



Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 08:45 pm BST

PDB ID : 2Z6G
Title : Crystal Structure of a Full-Length Zebrafish Beta-Catenin
Authors : Xing, Y.; Takemaru, K.; Liu, J.; Zheng, J.; Moon, R.; Xu, W.
Deposited on : 2007-08-01
Resolution : 3.40 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 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

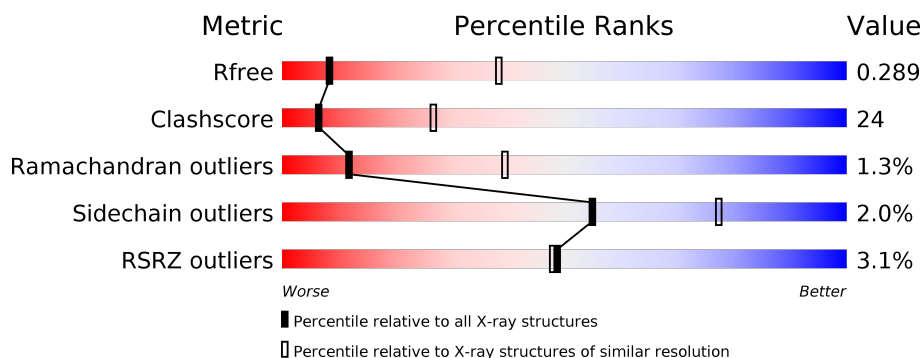
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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}	130704	1026 (3.48-3.32)
Clashscore	141614	1055 (3.48-3.32)
Ramachandran outliers	138981	1038 (3.48-3.32)
Sidechain outliers	138945	1038 (3.48-3.32)
RSRZ outliers	127900	2173 (3.50-3.30)

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 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	780	<div> <div>2%</div> <div> <div></div> <div>41%</div> <div>28%</div> <div>•</div> <div>29%</div> </div> </div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 4186 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 B-catenin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	550	4186	2623	760	776	27	0	0	0

- Molecule 1: B-catenin



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	71.62Å 112.82Å 123.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.69 – 3.40 29.69 – 3.31	Depositor EDS
% Data completeness (in resolution range)	78.2 (29.69-3.40) 84.4 (29.69-3.31)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.46 (at 3.31Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.281 , 0.319 0.259 , 0.289	Depositor DCC
R_{free} test set	712 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	90.7	Xtriage
Anisotropy	0.260	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 32.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	4186	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.76% 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	0.23	0/4244	0.44	0/5761

There are no bond length outliers.

There are no bond angle outliers.

