



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 04:57 AM UTC

PDB ID : 4AD8 / pdb_00004ad8
Title : Crystal structure of a deletion mutant of Deinococcus radiodurans RecN
Authors : Pellegrino, S.; Radzimanowski, J.; de Sanctis, D.; McSweeney, S.; Timmins, J.
Deposited on : 2011-12-22
Resolution : 4.00 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

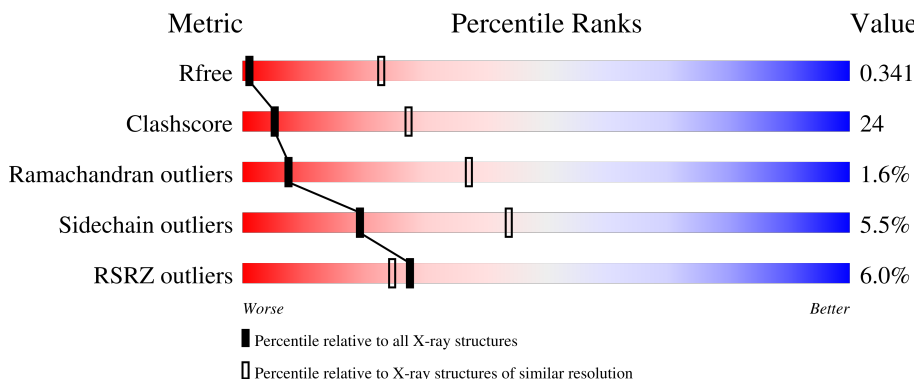
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.00 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	1082 (4.20-3.80)
Clashscore	190562	1129 (4.20-3.80)
Ramachandran outliers	187476	1064 (4.20-3.80)
Sidechain outliers	187428	1055 (4.20-3.80)
RSRZ outliers	180081	1082 (4.20-3.80)

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	517	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3416 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 DNA REPAIR PROTEIN REC�.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	452	Total	C	N	O	S	0	0	0
			3416	2111	630	670	5			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	GLY	-	expression tag	UNP Q9WXF2
A	-4	ILE	-	expression tag	UNP Q9WXF2
A	-3	ASP	-	expression tag	UNP Q9WXF2
A	-2	PRO	-	expression tag	UNP Q9WXF2
A	-1	PHE	-	expression tag	UNP Q9WXF2
A	0	THR	-	expression tag	UNP Q9WXF2
A	238	GLU	-	linker	UNP Q9WXF2
A	239	SER	-	linker	UNP Q9WXF2
A	240	SER	-	linker	UNP Q9WXF2
A	241	LYS	-	linker	UNP Q9WXF2
A	242	HIS	-	linker	UNP Q9WXF2
A	243	PRO	-	linker	UNP Q9WXF2
A	244	THR	-	linker	UNP Q9WXF2
A	245	SER	-	linker	UNP Q9WXF2
A	246	LEU	-	linker	UNP Q9WXF2
A	247	VAL	-	linker	UNP Q9WXF2
A	248	PRO	-	linker	UNP Q9WXF2
A	249	ARG	-	linker	UNP Q9WXF2
A	250	GLY	-	linker	UNP Q9WXF2
A	251	SER	-	linker	UNP Q9WXF2

4 Data and refinement statistics

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	72.20Å 62.49Å 145.53Å 90.00° 98.39° 90.00°	Depositor
Resolution (Å)	47.03 – 4.00 47.03 – 4.00	Depositor EDS
% Data completeness (in resolution range)	96.9 (47.03-4.00) 97.1 (47.03-4.00)	Depositor EDS
R_{merge}	0.28	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.96 (at 4.00Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.325 , 0.347 0.325 , 0.341	Depositor DCC
R_{free} test set	246 reflections (4.53%)	wwPDB-VP
Wilson B-factor (Å ²)	87.2	Xtriage
Anisotropy	0.384	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 6.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.36$, $\langle L^2 \rangle = 0.19$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	3416	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.59% 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	0.30	0/3458	0.76	6/4675 (0.1%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	190	GLU	N-CA-C	6.30	119.13	111.82
1	A	549	ASN	CB-CA-C	-6.08	109.55	116.54
1	A	547	SER	CB-CA-C	-5.42	110.35	116.63
1	A	155	LEU	N-CA-C	5.29	120.60	113.72
1	A	417	GLU	CA-C-N	5.02	124.33	118.85
1	A	417	GLU	C-N-CA	5.02	124.33	118.85

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	3416	0	3403	166	0
All	All	3416	0	3403	166	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 24.

