



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 02:18 AM UTC

PDB ID : 1JI6 / pdb_00001ji6
Title : CRYSTAL STRUCTURE OF THE INSECTICIDAL BACTERIAL DEL EN-
DOTOXIN CRY3Bb1 BACILLUS THURINGIENSIS
Authors : Cody, V.
Deposited on : 2001-06-29
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

<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
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

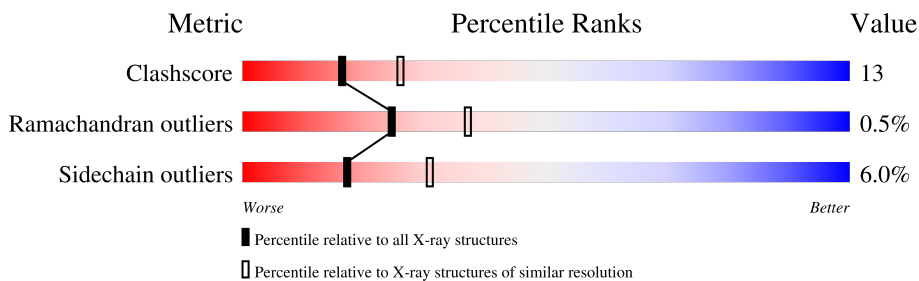
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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))
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (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 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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	589	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 5001 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 PESTICIDIAL CRYSTAL PROTEIN CRY3BB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	589	4750	3045	789	908	8	0	0	0

- Molecule 2 is water.

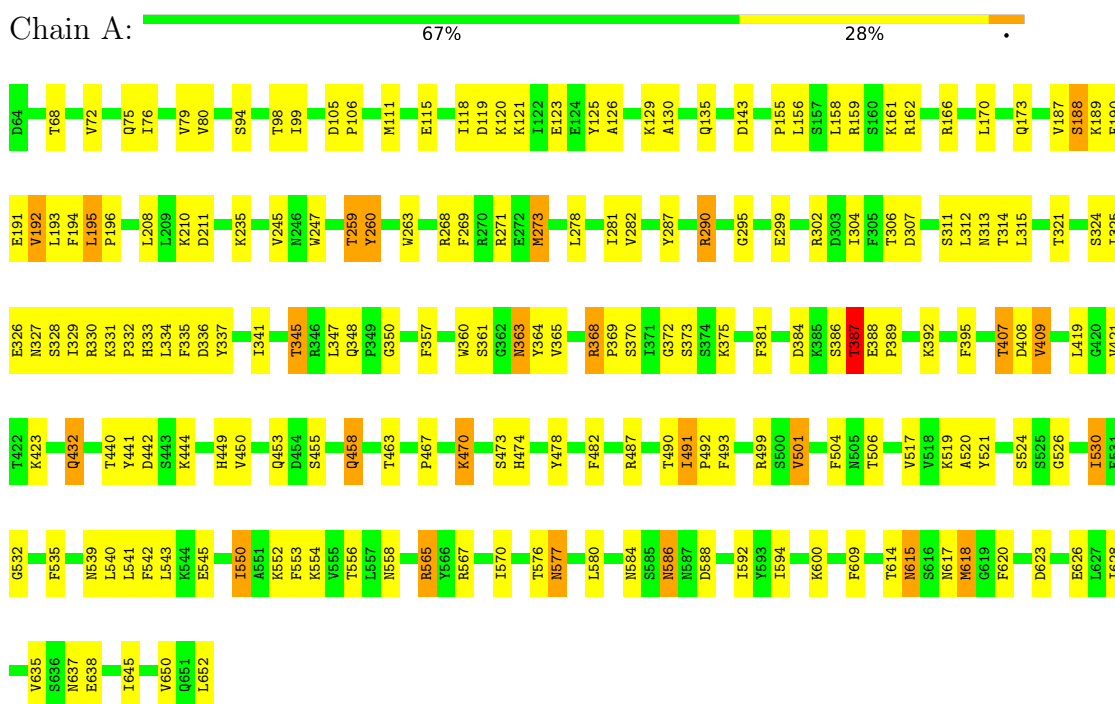
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	251	Total	O	0	0
			251	251		

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. 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. 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.

