



Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 08:42 am BST

PDB ID : 1QZ7
Title : Beta-catenin binding domain of Axin in complex with beta-catenin
Authors : Xing, Y.; Clements, W.K.; Kimelman, D.; Xu, W.
Deposited on : 2003-09-15
Resolution : 2.20 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

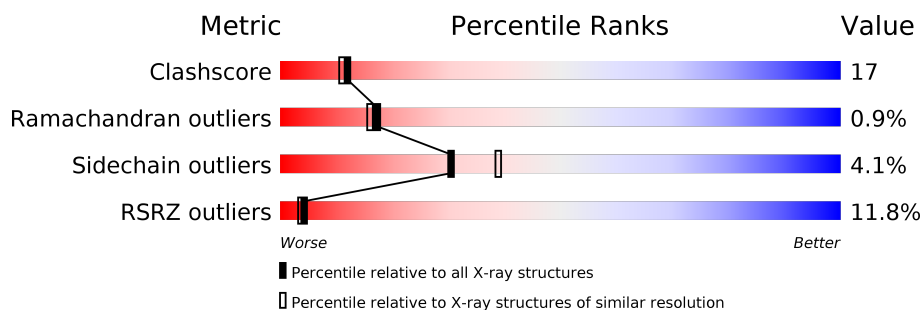
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 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	533	<div> <div>11%</div> <div>72%</div> <div>25%</div> <div>••</div> </div>
2	B	70	<div> <div>4%</div> <div>10%</div> <div>7%</div> <div>7%</div> <div>76%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4148 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-catenin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	524	Total	C	N	O	S	0	0	0
			3979	2496	721	735	27			

- Molecule 2 is a protein called Axin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	17	Total	C	N	O	S	0	0	0
			138	83	24	30	1			

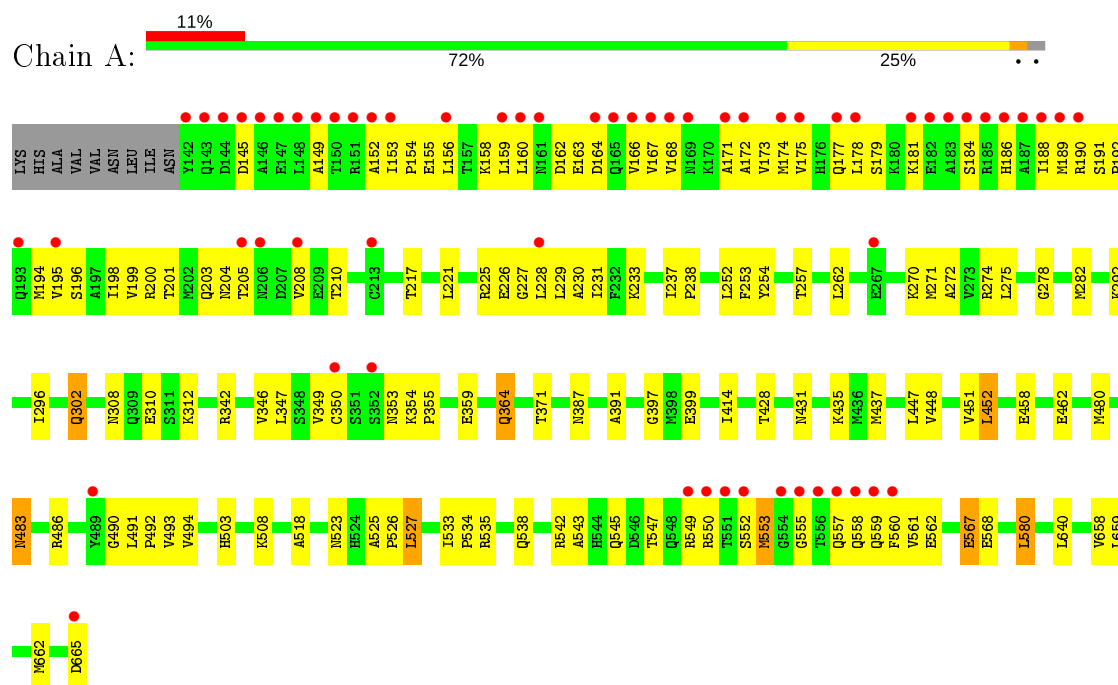
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	31	Total	O	0	0
			31	31		