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	4186	0	4306	203	0
All	All	4186	0	4306	203	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 (203) 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:582:ASP:HB3	1:A:585:ASN:HD22	1.30	0.94
1:A:201:MET:HG2	1:A:242:MET:HE3	1.56	0.87
1:A:269:LYS:HB3	1:A:273:ARG:HH12	1.40	0.87
1:A:279:GLN:NE2	1:A:279:GLN:H	1.78	0.82
1:A:670:LYS:HD3	1:A:671:LYS:N	1.98	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:665:LYS:HB3	1:A:666:PRO:HD2	1.65	0.77
1:A:590:ARG:HH12	1:A:625:GLU:HB2	1.53	0.73
1:A:311:LYS:HE2	1:A:345:VAL:HG12	1.69	0.72
1:A:139:ILE:O	1:A:143:ASP:HB2	1.88	0.72
1:A:132:LYS:O	1:A:135:VAL:HG12	1.91	0.70
1:A:524:ALA:HB3	1:A:525:PRO:HD3	1.72	0.69
1:A:490:LEU:HB2	1:A:491:PRO:HD3	1.76	0.68
1:A:590:ARG:HG3	1:A:595:ILE:HD11	1.76	0.67
1:A:236:ILE:HB	1:A:237:PRO:HD3	1.75	0.66
1:A:437:VAL:HG12	1:A:442:GLY:HA3	1.77	0.65
1:A:532:ILE:HB	1:A:533:PRO:HD3	1.78	0.65
1:A:545:ASP:HA	1:A:548:ARG:HH11	1.62	0.65
1:A:262:LEU:HD21	1:A:272:VAL:HG21	1.78	0.65
1:A:625:GLU:H	1:A:625:GLU:CD	2.00	0.65
1:A:140:ASN:HD22	1:A:141:TYR:N	1.95	0.65
1:A:457:GLU:HG2	1:A:505:LEU:HD22	1.78	0.64
1:A:189:ARG:O	1:A:191:PRO:HD3	1.97	0.64
1:A:398:GLU:H	1:A:398:GLU:CD	2.00	0.64
1:A:240:VAL:HG12	1:A:280:LYS:HD2	1.81	0.63
1:A:545:ASP:HA	1:A:548:ARG:NH1	2.14	0.63
1:A:287:LYS:HD3	1:A:288:THR:H	1.62	0.62
1:A:513:ILE:HG23	1:A:526:LEU:HD21	1.81	0.62
1:A:277:GLY:O	1:A:281:MET:HG3	1.99	0.62
1:A:152:ILE:HB	1:A:153:PRO:HD3	1.80	0.62
1:A:595:ILE:N	1:A:596:PRO:HD2	2.14	0.62
1:A:262:LEU:HD22	1:A:303:LEU:HD21	1.81	0.61
1:A:582:ASP:HB3	1:A:585:ASN:ND2	2.09	0.61
1:A:595:ILE:O	1:A:599:VAL:HG23	2.00	0.61
1:A:670:LYS:NZ	1:A:670:LYS:HB2	2.16	0.61
1:A:290:VAL:HG23	1:A:291:LYS:H	1.65	0.60
1:A:148:ALA:O	1:A:152:ILE:HG12	2.02	0.60
1:A:279:GLN:HE21	1:A:279:GLN:H	1.49	0.59
1:A:307:ASN:O	1:A:311:LYS:HG3	2.01	0.59
1:A:380:CYS:O	1:A:384:LEU:HG	2.01	0.59
1:A:139:ILE:O	1:A:139:ILE:HD13	2.04	0.58
1:A:532:ILE:HD11	1:A:585:ASN:OD1	2.03	0.58
1:A:590:ARG:HH12	1:A:625:GLU:CB	2.15	0.58
1:A:236:ILE:O	1:A:240:VAL:HG23	2.03	0.58
1:A:433:ASN:O	1:A:437:VAL:HG23	2.03	0.58
1:A:489:GLY:O	1:A:493:VAL:HG23	2.03	0.58
1:A:145:ALA:HB2	1:A:182:ALA:HB1	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:670:LYS:HZ3	1:A:670:LYS:HB2	1.69	0.58
1:A:159:LEU:HA	1:A:167:VAL:HG13	1.85	0.57
1:A:211:ARG:HB2	1:A:211:ARG:NH1	2.18	0.57
1:A:228:LEU:HD11	1:A:232:LYS:HE3	1.86	0.57
1:A:352:ASN:O	1:A:356:ILE:HG13	2.05	0.57
1:A:278:LEU:O	1:A:282:VAL:HG23	2.05	0.57
1:A:619:GLU:O	1:A:622:GLN:HG2	2.05	0.57
1:A:473:ARG:O	1:A:474:HIS:HB3	2.04	0.56
1:A:583:ILE:HA	1:A:586:ARG:CZ	2.35	0.56
1:A:227:LEU:HD22	1:A:261:LEU:HD23	1.87	0.56
1:A:497:LEU:HD11	1:A:513:ILE:CD1	2.35	0.56
1:A:611:ARG:HH12	1:A:649:GLY:HA3	1.70	0.56
1:A:353:LYS:HG3	1:A:387:LEU:HD23	1.87	0.56
1:A:144:ASP:HA	1:A:147:LEU:HD23	1.88	0.55
1:A:290:VAL:HG23	1:A:291:LYS:N	2.20	0.55
1:A:660:ARG:HG3	1:A:660:ARG:HH11	1.71	0.55
1:A:309:GLU:CD	1:A:309:GLU:H	2.10	0.55
1:A:519:CYS:HB3	1:A:522:ASN:HD22	1.72	0.54
