2.47	0.44
1:B:556:LEU:O	1:B:559:PRO:HD2	2.18	0.44
1:B:400:MET:HE3	1:B:400:MET:HB3	1.91	0.44
1:B:141:ARG:NH1	1:B:159:ASN:HB3	2.32	0.44
1:B:447:LYS:HE3	1:B:447:LYS:HB2	1.80	0.44
1:B:210:LEU:HD11	1:B:439:VAL:CG2	2.48	0.43
1:B:356:GLY:O	1:B:360:MET:HB2	2.17	0.43
1:B:376:ASP:OD1	1:B:376:ASP:N	2.48	0.43
1:A:341:ILE:HD11	1:A:477:ASP:HB3	2.01	0.43
1:B:430:ASN:ND2	1:B:433:SER:H	2.16	0.43
1:A:58:VAL:O	1:A:62:ILE:HG13	2.18	0.43
1:A:394:THR:HG22	1:A:395:ARG:HG3	2.01	0.43
1:B:173:LEU:CD1	1:B:443:THR:HG21	2.48	0.43
1:B:174:LEU:O	1:B:203:GLY:HA3	2.19	0.43
1:B:294:MET:HE2	1:B:294:MET:HB2	1.48	0.43
1:A:24:LEU:HD21	1:A:181:GLU:HG2	2.01	0.43
1:A:363:TRP:CD1	1:B:448:PRO:HB3	2.54	0.43
1:A:236:THR:CG2	1:A:238:GLU:HG3	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:288:ILE:HG12	1:B:414:PHE:HE2	1.83	0.42
1:A:478:VAL:HG11	1:A:497:LYS:HA	2.01	0.42
1:B:544:TRP:HB2	1:B:547:GLY:HA3	2.01	0.42
1:A:363:TRP:HD1	1:B:448:PRO:HG3	1.84	0.42
1:A:475:MET:HA	1:A:478:VAL:HG23	2.02	0.42
1:B:147:LEU:O	1:B:150:ILE:HG22	2.18	0.42
1:B:152:LYS:HG2	1:B:153:ASP:H	1.84	0.42
1:A:173:LEU:CD1	1:A:443:THR:HG21	2.49	0.42
1:B:563:TYR:HE2	1:B:573:ILE:HG13	1.84	0.42
1:A:22:GLN:O	1:A:180:TYR:HA	2.20	0.42
1:B:372:LYS:HG3	1:B:382:GLU:OE2	2.19	0.42
1:A:32:TYR:HB2	1:A:207:TYR:CD1	2.54	0.42
1:A:155:TYR:CZ	1:A:175:HIS:CD2	3.08	0.42
1:A:236:THR:HG23	1:A:453:ASN:O	2.19	0.42
1:B:401:LYS:HD2	1:B:401:LYS:HA	1.75	0.42
1:A:214:LEU:HD11	1:A:560:VAL:HG12	2.02	0.42
1:B:151:ASP:OD1	1:B:151:ASP:N	2.48	0.42
1:A:360:MET:HE1	1:A:404:THR:CG2	2.50	0.41
1:A:520:ARG:HG3	1:A:520:ARG:HH11	1.85	0.41
1:A:456:ASP:C	1:B:452:ARG:HG3	2.45	0.41
1:B:489:THR:HG23	1:B:492:TYR:O	2.19	0.41
1:A:86:ALA:HB1	1:A:90:GLU:HG2	2.02	0.41
1:A:261:ASP:O	1:A:264:SER:OG	2.34	0.41
1:B:293:ALA:HB1	1:B:336:MET:HE2	2.00	0.41
1:A:25:PRO:HB3	1:A:157:GLY:CA	2.50	0.41
1:A:74:GLU:OE2	1:A:78:ARG:NH1	2.53	0.41
1:A:134:HIS:O	1:A:275:ASN:ND2	2.53	0.41
1:A:352:ALA:HB2	1:A:408:SER:CB	2.48	0.41
1:B:487:ILE:HD13	1:B:487:ILE:HA	1.79	0.41
1:A:99:THR:H	1:A:99:THR:HG23	1.64	0.41
1:A:464:THR:HG22	1:A:466:GLU:H	1.85	0.41
1:A:130:ASP:O	1:A:247:SER:OG	2.37	0.41
1:A:373:THR:HG22	1:A:423:MET:HE1	2.03	0.41
1:B:50:LEU:HD13	1:B:94:ILE:HD11	2.02	0.41
1:A:291:MET:CB	1:A:364:MET:HE1	2.50	0.41
1:A:324:ARG:HE	1:A:324:ARG:HB3	1.46	0.41
1:B:302:VAL:HG12	1:B:303:ASP:N	2.36	0.41
1:A:52:LYS:HD2	1:A:83:ILE:HG23	2.02	0.41
1:A:411:GLN:HB3	1:A:412:GLY:H	1.77	0.41
1:B:246:PRO:HG3	1:B:270:ASP:CB	2.50	0.41
1:A:62:ILE:HG13	1:A:62:ILE:H	1.57	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:66:GLN:HG3	1:A:71:LEU:HB2	2.02	0.41
1:A:167:GLU:OE1	1:A:174:LEU:HD13	2.21	0.41
1:A:209:SER:HB2	1:A:238:GLU:HB3	2.03	0.41
1:B:50:LEU:HD22	1:B:79:PHE:HZ	1.86	0.41
1:B:173:LEU:HD23	1:B:173:LEU:HA	1.86	0.41
1:B:173:LEU:HD13	1:B:443:THR:HG21	2.02	0.41
1:B:375:VAL:HA	1:B:437:PRO:O	2.21	0.41
1:B:391:LYS:HE2	1:B:397:SER:HB2	2.02	0.41
1:B:548:ARG:HB3	1:B:549:HIS:H	1.69	0.41
1:A:25:PRO:HB3	1:A:157:GLY:HA3	2.03	0.41
1:A:149:SER:O	1:A:152:LYS:N	2.54	0.41
1:B:264:SER:O	1:B:268:ASN:HB2	2.21	0.41
1:B:294:MET:HA	1:B:297:LEU:HD12	2.03	0.40
1:A:227:GLY:HA3	1:A:543:ILE:O	2.22	0.40
1:A:42:ASN:HA	1:A:123:THR:O	2.21	0.40
1:A:532:PRO:HD2	1:A:537:GLU:HG3	2.02	0.40
1:B:503:VAL:HG11	1:B:521:GLN:O	2.20	0.40
1:B:69:LEU:HA	1:B:102:ASN:HB2	2.03	0.40
1:B:275:ASN:CG	1:B:278:VAL:HG22	2.47	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:466:GLU:OE1	1:A:472:ARG:NH2[3_656]	2.09	0.11