Note EDS was not executed.

- Molecule 1: PESTICIDIAL CRYSTAL PROTEIN CRY3BB



4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	122.44Å 131.81Å 105.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.40	Depositor
% Data completeness (in resolution range)	72.2 (8.00-2.40)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	0.02	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.175 , 0.253	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	5001	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

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	0.77	5/4867 (0.1%)	1.14	36/6602 (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	1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	618	MET	SD-CE	-9.73	1.55	1.79
1	A	273	MET	SD-CE	-8.79	1.57	1.79
1	A	190	PHE	C-N	8.13	1.45	1.33
1	A	119	ASP	C-N	-7.41	1.23	1.33
1	A	192	VAL	C-N	5.44	1.41	1.33

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	192	VAL	O-C-N	-10.42	111.34	121.87
1	A	450	VAL	N-CA-C	-9.19	97.58	109.80
1	A	295	GLY	N-CA-C	-9.02	103.39	111.95
1	A	453	GLN	N-CA-C	8.61	122.89	110.24
1	A	387	THR	N-CA-C	-7.90	103.86	113.97
1	A	577	ASN	N-CA-C	-7.30	99.68	110.48
1	A	190	PHE	O-C-N	7.10	131.72	121.78
1	A	532	GLY	CA-C-N	6.74	126.69	119.28
1	A	532	GLY	C-N-CA	6.74	126.69	119.28
1	A	287	TYR	N-CA-C	-6.69	105.12	113.28
1	A	440	THR	N-CA-C	6.51	119.32	109.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	260	TYR	N-CA-C	-6.46	104.32	111.36
1	A	588	ASP	N-CA-C	-6.35	101.08	110.48
1	A	269	PHE	N-CA-C	-6.34	104.29	111.14
1	A	295	GLY	CA-C-O	-6.21	118.18	122.22
1	A	567	ARG	N-CA-C	-6.11	99.75	109.76
1	A	504	PHE	N-CA-C	5.95	120.40	113.20
1	A	190	PHE	CA-C-N	-5.86	109.16	121.64
1	A	190	PHE	C-N-CA	-5.86	109.16	121.64
1	A	449	HIS	N-CA-C	5.84	119.44	107.69
1	A	194	PHE	O-C-N	-5.74	113.89	122.39
1	A	586	ASN	N-CA-C	-5.67	106.22	113.02
1	A	623	ASP	N-CA-C	5.64	120.28	113.17
1	A	306	THR	N-CA-C	-5.61	103.12	110.53
1	A	580	LEU	N-CA-C	-5.61	100.98	109.85
1	A	645	ILE	N-CA-C	-5.61	99.67	107.80
1	A	345	THR	N-CA-C	5.56	118.54	109.59
1	A	68	THR	N-CA-C	-5.53	105.16	111.14
1	A	368	ARG	CA-C-N	5.46	126.22	120.11
1	A	368	ARG	C-N-CA	5.46	126.22	120.11
1	A	350	GLY	N-CA-C	-5.45	102.78	112.54
1	A	290	ARG	N-CA-C	-5.33	106.45	113.12
1	A	487	ARG	N-CA-C	5.13	118.28	111.30
1	A	501	VAL	N-CA-C	5.06	115.76	108.93
1	A	455	SER	N-CA-C	5.03	117.15	111.11
1	A	195	LEU	N-CA-C	5.03	120.92	109.81

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	192	VAL	Mainchain

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	4750	0	4623	122	9

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	251	0	0	9	9
All	All	5001	0	4623	122	9

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.