All (166) 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:450:LEU:HD23	1:A:451:SER:N	1.90	0.86
1:A:125:LEU:O	1:A:127:GLY:N	2.10	0.83
1:A:431:SER:HB2	1:A:436:GLU:HB3	1.61	0.82
1:A:185:ALA:HB1	1:A:365:VAL:HG22	1.60	0.81
1:A:471:ASP:OD1	1:A:472:GLU:HG2	1.78	0.81
1:A:423:LEU:H	1:A:423:LEU:HD23	1.46	0.80
1:A:469:VAL:HG22	1:A:499:LEU:HB2	1.63	0.80
1:A:449:GLU:H	1:A:449:GLU:CD	1.91	0.79
1:A:94:LEU:CD2	1:A:115:LEU:HB2	2.17	0.73
1:A:376:GLY:HA3	1:A:423:LEU:HD21	1.70	0.73
1:A:125:LEU:HD13	1:A:130:VAL:HB	1.69	0.73
1:A:543:ALA:O	1:A:546:LEU:O	2.06	0.73
1:A:190:GLU:OE1	1:A:191:ARG:N	2.22	0.72
1:A:460:VAL:HG13	1:A:461:LEU:HD13	1.74	0.69
1:A:327:LYS:HG3	1:A:332:PRO:O	1.93	0.69
1:A:160:GLN:O	1:A:163:LEU:HG	1.92	0.69
1:A:486:ALA:HB2	1:A:507:ILE:HG12	1.76	0.68
1:A:120:ARG:HG3	1:A:121:GLY:H	1.59	0.68
1:A:415:LEU:HD12	1:A:416:ALA:H	1.57	0.68
1:A:82:ALA:HB1	1:A:115:LEU:HD11	1.76	0.67
1:A:168:VAL:HG11	1:A:382:ALA:HB1	1.77	0.67
1:A:452:ARG:HG3	1:A:473:VAL:HG23	1.77	0.66
1:A:130:VAL:HG12	1:A:131:SER:H	1.61	0.64
1:A:175:TYR:OH	1:A:418:PRO:O	2.15	0.64
1:A:195:SER:O	1:A:199:ARG:HB2	1.97	0.64
1:A:452:ARG:NH1	1:A:473:VAL:O	2.31	0.64
1:A:335:GLU:N	1:A:335:GLU:OE1	2.31	0.63
1:A:415:LEU:HD12	1:A:416:ALA:N	2.12	0.63
1:A:459:THR:HG21	1:A:488:GLN:HG3	1.80	0.63
1:A:437:GLU:O	1:A:438:LEU:HB2	1.98	0.62
1:A:450:LEU:HD23	1:A:450:LEU:C	2.25	0.61
1:A:154:LEU:HB2	1:A:454:MET:HE1	1.83	0.61
1:A:413:SER:O	1:A:424:SER:HA	2.00	0.61
1:A:452:ARG:CG	1:A:473:VAL:HG23	2.31	0.61
1:A:45:ILE:HG12	1:A:69:ILE:HD11	1.82	0.60
1:A:431:SER:HB3	1:A:438:LEU:HA	1.83	0.59
1:A:150:SER:OG	1:A:454:MET:SD	2.52	0.58
1:A:175:TYR:CZ	1:A:422:GLY:HA2	2.37	0.58
1:A:466:PRO:HA	1:A:496:ARG:HH11	1.68	0.58
1:A:92:LYS:HG3	1:A:93:GLU:HG2	1.85	0.57
1:A:395:LEU:HB3	1:A:399:ARG:HD2	1.86	0.57
1:A:449:GLU:N	1:A:449:GLU:OE2	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:38:GLU:HB3	1:A:97:THR:OG1	2.04	0.57
1:A:449:GLU:CD	1:A:449:GLU:N	2.60	0.57
1:A:212:GLU:OE1	1:A:330:TYR:OH	2.23	0.57
1:A:147:TRP:H	1:A:150:SER:HB2	1.70	0.56
1:A:521:VAL:HG22	1:A:526:THR:HG23	1.88	0.56
1:A:69:ILE:HG22	1:A:70:ILE:HD12	1.88	0.56
1:A:333:THR:HG22	1:A:335:GLU:H	1.70	0.55
1:A:163:LEU:HD12	1:A:164:LEU:N	2.21	0.55
1:A:32:PRO:O	1:A:466:PRO:HB3	2.07	0.54
1:A:450:LEU:HD23	1:A:451:SER:CA	2.37	0.54
1:A:151:ALA:HA	1:A:155:LEU:CB	2.37	0.54
1:A:151:ALA:HA	1:A:155:LEU:HB2	1.89	0.54
1:A:151:ALA:O	1:A:156:SER:OG	2.20	0.54