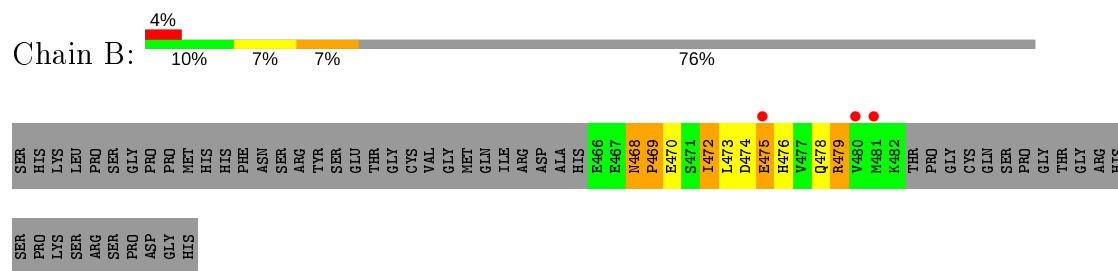
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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 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 ($\text{RSRZ} > 2$). 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: Beta-catenin



• Molecule 2: Axin



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	85.14Å 75.04Å 101.40Å 90.00° 97.47° 90.00°	Depositor
Resolution (Å)	42.21 – 2.20 42.21 – 2.09	Depositor EDS
% Data completeness (in resolution range)	81.1 (42.21-2.20) 93.4 (42.21-2.09)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.80 (at 2.10Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.221 , 0.256 0.222 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	35.2	Xtriage
Anisotropy	0.068	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 49.9	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	0.94	EDS
Total number of atoms	4148	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.76% 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	0.31	0/4035	0.53	0/5476
2	B	0.28	0/139	0.87	1/187 (0.5%)
All	All	0.31	0/4174	0.55	1/5663 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	475	GLU	CB-CA-C	9.99	130.38	110.40

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	3979	0	4094	129	0
2	B	138	0	124	21	0
3	A	31	0	0	0	0
All	All	4148	0	4218	143	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 17.