All (122) 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:189:LYS:HB2	2:A:780:HOH:O	1.42	1.17
1:A:618:MET:HE2	1:A:620:PHE:CZ	2.12	0.84
1:A:552:LYS:HG2	1:A:628:ILE:HD12	1.59	0.84
1:A:565:ARG:HD3	1:A:617:ASN:ND2	1.95	0.82
1:A:360:TRP:HB3	1:A:441:TYR:CZ	2.17	0.79
1:A:331:LYS:HB2	1:A:332:PRO:HD2	1.65	0.78
1:A:75:GLN:HE22	1:A:98:THR:HG21	1.53	0.72
1:A:584:ASN:HB3	1:A:618:MET:HE1	1.74	0.70
1:A:341:ILE:HG13	1:A:395:PHE:HE1	1.61	0.66
1:A:325:ILE:O	1:A:329:ILE:HG12	1.96	0.66
1:A:565:ARG:HH21	1:A:617:ASN:ND2	1.94	0.66
1:A:345:THR:H	1:A:386:SER:HB3	1.62	0.63
1:A:473:SER:OG	1:A:474:HIS:HD2	1.81	0.63
1:A:361:SER:O	1:A:490:THR:HG21	1.99	0.63
1:A:345:THR:N	1:A:386:SER:HB3	2.13	0.62
1:A:94:SER:O	1:A:98:THR:HG22	2.01	0.61
1:A:299:GLU:OE1	1:A:519:LYS:HE2	2.01	0.61
1:A:268:ARG:HD2	2:A:723:HOH:O	2.02	0.60
1:A:75:GLN:NE2	1:A:98:THR:HG21	2.16	0.60
1:A:565:ARG:HD3	1:A:617:ASN:HD21	1.64	0.60
1:A:570:ILE:HD12	1:A:592:ILE:HD12	1.84	0.60
1:A:195:LEU:HB3	1:A:196:PRO:HD3	1.83	0.59
1:A:312:LEU:HB3	1:A:315:LEU:HB2	1.84	0.59
1:A:530:ILE:O	1:A:539:ASN:HB3	2.02	0.59
1:A:423:LYS:HA	1:A:441:TYR:O	2.03	0.59
1:A:72:VAL:HG21	1:A:99:ILE:HD11	1.84	0.58
1:A:123:GLU:HB2	1:A:125:TYR:CE2	2.39	0.58
1:A:409:VAL:HG13	1:A:419:LEU:CD2	2.34	0.58
1:A:120:LYS:HG2	1:A:121:LYS:H	1.69	0.57
1:A:392:LYS:HE2	2:A:876:HOH:O	2.03	0.57
1:A:360:TRP:CD1	1:A:421:VAL:HB	2.39	0.57
1:A:584:ASN:HB3	1:A:618:MET:CE	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:650:VAL:HG12	1:A:652:LEU:HG	1.88	0.56
1:A:278:LEU:O	1:A:282:VAL:HG23	2.05	0.56
1:A:189:LYS:HG2	1:A:189:LYS:O	2.05	0.55
1:A:584:ASN:HD21	1:A:586:ASN:HB3	1.72	0.55
1:A:409:VAL:HG13	1:A:419:LEU:HG	1.89	0.55
1:A:615:ASN:OD1	1:A:615:ASN:N	2.39	0.54
1:A:577:ASN:HB3	2:A:695:HOH:O	2.07	0.54
1:A:369:PRO:HD3	1:A:375:LYS:O	2.07	0.54
1:A:614:THR:HG23	2:A:895:HOH:O	2.08	0.53
1:A:361:SER:HB2	1:A:384:ASP:HB2	1.91	0.53
1:A:125:TYR:CG	1:A:126:ALA:N	2.77	0.53
1:A:307:ASP:H	1:A:458:GLN:HE22	1.57	0.52
1:A:307:ASP:H	1:A:458:GLN:NE2	2.08	0.52
1:A:120:LYS:HB3	1:A:193:LEU:HD11	1.91	0.52
1:A:290:ARG:HH11	1:A:290:ARG:HG2	1.74	0.52
1:A:321:THR:O	1:A:325:ILE:HG13	2.09	0.52
1:A:407:THR:HG23	1:A:408:ASP:N	2.24	0.52
1:A:191:GLU:HB3	1:A:247:TRP:CD2	2.45	0.52
1:A:442:ASP:O	1:A:444:LYS:HG3	2.11	0.51
1:A:360:TRP:HB3	1:A:441:TYR:OH	2.10	0.50
1:A:584:ASN:ND2	1:A:586:ASN:HB3	2.26	0.50
1:A:208:LEU:O	1:A:211:ASP:HB2	2.10	0.50
1:A:76:ILE:HA	1:A:79:VAL:HG12	1.93	0.50
1:A:118:ILE:HD11	1:A:193:LEU:HG	1.93	0.50
1:A:135:GLN:HB2	2:A:837:HOH:O	2.10	0.50
1:A:302:ARG:N	1:A:302:ARG:HD3	2.28	0.49
1:A:196:PRO:HD3	1:A:273:MET:HE1	1.94	0.49
1:A:268:ARG:HG3	1:A:271:ARG:NH2	2.28	0.49
1:A:372:GLY:HA3	1:A:521:TYR:CD2	2.48	0.49