1:A:156:SER:HB3	1:A:157:PRO:CD	2.38	0.54
1:A:70:ILE:O	1:A:74:LEU:HB2	2.08	0.53
1:A:400:GLU:O	1:A:402:GLY:N	2.43	0.52
1:A:442:SER:C	1:A:444:VAL:H	2.16	0.52
1:A:448:GLY:N	1:A:449:GLU:OE2	2.42	0.52
1:A:120:ARG:HG3	1:A:121:GLY:N	2.24	0.52
1:A:70:ILE:HA	1:A:74:LEU:HD13	1.91	0.52
1:A:62:GLU:HG3	1:A:519:LYS:HE3	1.91	0.52
1:A:541:GLU:O	1:A:545:MET:HG3	2.10	0.52
1:A:518:GLU:HG2	1:A:519:LYS:H	1.72	0.52
1:A:42:LEU:HG	1:A:94:LEU:HD12	1.92	0.52
1:A:52:LEU:HD12	1:A:52:LEU:O	2.09	0.52
1:A:459:THR:HG22	1:A:492:LEU:HB2	1.92	0.52
1:A:361:LEU:O	1:A:365:VAL:HG23	2.10	0.51
1:A:394:LEU:O	1:A:397:VAL:HG12	2.11	0.51
1:A:395:LEU:HD21	1:A:408:MET:HB3	1.92	0.51
1:A:506:GLN:H	1:A:506:GLN:CD	2.15	0.51
1:A:546:LEU:HD12	1:A:547:SER:N	2.26	0.51
1:A:146:HIS:HA	1:A:150:SER:HB2	1.91	0.51
1:A:56:PHE:C	1:A:56:PHE:CD1	2.88	0.50
1:A:492:LEU:O	1:A:492:LEU:HD23	2.11	0.50
1:A:199:ARG:NH1	1:A:202:GLN:OE1	2.44	0.50
1:A:539:LEU:O	1:A:542:ILE:HG12	2.11	0.50
1:A:517:VAL:HG22	1:A:530:VAL:HG22	1.93	0.50
1:A:41:ASN:ND2	1:A:91:GLU:HG3	2.27	0.50
1:A:88:ARG:HB3	1:A:91:GLU:HB2	1.92	0.50
1:A:130:VAL:HG12	1:A:131:SER:N	2.26	0.49
1:A:132:VAL:O	1:A:136:GLN:HG3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:156:SER:HB3	1:A:157:PRO:HD2	1.93	0.49
1:A:456:ALA:O	1:A:460:VAL:HG12	2.12	0.49
1:A:161:ARG:NE	1:A:165:ASP:OD2	2.46	0.49
1:A:144:THR:HB	1:A:468:VAL:HG12	1.94	0.49
1:A:125:LEU:HB2	1:A:130:VAL:HG21	1.95	0.48
1:A:94:LEU:HD21	1:A:115:LEU:HB2	1.94	0.48
1:A:36:ARG:HB3	1:A:99:PHE:HB2	1.95	0.48
1:A:546:LEU:HD12	1:A:547:SER:H	1.79	0.48
1:A:125:LEU:HD13	1:A:130:VAL:CB	2.40	0.48
1:A:527:VAL:HG12	1:A:528:SER:N	2.29	0.47
1:A:70:ILE:HG23	1:A:469:VAL:HG11	1.96	0.47
1:A:366:ASP:O	1:A:369:HIS:HB3	2.14	0.47
1:A:219:ASP:O	1:A:222:GLU:HB2	2.14	0.47
1:A:125:LEU:CD1	1:A:130:VAL:HB	2.43	0.46
1:A:458:SER:O	1:A:462:GLY:N	2.46	0.46
1:A:511:ALA:O	1:A:538:ARG:NH2	2.46	0.46
1:A:523:ASP:HA	1:A:524:GLY:HA2	1.51	0.46
1:A:423:LEU:H	1:A:423:LEU:CD2	2.23	0.46
1:A:471:ASP:OD1	1:A:472:GLU:N	2.49	0.46
1:A:388:GLU:N	1:A:389:PRO:HD2	2.31	0.46
1:A:34:LEU:HG	1:A:52:LEU:HD11	1.98	0.46
1:A:485:VAL:O	1:A:489:LEU:HG	2.16	0.46
1:A:72:ASP:O	1:A:76:LEU:HD23	2.16	0.45
1:A:562:LEU:C	1:A:562:LEU:HD12	2.42	0.45
1:A:537:GLU:O	1:A:541:GLU:HG2	2.16	0.45
1:A:539:LEU:HD11	1:A:559:ARG:CG	2.47	0.45
1:A:110:SER:O	1:A:110:SER:OG	2.30	0.45
1:A:348:LEU:C	1:A:348:LEU:HD23	2.42	0.44
1:A:188:ARG:O	1:A:191:ARG:HG2	2.18	0.44