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	504/631 (80%)	481 (95%)	23 (5%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	495/631 (78%)	470 (95%)	24 (5%)	1 (0%)	43	72
All	All	999/1262 (79%)	951 (95%)	47 (5%)	1 (0%)	48	76

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	144	ASP

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	430/521 (82%)	430 (100%)	0	100	100
1	B	419/521 (80%)	419 (100%)	0	100	100
All	All	849/1042 (82%)	849 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	42	ASN
1	A	279	GLN
1	A	331	HIS
1	A	371	GLN
1	B	64	GLN
1	B	121	GLN
1	B	159	ASN
1	B	279	GLN
1	B	331	HIS
1	B	362	GLN
1	B	366	GLN
1	B	411	GLN
1	B	430	ASN

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Mol	Chain	Res	Type
1	B	546	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 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	516/631 (81%)	-0.15	3 (0%) 85 73	19, 38, 83, 99	0
1	B	509/631 (80%)	0.03	12 (2%) 59 40	21, 46, 107, 132	0
All	All	1025/1262 (81%)	-0.06	15 (1%) 72 53	19, 41, 94, 132	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	570	LYS	3.1
1	A	575	PRO	3.1
1	B	83	ILE	3.1
1	B	57	ASN	2.7
1	B	321	HIS	2.6
1	A	149	SER	2.5
1	B	333	ILE	2.4
1	B	150	ILE	2.4
1	B	94	ILE	2.3
1	B	344	CYS	2.3
1	B	111	TYR	2.2
1	B	152	LYS	2.1
1	B	411	GLN	2.1
1	B	519	GLU	2.0
1	A	573	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.