1:A:105:ASP:N	1:A:106:PRO:CD	2.76	0.48
1:A:245:VAL:HG21	1:A:535:PHE:HD2	1.77	0.48
1:A:155:PRO:HD2	1:A:158:LEU:HD12	1.95	0.48
1:A:302:ARG:HD3	1:A:302:ARG:H	1.77	0.48
1:A:552:LYS:HG2	1:A:628:ILE:CD1	2.36	0.48
1:A:473:SER:C	1:A:474:HIS:CD2	2.92	0.48
1:A:388:GLU:HB3	1:A:389:PRO:CD	2.44	0.47
1:A:541:LEU:C	1:A:541:LEU:HD23	2.39	0.47
1:A:330:ARG:HH12	1:A:336:ASP:CG	2.22	0.47
1:A:123:GLU:CB	1:A:125:TYR:CE2	2.98	0.47
1:A:111:MET:HE1	1:A:130:ALA:CB	2.45	0.46
1:A:162:ARG:HH21	1:A:166:ARG:NH2	2.13	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:360:TRP:HZ3	1:A:363:ASN:HB3	1.80	0.46
1:A:364:TYR:CE2	1:A:381:PHE:HB2	2.51	0.46
1:A:565:ARG:HD3	1:A:617:ASN:HD22	1.76	0.46
1:A:577:ASN:HA	1:A:594:ILE:O	2.17	0.45
1:A:482:PHE:HB2	1:A:491:ILE:HD12	1.97	0.45
1:A:302:ARG:HH12	1:A:474:HIS:HE1	1.63	0.45
1:A:304:ILE:HD13	1:A:304:ILE:HA	1.73	0.45
1:A:115:GLU:HA	1:A:193:LEU:CD2	2.46	0.45
1:A:365:VAL:HG11	1:A:478:TYR:CE1	2.52	0.45
1:A:650:VAL:CG1	1:A:652:LEU:HG	2.46	0.45
1:A:408:ASP:O	1:A:419:LEU:HD23	2.17	0.45
1:A:554:LYS:HE3	2:A:833:HOH:O	2.16	0.45
1:A:409:VAL:HG13	1:A:419:LEU:CG	2.47	0.45
1:A:191:GLU:HB2	1:A:247:TRP:CE3	2.53	0.44
1:A:195:LEU:HB3	1:A:273:MET:HE1	2.00	0.44
1:A:348:GLN:HG2	1:A:357:PHE:CZ	2.51	0.44
1:A:387:THR:HG21	2:A:767:HOH:O	2.16	0.44
1:A:600:LYS:HE2	1:A:638:GLU:OE1	2.18	0.44
1:A:520:ALA:HA	1:A:553:PHE:CD2	2.53	0.44
1:A:324:SER:O	1:A:328:SER:HB2	2.18	0.44
1:A:368:ARG:HA	1:A:369:PRO:HD3	1.84	0.43
1:A:526:GLY:HA3	1:A:545:GLU:HB2	2.00	0.43
1:A:76:ILE:O	1:A:79:VAL:HG12	2.18	0.43
1:A:520:ALA:HB2	1:A:553:PHE:CE2	2.53	0.43
1:A:467:PRO:HG2	1:A:470:LYS:HB2	2.00	0.43
1:A:263:TRP:HE1	1:A:326:GLU:HG2	1.83	0.43
1:A:187:VAL:HG12	1:A:188:SER:N	2.34	0.43
1:A:330:ARG:NH1	1:A:336:ASP:OD2	2.52	0.42
1:A:331:LYS:HB2	1:A:332:PRO:CD	2.44	0.42
1:A:506:THR:HA	1:A:556:THR:O	2.20	0.42
1:A:115:GLU:HA	1:A:193:LEU:HD21	2.01	0.42
1:A:259:THR:HG22	1:A:260:TYR:H	1.84	0.42
1:A:540:LEU:HD11	1:A:609:PHE:HZ	1.84	0.42
1:A:335:PHE:CE2	1:A:501:VAL:HG11	2.55	0.42
1:A:369:PRO:CD	1:A:375:LYS:O	2.67	0.42
1:A:333:HIS:HD2	1:A:334:LEU:O	2.03	0.42
1:A:373:SER:OG	1:A:375:LYS:HG2	2.20	0.42
1:A:170:LEU:HD23	1:A:170:LEU:HA	1.76	0.41
1:A:347:LEU:HG	1:A:348:GLN:N	2.36	0.41
1:A:161:LYS:HB3	2:A:799:HOH:O	2.20	0.41
1:A:195:LEU:HB3	1:A:273:MET:CE	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:530:ILE:HD12	1:A:542:PHE:CB	2.51	0.41
1:A:337:TYR:OH	1:A:519:LYS:NZ	2.54	0.41
1:A:191:GLU:CB	1:A:247:TRP:CD2	3.04	0.41
1:A:337:TYR:CD1	1:A:337:TYR:N	2.88	0.40
1:A:72:VAL:O	1:A:76:ILE:HG12	2.20	0.40
1:A:543:LEU:HD11	1:A:550:ILE:HD11	2.03	0.40
1:A:156:LEU:HA	1:A:159:ARG:HD2	2.03	0.40
1:A:492:PRO:C	1:A:493:PHE:HD1	2.29	0.40