All (143) 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:159:LEU:HD23	1:A:171:ALA:HB2	1.48	0.96
1:A:271:MET:O	1:A:275:LEU:HG	1.84	0.78
1:A:550:ARG:HH22	1:A:561:VAL:CG2	1.99	0.76
1:A:272:ALA:HA	1:A:275:LEU:HD12	1.68	0.75
1:A:364:GLN:H	1:A:364:GLN:HE21	1.35	0.74
1:A:364:GLN:H	1:A:364:GLN:NE2	1.85	0.74
1:A:355:PRO:O	1:A:359:GLU:HG2	1.87	0.74
1:A:270:LYS:HB3	1:A:274:ARG:HH12	1.55	0.70
1:A:154:PRO:O	1:A:158:LYS:HG3	1.91	0.70
2:B:468:ASN:HD22	2:B:469:PRO:CD	2.05	0.70
1:A:257:THR:HG23	2:B:476:HIS:ND1	2.07	0.69
1:A:153:ILE:HB	1:A:154:PRO:HD3	1.75	0.69
1:A:508:LYS:HE3	1:A:568:GLU:OE1	1.92	0.68
1:A:201:THR:O	1:A:205:THR:HG22	1.93	0.68
1:A:188:ILE:HG23	1:A:194:MET:HB3	1.77	0.67
1:A:371:THR:HG22	1:A:371:THR:O	1.95	0.66
2:B:468:ASN:HD22	2:B:469:PRO:HD2	1.60	0.66
1:A:200:ARG:HA	1:A:203:GLN:HE21	1.61	0.66
1:A:292:LYS:O	1:A:296:ILE:HG12	1.95	0.66
1:A:278:GLY:O	1:A:282:MET:HG3	1.97	0.65
1:A:189:MET:SD	1:A:226:GLU:HB2	2.38	0.63
1:A:483:ASN:ND2	1:A:486:ARG:NH2	2.48	0.62
1:A:189:MET:HB2	1:A:221:LEU:HD22	1.80	0.61
1:A:270:LYS:HB3	1:A:274:ARG:NH1	2.14	0.61
1:A:533:ILE:HB	1:A:534:PRO:HD3	1.83	0.60
1:A:190:ARG:O	1:A:192:PRO:HD3	2.02	0.60
2:B:468:ASN:HD22	2:B:469:PRO:N	2.00	0.59
1:A:173:VAL:HG12	1:A:177:GLN:HE21	1.68	0.58
1:A:458:GLU:OE2	1:A:503:HIS:HD2	1.86	0.58
1:A:557:GLN:O	1:A:558:GLN:HG2	2.03	0.58
1:A:550:ARG:HD3	1:A:558:GLN:OE1	2.04	0.58
1:A:159:LEU:HD11	1:A:167:VAL:HG12	1.85	0.57
1:A:296:ILE:HD12	2:B:476:HIS:HD2	1.69	0.57
1:A:181:LYS:HB2	1:A:184:SER:OG	2.03	0.57
1:A:399:GLU:H	1:A:399:GLU:CD	2.08	0.56
1:A:518:ALA:CB	1:A:580:LEU:HD13	2.36	0.56
1:A:200:ARG:HA	1:A:203:GLN:NE2	2.22	0.55
1:A:159:LEU:CD2	1:A:171:ALA:HB2	2.29	0.54
1:A:371:THR:CG2	1:A:371:THR:O	2.55	0.54
1:A:525:ALA:HB3	1:A:526:PRO:HD3	1.90	0.53
1:A:347:LEU:O	1:A:350:CYS:HB3	2.09	0.53
1:A:174:MET:HA	1:A:177:GLN:NE2	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:188:ILE:HG23	1:A:194:MET:CB	2.38	0.53
1:A:559:GLN:HG2	1:A:560:PHE:N	2.23	0.53
1:A:171:ALA:O	1:A:175:VAL:HG23	2.09	0.53
1:A:547:THR:HA	1:A:558:GLN:NE2	2.23	0.52
2:B:472:ILE:C	2:B:472:ILE:HD13	2.29	0.52
1:A:164:ASP:OD2	1:A:167:VAL:HG23	2.09	0.52
1:A:354:LYS:HZ3	1:A:354:LYS:HB2	1.74	0.52
1:A:558:GLN:OE1	1:A:558:GLN:HA	2.10	0.52
1:A:205:THR:O	1:A:205:THR:HG23	2.10	0.52
1:A:550:ARG:HH22	1:A:561:VAL:HG21	1.73	0.51
1:A:543:ALA:O	1:A:547:THR:HG23	2.10	0.51
1:A:542:ARG:HG2	1:A:542:ARG:HH11	1.75	0.51
1:A:535:ARG:HH11	1:A:538:GLN:NE2	2.09	0.51
1:A:200:ARG:O	1:A:204:ASN:ND2	2.44	0.51
1:A:149:ALA:O	1:A:153:ILE:HG12	2.11	0.50
1:A:535:ARG:NH1	1:A:538:GLN:NE2	2.59	0.50
1:A:171:ALA:HA	1:A:174:MET:HE3	1.94	0.50
1:A:186:HIS:HA	1:A:189:MET:HE2	1.93	0.50
1:A:230:ALA:HA	1:A:233:LYS:CE	2.41	0.50
2:B:468:ASN:C	2:B:470:GLU:H	2.14	0.49
1:A:227:GLY:O	1:A:231:ILE:HG13	2.12	0.49
1:A:658:VAL:HG12	1:A:662:MET:CE	2.42	0.49
1:A:257:THR:HG23	2:B:476:HIS:CE1	2.46	0.49
1:A:483:ASN:HD21	1:A:486:ARG:NH2	2.11	0.49
2:B:479:ARG:CB	2:B:479:ARG:HH11	2.26	0.48
1:A:159:LEU:HD21	1:A:167:VAL:HG12	1.94	0.48
1:A:178:LEU:HB3	1:A:184:SER:HB2	1.95	0.48
1:A:160:LEU:HD12	1:A:201:THR:OG1	2.14	0.48
1:A:518:ALA:HB2	1:A:580:LEU:HD13	1.95	0.48