1:A:144:THR:O	1:A:469:VAL:N	2.46	0.44
1:A:436:GLU:O	1:A:437:GLU:HB3	2.17	0.44
1:A:394:LEU:O	1:A:398:ILE:HG13	2.18	0.44
1:A:370:ALA:O	1:A:373:LEU:HB3	2.17	0.44
1:A:81:ARG:HB2	1:A:81:ARG:NH1	2.33	0.44
1:A:171:GLU:OE1	1:A:171:GLU:N	2.43	0.44
1:A:146:HIS:ND1	1:A:454:MET:SD	2.91	0.43
1:A:455:LEU:HD21	1:A:488:GLN:HB3	2.00	0.43
1:A:36:ARG:HG2	1:A:37:LEU:N	2.33	0.43
1:A:394:LEU:CD2	1:A:460:VAL:HG11	2.48	0.43
1:A:466:PRO:O	1:A:496:ARG:HB3	2.19	0.43
1:A:169:THR:O	1:A:173:GLN:HG3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:324:SER:HA	1:A:327:LYS:HE2	2.01	0.43
1:A:401:LEU:HD23	1:A:485:VAL:HG22	2.01	0.43
1:A:45:ILE:HD12	1:A:45:ILE:N	2.33	0.43
1:A:56:PHE:HE1	1:A:500:VAL:HG12	1.83	0.43
1:A:442:SER:C	1:A:444:VAL:N	2.77	0.43
1:A:544:ARG:HA	1:A:549:ASN:O	2.17	0.43
1:A:40:ARG:NE	1:A:41:ASN:OD1	2.52	0.43
1:A:394:LEU:HD12	1:A:408:MET:HE1	2.01	0.43
1:A:486:ALA:HA	1:A:489:LEU:HD12	2.00	0.43
1:A:327:LYS:O	1:A:331:GLY:HA3	2.19	0.43
1:A:431:SER:HB3	1:A:438:LEU:CA	2.49	0.43
1:A:450:LEU:O	1:A:454:MET:CG	2.67	0.42
1:A:146:HIS:O	1:A:147:TRP:HB2	2.18	0.42
1:A:183:ARG:HD3	1:A:183:ARG:HA	1.84	0.42
1:A:416:ALA:O	1:A:417:GLU:HB2	2.19	0.42
1:A:412:LEU:HA	1:A:425:ASP:O	2.19	0.42
1:A:142:ARG:HA	1:A:466:PRO:HD2	2.01	0.42
1:A:418:PRO:O	1:A:419:ALA:HB3	2.18	0.42
1:A:163:LEU:HD13	1:A:390:LEU:HD21	2.02	0.42
1:A:166:ARG:HH21	1:A:461:LEU:HG	1.84	0.42
1:A:161:ARG:CD	1:A:421:TYR:HB2	2.50	0.42
1:A:474:ASP:OD2	1:A:502:THR:HG22	2.20	0.42
1:A:56:PHE:C	1:A:56:PHE:HD1	2.28	0.42
1:A:152:VAL:O	1:A:152:VAL:HG12	2.20	0.42
1:A:226:LEU:HD11	1:A:316:VAL:HG13	2.02	0.42
1:A:416:ALA:O	1:A:417:GLU:CB	2.68	0.42
1:A:161:ARG:HG2	1:A:165:ASP:OD2	2.20	0.41
1:A:182:TRP:O	1:A:186:VAL:HG23	2.20	0.41
1:A:148:GLN:OE1	1:A:148:GLN:HA	2.20	0.41
1:A:385:ARG:NH1	1:A:386:GLU:OE2	2.54	0.41
1:A:39:ILE:O	1:A:47:GLN:HA	2.20	0.41
1:A:66:GLY:C	1:A:501:VAL:HG21	2.45	0.41
1:A:161:ARG:HG3	1:A:426:VAL:HG21	2.02	0.41
1:A:236:LEU:C	1:A:236:LEU:HD23	2.46	0.41
1:A:372:LEU:C	1:A:372:LEU:HD23	2.46	0.41
1:A:449:GLU:O	1:A:453:VAL:HG23	2.21	0.41
1:A:147:TRP:CE3	1:A:147:TRP:HA	2.56	0.41
1:A:38:GLU:HA	1:A:48:LEU:O	2.20	0.40
1:A:514:HIS:CG	1:A:533:LEU:HD12	2.56	0.40
1:A:56:PHE:HD1	1:A:57:CYS:N	2.19	0.40
1:A:428:LEU:C	1:A:428:LEU:HD23	2.46	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:546:LEU:O	1:A:547:SER:OG	2.25	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	446/517 (86%)	403 (90%)	36 (8%)	7 (2%)	7	37