1:A:663:GLU:O	1:A:664:ASP:HB2	2.07	0.54
1:A:662:SER:HB2	1:A:673:LEU:HD12	1.89	0.54
1:A:435:MET:HE3	1:A:475:GLN:HB2	1.88	0.54
1:A:280:LYS:O	1:A:284:LEU:HG	2.08	0.54
1:A:208:GLU:HA	1:A:211:ARG:HG2	1.90	0.54
1:A:613:ALA:O	1:A:616:VAL:HG12	2.07	0.54
1:A:455:ASP:O	1:A:457:GLU:N	2.41	0.53
1:A:362:MET:HE2	1:A:388:SER:HA	1.91	0.53
1:A:208:GLU:OE1	1:A:211:ARG:HD3	2.08	0.53
1:A:457:GLU:HA	1:A:460:THR:OG1	2.09	0.53
1:A:545:ASP:O	1:A:549:ARG:HG2	2.09	0.53
1:A:489:GLY:O	1:A:492:VAL:HG12	2.08	0.53
1:A:478:GLU:HA	1:A:481:GLN:NE2	2.23	0.52
1:A:215:GLY:HA2	1:A:253:HIS:ND1	2.24	0.52
1:A:287:LYS:HE3	1:A:287:LYS:HA	1.90	0.52
1:A:132:LYS:O	1:A:136:VAL:HG23	2.10	0.52
1:A:626:ALA:O	1:A:630:ILE:HG13	2.09	0.52
1:A:188:MET:SD	1:A:225:GLU:HB2	2.50	0.51
1:A:287:LYS:CD	1:A:288:THR:H	2.23	0.51
1:A:595:ILE:HG23	1:A:630:ILE:HG12	1.91	0.51
1:A:218:HIS:NE2	1:A:256:THR:HG21	2.26	0.51
1:A:140:ASN:HD22	1:A:141:TYR:H	1.58	0.51
1:A:155:LEU:HD23	1:A:158:LEU:HD22	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:289:ASN:HB3	1:A:292:PHE:HB3	1.93	0.51
1:A:611:ARG:NH1	1:A:649:GLY:HA3	2.25	0.51
1:A:438:CYS:HB3	1:A:479:MET:CE	2.41	0.50
1:A:452:ARG:HH21	1:A:452:ARG:HG2	1.76	0.50
1:A:138:LEU:O	1:A:142:GLN:HG2	2.12	0.50
1:A:396:GLY:HA2	1:A:398:GLU:OE1	2.11	0.50
1:A:418:CYS:O	1:A:422:ILE:HG13	2.10	0.50
1:A:503:TRP:N	1:A:504:PRO:HD2	2.26	0.50
1:A:193:MET:O	1:A:197:ILE:HG13	2.11	0.50
1:A:353:LYS:O	1:A:357:VAL:HG23	2.12	0.50
1:A:443:ILE:O	1:A:447:VAL:HG23	2.11	0.49
1:A:506:ILE:O	1:A:510:VAL:HG23	2.11	0.49
1:A:298:ASP:O	1:A:302:ILE:HG13	2.12	0.49
1:A:543:HIS:CD2	1:A:597:LEU:HD11	2.48	0.49
1:A:377:VAL:O	1:A:381:LEU:HG	2.13	0.49
1:A:545:ASP:HA	1:A:548:ARG:HG2	1.94	0.49
1:A:136:VAL:O	1:A:139:ILE:HG22	2.13	0.49
1:A:405:VAL:HG21	1:A:440:VAL:HG21	1.95	0.48
1:A:519:CYS:HB3	1:A:522:ASN:ND2	2.27	0.48
1:A:532:ILE:O	1:A:536:VAL:HG23	2.12	0.48
1:A:324:VAL:HG12	1:A:328:ARG:HD2	1.94	0.48
1:A:412:ASP:HB3	1:A:415:VAL:HG23	1.95	0.48
1:A:670:LYS:C	1:A:670:LYS:HD3	2.33	0.48
1:A:278:LEU:HD12	1:A:313:ILE:HD12	1.95	0.48
1:A:262:LEU:CD2	1:A:303:LEU:HD21	2.44	0.48
1:A:401:LEU:O	1:A:405:VAL:HG23	2.13	0.48
1:A:291:LYS:O	1:A:295:ILE:HG12	2.13	0.48
1:A:145:ALA:CA	1:A:182:ALA:HB1	2.44	0.47
1:A:225:GLU:CD	1:A:225:GLU:H	2.18	0.47
1:A:435:MET:O	1:A:439:GLN:HG2	2.13	0.47
1:A:583:ILE:HA	1:A:586:ARG:NH1	2.29	0.47
1:A:202:GLN:HB3	1:A:238:ALA:HB1	1.97	0.47
1:A:279:GLN:HE21	1:A:279:GLN:N	2.11	0.47
1:A:405:VAL:HG21	1:A:440:VAL:CG2	2.45	0.47
1:A:195:SER:HA	1:A:233:SER:HB2	1.97	0.46
1:A:514:ARG:HH11	1:A:514:ARG:HG2	1.80	0.46
1:A:211:ARG:CB	1:A:211:ARG:HH11	2.28	0.46
1:A:594:THR:HG1	1:A:598:PHE:HE2	1.63	0.46
1:A:524:ALA:HA	1:A:527:ARG:NH1	2.30	0.46
1:A:603:TYR:CE2	1:A:638:PRO:HB3	2.51	0.46
1:A:582:ASP:CB	1:A:585:ASN:HD22	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:158:LEU:HB3	1:A:170:ALA:HB2	1.97	0.46
1:A:310:SER:O	1:A:314:ILE:HG13	2.16	0.46
1:A:353:LYS:HB3	1:A:354:PRO:CD	2.46	0.46
1:A:135:VAL:O	1:A:139:ILE:HB	2.16	0.45
1:A:412:ASP:HB3	1:A:415:VAL:CG2	2.46	0.45
1:A:658:LEU:HA	1:A:661:MET:CE	2.47	0.45