1:A:431:ASN:O	1:A:435:LYS:HG3	2.13	0.48
1:A:448:VAL:O	1:A:452:LEU:HD22	2.15	0.47
1:A:552:SER:O	1:A:553:MET:HB2	2.15	0.47
1:A:253:PHE:HB3	2:B:472:ILE:HD12	1.97	0.47
1:A:354:LYS:HE3	1:A:387:ASN:O	2.15	0.47
1:A:159:LEU:HD11	1:A:167:VAL:CG1	2.45	0.47
1:A:354:LYS:HB2	1:A:354:LYS:NZ	2.30	0.47
1:A:547:THR:HA	1:A:558:GLN:HE22	1.80	0.47
1:A:145:ASP:O	1:A:149:ALA:HB3	2.15	0.47
1:A:490:GLY:O	1:A:493:VAL:HG12	2.15	0.47
1:A:253:PHE:HD2	2:B:469:PRO:O	1.98	0.47
1:A:149:ALA:HA	1:A:152:ALA:HB3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:468:ASN:HD22	2:B:468:ASN:C	2.18	0.46
1:A:172:ALA:CB	1:A:210:THR:HG23	2.46	0.46
1:A:308:ASN:OD1	1:A:310:GLU:HB2	2.15	0.46
1:A:428:THR:O	1:A:435:LYS:HE2	2.15	0.46
1:A:177:GLN:C	1:A:179:SER:H	2.18	0.46
2:B:475:GLU:O	2:B:478:GLN:HB2	2.15	0.46
1:A:179:SER:OG	1:A:217:THR:HG23	2.16	0.46
1:A:226:GLU:H	1:A:226:GLU:CD	2.19	0.46
1:A:346:VAL:O	1:A:349:VAL:HG22	2.16	0.46
1:A:561:VAL:O	1:A:562:GLU:HB2	2.16	0.46
1:A:491:LEU:HB2	1:A:492:PRO:HD3	1.98	0.45
1:A:152:ALA:O	1:A:155:GLU:HB3	2.16	0.45
1:A:173:VAL:HG12	1:A:177:GLN:NE2	2.30	0.45
1:A:164:ASP:O	1:A:168:VAL:HG23	2.16	0.45
1:A:538:GLN:NE2	1:A:542:ARG:HH21	2.15	0.45
1:A:447:LEU:O	1:A:451:VAL:HG23	2.16	0.45
1:A:414:ILE:H	1:A:414:ILE:HG13	1.60	0.45
1:A:198:ILE:HD13	1:A:217:THR:HG21	1.99	0.45
1:A:518:ALA:HB1	1:A:580:LEU:HD13	1.99	0.45
2:B:468:ASN:O	2:B:470:GLU:N	2.50	0.44
1:A:173:VAL:O	1:A:177:GLN:HG3	2.16	0.44
1:A:308:ASN:O	1:A:312:LYS:HG3	2.16	0.44
1:A:640:LEU:CD1	1:A:662:MET:HE1	2.48	0.44
1:A:523:ASN:O	1:A:527:LEU:HB2	2.17	0.44
1:A:195:VAL:O	1:A:199:VAL:HG23	2.17	0.44
1:A:354:LYS:HD3	1:A:391:ALA:HB2	2.00	0.44
1:A:560:PHE:N	1:A:560:PHE:CD1	2.86	0.44
1:A:458:GLU:OE2	1:A:503:HIS:CD2	2.70	0.44
1:A:567:GLU:H	1:A:567:GLU:CD	2.20	0.44
1:A:196:SER:O	1:A:200:ARG:HG3	2.18	0.43
1:A:350:CYS:HB3	1:A:353:ASN:HB2	1.99	0.43
2:B:479:ARG:HB3	2:B:479:ARG:HH11	1.82	0.43
1:A:162:ASP:HB3	1:A:168:VAL:HG22	2.01	0.43
2:B:479:ARG:HB2	2:B:479:ARG:NH1	2.33	0.43
1:A:225:ARG:HG3	1:A:225:ARG:HH11	1.84	0.43
1:A:545:GLN:O	1:A:549:ARG:HG3	2.19	0.43
1:A:237:ILE:HB	1:A:238:PRO:HD3	2.01	0.43
1:A:257:THR:HG23	2:B:476:HIS:CG	2.53	0.43
1:A:658:VAL:HG12	1:A:662:MET:HE1	1.99	0.43
1:A:658:VAL:O	1:A:662:MET:HG3	2.19	0.43
1:A:270:LYS:O	1:A:274:ARG:HG3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:549:ARG:HH11	1:A:549:ARG:HG2	1.83	0.42
1:A:659:LEU:HD23	1:A:662:MET:HE3	2.00	0.42
1:A:659:LEU:HA	1:A:662:MET:HE2	2.01	0.42
2:B:479:ARG:CB	2:B:479:ARG:NH1	2.82	0.42
1:A:397:GLY:HA2	1:A:399:GLU:OE1	2.19	0.42
2:B:472:ILE:HG23	2:B:473:LEU:N	2.35	0.42
1:A:296:ILE:HD12	2:B:476:HIS:CD2	2.52	0.42
1:A:230:ALA:HA	1:A:233:LYS:HE3	2.00	0.41
1:A:153:ILE:HG21	1:A:191:SER:OG	2.21	0.41
1:A:160:LEU:HD22	1:A:171:ALA:CB	2.51	0.41
1:A:228:LEU:HD22	1:A:262:LEU:HD23	2.03	0.41
1:A:483:ASN:HD21	1:A:486:ARG:HH22	1.68	0.41
1:A:156:LEU:HD12	1:A:178:LEU:HD12	2.02	0.41
1:A:188:ILE:HG12	1:A:194:MET:HE2	2.02	0.40
1:A:302:GLN:NE2	1:A:342:ARG:HH21	2.19	0.40
1:A:354:LYS:HB3	1:A:355:PRO:CD	2.51	0.40
1:A:493:VAL:HG13	1:A:494:VAL:N	2.36	0.40
1:A:229:LEU:HG	1:A:233:LYS:HE2	2.02	0.40
2:B:468:ASN:ND2	2:B:469:PRO:HD2	2.33	0.40