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	126	SER
1	A	147	TRP
1	A	47	GLN
1	A	401	LEU
1	A	417	GLU
1	A	535	GLY
1	A	332	PRO

5.3.2 Protein sidechains [i](#)

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	348/399 (87%)	329 (94%)	19 (6%)	19	44

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	ARG
1	A	70	ILE
1	A	85	ASP
1	A	94	LEU
1	A	126	SER
1	A	147	TRP
1	A	155	LEU
1	A	190	GLU
1	A	227	ASN
1	A	330	TYR
1	A	415	LEU
1	A	421	TYR
1	A	449	GLU
1	A	450	LEU
1	A	454	MET
1	A	473	VAL
1	A	534	THR
1	A	546	LEU
1	A	552	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	179	HIS
1	A	211	GLN
1	A	227	ASN
1	A	369	HIS
1	A	488	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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 ⓘ

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	452/517 (87%)	0.76	27 (5%)	27 24	70, 70, 70, 70	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	92	LYS	4.9
1	A	129	VAL	4.2
1	A	118	ALA	3.9
1	A	117	SER	3.4
1	A	119	GLY	3.4
1	A	110	SER	3.4
1	A	507	ILE	3.0
1	A	406	ALA	2.8
1	A	530	VAL	2.6
1	A	403	MET	2.6
1	A	505	ALA	2.4
1	A	37	LEU	2.4
1	A	408	MET	2.3
1	A	123	ALA	2.3
1	A	346	GLU	2.2
1	A	525	ARG	2.2
1	A	134	GLU	2.2
1	A	42	LEU	2.2
1	A	188	ARG	2.1
1	A	434	PRO	2.1
1	A	553	ALA	2.1
1	A	125	LEU	2.1
1	A	86	LEU	2.1
1	A	390	LEU	2.1
1	A	124	ARG	2.0
1	A	111	ALA	2.0
1	A	157	PRO	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.