1:A:524:ALA:O	1:A:528:GLU:HG3	2.17	0.45
1:A:583:ILE:HG23	1:A:584:HIS:N	2.32	0.45
1:A:337:TRP:O	1:A:341:ARG:HG3	2.17	0.45
1:A:660:ARG:O	1:A:663:GLU:HB3	2.17	0.45
1:A:198:VAL:HG11	1:A:234:GLY:O	2.17	0.45
1:A:583:ILE:HG23	1:A:584:HIS:H	1.81	0.45
1:A:666:PRO:C	1:A:668:ASP:H	2.20	0.45
1:A:476:ASP:O	1:A:479:MET:HB3	2.17	0.44
1:A:312:LEU:O	1:A:315:LEU:HB3	2.17	0.44
1:A:204:THR:C	1:A:205:ASN:HD22	2.20	0.44
1:A:615:GLY:O	1:A:618:CYS:HB3	2.17	0.44
1:A:640:THR:HA	1:A:658:LEU:HD11	2.00	0.44
1:A:228:LEU:CD1	1:A:232:LYS:HE3	2.46	0.44
1:A:481:GLN:OE1	1:A:518:LEU:HB2	2.17	0.44
1:A:536:VAL:HG21	1:A:592:LEU:HD12	1.99	0.44
1:A:140:ASN:ND2	1:A:141:TYR:N	2.64	0.44
1:A:185:HIS:HA	1:A:188:MET:HE2	1.98	0.44
1:A:467:LEU:O	1:A:471:THR:HG23	2.18	0.44
1:A:240:VAL:HG13	1:A:277:GLY:HA2	1.99	0.43
1:A:514:ARG:NH1	1:A:514:ARG:HG2	2.32	0.43
1:A:215:GLY:O	1:A:218:HIS:HB3	2.18	0.43
1:A:585:ASN:O	1:A:589:ILE:HG13	2.19	0.43
1:A:662:SER:CB	1:A:673:LEU:HD12	2.48	0.43
1:A:534:ARG:CZ	1:A:538:LEU:HD21	2.49	0.43
1:A:637:ALA:N	1:A:638:PRO:HD2	2.34	0.43
1:A:662:SER:HB2	1:A:673:LEU:CD1	2.48	0.43
1:A:611:ARG:HH11	1:A:611:ARG:HG3	1.84	0.43
1:A:337:TRP:CE2	1:A:341:ARG:HD2	2.54	0.42
1:A:148:ALA:C	1:A:150:ARG:N	2.73	0.42
1:A:305:TYR:HA	1:A:345:VAL:HG11	2.01	0.42
1:A:365:LEU:HB2	1:A:384:LEU:HD21	2.01	0.42
1:A:665:LYS:HB3	1:A:666:PRO:CD	2.44	0.42
1:A:477:ALA:O	1:A:481:GLN:HG3	2.19	0.42
1:A:658:LEU:HD23	1:A:661:MET:CE	2.50	0.42
1:A:662:SER:HG	1:A:669:TYR:HE2	1.65	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:438:CYS:HB3	1:A:479:MET:HE1	2.01	0.42
1:A:145:ALA:CB	1:A:182:ALA:HB1	2.49	0.42
1:A:228:LEU:O	1:A:232:LYS:HG3	2.20	0.42
1:A:258:LEU:O	1:A:262:LEU:HG	2.20	0.42
1:A:461:GLU:N	1:A:462:PRO:HD2	2.35	0.42
1:A:536:VAL:O	1:A:540:VAL:HG23	2.20	0.42
1:A:240:VAL:CG1	1:A:280:LYS:HD2	2.47	0.41
1:A:211:ARG:CB	1:A:211:ARG:NH1	2.83	0.41
1:A:308:GLN:O	1:A:312:LEU:HG	2.21	0.41
1:A:180:LYS:O	1:A:184:ARG:HB2	2.20	0.41
1:A:247:VAL:O	1:A:251:LEU:HG	2.20	0.41
1:A:616:VAL:O	1:A:620:LEU:HG	2.20	0.41
1:A:208:GLU:CD	1:A:211:ARG:HD3	2.40	0.41
1:A:388:SER:C	1:A:390:ALA:H	2.24	0.41
1:A:474:HIS:O	1:A:477:ALA:HB2	2.21	0.41
1:A:201:MET:HB2	1:A:213:THR:HB	2.03	0.41
1:A:353:LYS:HB3	1:A:354:PRO:HD3	2.02	0.41
1:A:138:LEU:HD13	1:A:138:LEU:C	2.42	0.41
1:A:662:SER:HA	1:A:665:LYS:HG3	2.03	0.41
1:A:519:CYS:SG	1:A:521:ALA:HB3	2.61	0.41
1:A:624:LYS:O	1:A:627:ALA:HB3	2.21	0.41
1:A:163:ASP:CG	1:A:166:VAL:HG23	2.42	0.41
1:A:534:ARG:NH2	1:A:538:LEU:HD21	2.36	0.41
1:A:536:VAL:O	1:A:539:LEU:HB3	2.21	0.40
1:A:595:ILE:N	1:A:596:PRO:CD	2.81	0.40
1:A:598:PHE:CD1	1:A:616:VAL:HG11	2.56	0.40
1:A:148:ALA:C	1:A:150:ARG:H	2.23	0.40
1:A:401:LEU:HD11	1:A:433:ASN:ND2	2.36	0.40
1:A:641:GLU:C	1:A:643:LEU:H	2.24	0.40
1:A:168:ASN:O	1:A:172:VAL:HG23	2.21	0.40
1:A:471:THR:O	1:A:515:ASN:HB3	2.22	0.40
1:A:531:ALA:O	1:A:535:LEU:HG	2.21	0.40
1:A:607:GLU:O	1:A:610:GLN:N	2.54	0.40
1:A:301:GLN:HE21	1:A:302:ILE:N	2.19	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	546/780 (70%)	472 (86%)	67 (12%)	7 (1%)	12	39