There are no symmetry-related clashes.

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	522/533 (98%)	488 (94%)	30 (6%)	4 (1%)	19	19
2	B	15/70 (21%)	13 (87%)	1 (7%)	1 (7%)	1	0
All	All	537/603 (89%)	501 (93%)	31 (6%)	5 (1%)	17	16

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	553	MET
1	A	208	VAL
1	A	555	GLY
2	B	469	PRO
1	A	166	VAL

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	428/442 (97%)	414 (97%)	14 (3%)	38	49
2	B	16/62 (26%)	12 (75%)	4 (25%)	0	0
All	All	444/504 (88%)	426 (96%)	18 (4%)	30	39

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	163	GLU
1	A	252	LEU
1	A	254	TYR
1	A	302	GLN
1	A	364	GLN
1	A	437	MET
1	A	452	LEU
1	A	462	GLU
1	A	480	MET
1	A	483	ASN
1	A	527	LEU
1	A	567	GLU
1	A	580	LEU
1	A	665	ASP
2	B	468	ASN
2	B	472	ILE
2	B	474	ASP
2	B	479	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	177	GLN
1	A	186	HIS
1	A	193	GLN
1	A	203	GLN
1	A	220	ASN
1	A	302	GLN
1	A	322	GLN
1	A	326	ASN
1	A	364	GLN
1	A	415	ASN
1	A	483	ASN
1	A	499	HIS
1	A	503	HIS
1	A	538	GLN
1	A	601	GLN
1	A	611	GLN
2	B	468	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 ⓘ

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	524/533 (98%)	0.64	61 (11%) 4 4	22, 47, 99, 108	0
2	B	17/70 (24%)	1.33	3 (17%) 1 1	71, 81, 94, 94	0
All	All	541/603 (89%)	0.66	64 (11%) 4 4	22, 48, 99, 108	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	142	TYR	11.0
1	A	160	LEU	10.8
1	A	551	THR	9.7
1	A	144	ASP	8.4
1	A	552	SER	8.3
1	A	148	LEU	8.3
1	A	556	THR	8.1
1	A	143	GLN	8.1
1	A	146	ALA	7.3
1	A	149	ALA	7.1
2	B	481	MET	6.9
1	A	167	VAL	6.7
1	A	183	ALA	6.6
1	A	178	LEU	6.4
1	A	159	LEU	5.8
1	A	557	GLN	5.7
1	A	165	GLN	5.6
1	A	174	MET	5.5
1	A	145	ASP	5.5
1	A	150	THR	5.2
1	A	181	LYS	5.1
1	A	555	GLY	5.1
1	A	177	GLN	4.9
1	A	153	ILE	4.8

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Mol	Chain	Res	Type	RSRZ
1	A	147	GLU	4.7
1	A	166	VAL	4.4
1	A	168	VAL	4.4
1	A	558	GLN	4.4
1	A	352	SER	4.3
1	A	164	ASP	4.2
1	A	206	ASN	4.1
1	A	186	HIS	4.1
1	A	665	ASP	4.0
1	A	189	MET	4.0
1	A	184	SER	3.9
1	A	156	LEU	3.8
1	A	151	ARG	3.8
1	A	550	ARG	3.8
1	A	185	ARG	3.4
1	A	172	ALA	3.3
1	A	549	ARG	3.2
1	A	169	ASN	3.1
2	B	480	VAL	3.0
1	A	161	ASN	3.0
1	A	208	VAL	3.0
2	B	475	GLU	2.9
1	A	175	VAL	2.7
1	A	228	LEU	2.7
1	A	559	GLN	2.6
1	A	182	GLU	2.6
1	A	205	THR	2.5
1	A	489	TYR	2.5
1	A	190	ARG	2.4
1	A	188	ILE	2.4
1	A	152	ALA	2.4
1	A	171	ALA	2.3
1	A	187	ALA	2.3
1	A	213	CYS	2.3
1	A	560	PHE	2.2
1	A	350	CYS	2.2
1	A	193	GLN	2.2
1	A	267	GLU	2.1
1	A	195	VAL	2.1
1	A	554	GLY	2.1

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.