All (9) 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:173:GLN:CD	2:A:843:HOH:O[3_655]	0.60	1.60
1:A:173:GLN:OE1	2:A:843:HOH:O[3_655]	1.35	0.85
1:A:173:GLN:NE2	2:A:843:HOH:O[3_655]	1.40	0.80
1:A:314:THR:O	2:A:861:HOH:O[6_555]	1.53	0.67
1:A:314:THR:C	2:A:861:HOH:O[6_555]	1.71	0.49
1:A:173:GLN:CG	2:A:843:HOH:O[3_655]	1.75	0.45
1:A:314:THR:CG2	2:A:861:HOH:O[6_555]	1.81	0.39
1:A:314:THR:CA	2:A:861:HOH:O[6_555]	1.81	0.39
1:A:314:THR:CB	2:A:861:HOH:O[6_555]	1.99	0.21

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	587/589 (100%)	556 (95%)	28 (5%)	3 (0%)	24 37

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	313	ASN
1	A	432	GLN
1	A	637	ASN

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	521/522 (100%)	490 (94%)	31 (6%)	17 31

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	80	VAL
1	A	129	LYS
1	A	143	ASP
1	A	188	SER
1	A	210	LYS
1	A	235	LYS
1	A	259	THR
1	A	281	ILE
1	A	311	SER
1	A	327	ASN
1	A	363	ASN
1	A	370	SER
1	A	387	THR
1	A	407	THR
1	A	409	VAL
1	A	432	GLN
1	A	458	GLN
1	A	463	THR
1	A	470	LYS
1	A	491	ILE
1	A	499	ARG
1	A	517	VAL
1	A	524	SER
1	A	530	ILE

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Mol	Chain	Res	Type
1	A	550	ILE
1	A	558	ASN
1	A	565	ARG
1	A	576	THR
1	A	615	ASN
1	A	626	GLU
1	A	635	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	75	GLN
1	A	97	ASN
1	A	113	GLN
1	A	173	GLN
1	A	200	GLN
1	A	327	ASN
1	A	348	GLN
1	A	358	ASN
1	A	363	ASN
1	A	414	ASN
1	A	434	ASN
1	A	439	GLN
1	A	446	ASN
1	A	449	HIS
1	A	458	GLN
1	A	474	HIS
1	A	477	ASN
1	A	485	GLN
1	A	558	ASN
1	A	586	ASN
1	A	595	ASN
1	A	617	ASN
1	A	651	GLN

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](#)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.