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	456	ARG
1	A	287	LYS
1	A	430	ASN
1	A	476	ASP
1	A	474	HIS
1	A	475	GLN
1	A	320	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	455/651 (70%)	446 (98%)	9 (2%)	55	77

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	139	ILE
1	A	140	ASN
1	A	147	LEU
1	A	279	GLN

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Mol	Chain	Res	Type
1	A	287	LYS
1	A	301	GLN
1	A	670	LYS
1	A	671	LYS
1	A	673	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	137	ASN
1	A	140	ASN
1	A	168	ASN
1	A	203	ASN
1	A	205	ASN
1	A	219	ASN
1	A	260	ASN
1	A	279	GLN
1	A	301	GLN
1	A	325	ASN
1	A	379	ASN
1	A	406	GLN
1	A	414	ASN
1	A	425	ASN
1	A	433	ASN
1	A	481	GLN
1	A	502	HIS
1	A	543	HIS
1	A	544	GLN
1	A	644	HIS
1	A	667	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 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 [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	550/780 (70%)	-0.00	17 (3%) 49 48	26, 65, 96, 115	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	126	GLU	7.5
1	A	128	SER	6.2
1	A	127	PRO	6.1
1	A	551	SER	5.5
1	A	559	PHE	4.1
1	A	550	THR	3.8
1	A	678	THR	3.4
1	A	667	GLN	3.3
1	A	561	GLU	3.0
1	A	130	MET	2.8
1	A	548	ARG	2.5
1	A	674	SER	2.4
1	A	562	GLY	2.2
1	A	332	TYR	2.1
1	A	162	GLU	2.1
1	A	670	LYS	2.1
1	A	679	SER	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.