



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:10 AM UTC

PDB ID : 1LUJ / pdb_00001luj
Title : Crystal Structure of the Beta-catenin/ICAT Complex
Authors : Graham, T.A.; Clements, W.K.; Kimelman, D.; Xu, W.
Deposited on : 2002-05-22
Resolution : 2.50 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) : **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

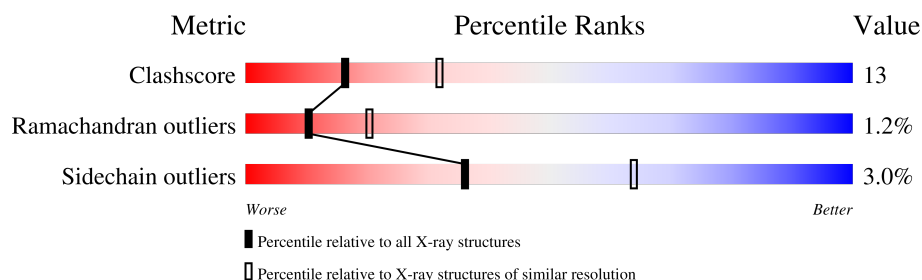
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)

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	514	
2	B	75	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4216 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 Catenin beta-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	501	Total	C	N	O	S	0	0	0
			3699	2331	669	673	26			

- Molecule 2 is a protein called Beta-catenin-interacting protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	71	Total	C	N	O	S	0	0	0
			517	323	89	102	3			

There are 2 discrepancies between the modelled and reference sequences:

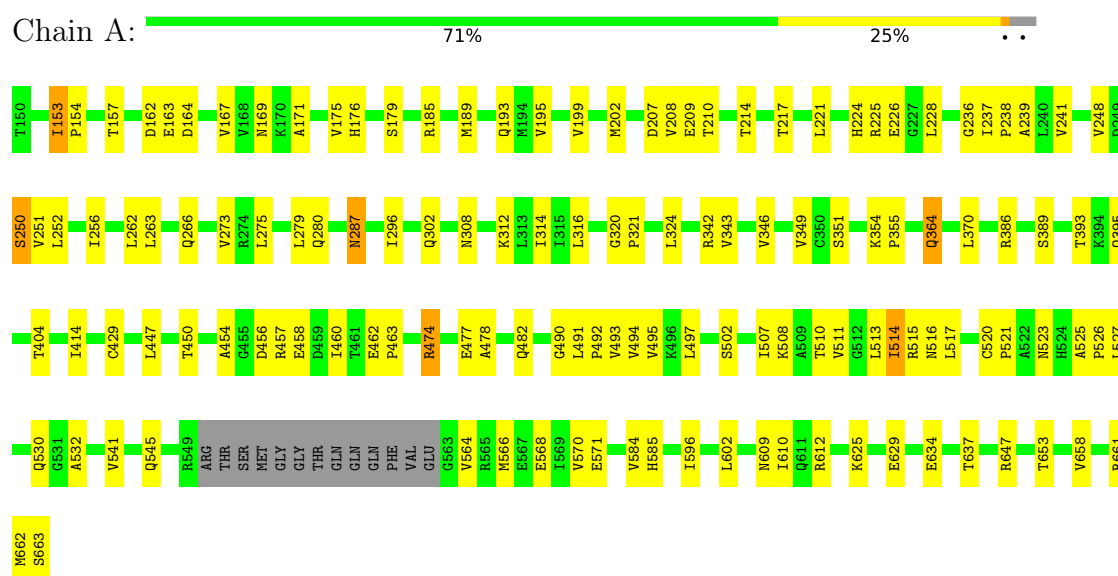
Chain	Residue	Modelled	Actual	Comment	Reference
B	8	ALA	GLY	conflict	UNP Q9JJN6
B	63	ALA	GLY	conflict	UNP Q9JJN6

3 Residue-property plots

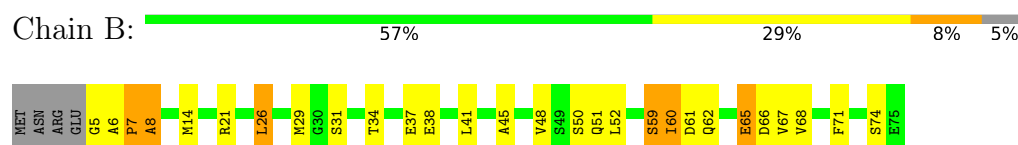
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: Catenin beta-1



• Molecule 2: Beta-catenin-interacting protein 1



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	95.17Å 98.50Å 86.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.74 – 2.50	Depositor
% Data completeness (in resolution range)	82.8 (43.74-2.50)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.210 , 0.255	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4216	wwPDB-VP
Average B, all atoms (Å ²)	32.0	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	0.45	0/3752	0.90	8/5111 (0.2%)
2	B	0.52	0/524	0.94	2/709 (0.3%)
All	All	0.45	0/4276	0.91	10/5820 (0.2%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	59	SER	N-CA-C	6.77	117.17	108.24
1	A	474	ARG	N-CA-C	6.63	120.23	111.28
1	A	153	ILE	CB-CA-C	-6.35	107.67	113.70
1	A	251	VAL	N-CA-C	-6.02	104.48	110.62
2	B	45	ALA	N-CA-C	-5.70	105.15	111.71
1	A	596	ILE	CB-CA-C	-5.62	108.36	113.70
1	A	389	SER	N-CA-C	5.22	117.64	111.33
1	A	637	THR	N-CA-C	5.12	117.52	111.33
1	A	532	ALA	N-CA-C	5.05	116.78	111.28
1	A	514	ILE	N-CA-C	-5.04	105.48	110.62

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	3699	0	3758	94	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	517	0	477	27	0
All	All	4216	0	4235	110	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 13.

All (110) 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:MET:HE3	1:A:226:GLU:HB2	1.50	0.93
2:B:8:ALA:HB3	2:B:14:MET:SD	2.12	0.90
2:B:26:LEU:HD22	2:B:31:SER:HB2	1.55	0.87
2:B:6:ALA:HB1	2:B:7:PRO:HD2	1.59	0.83
1:A:364:GLN:HE21	1:A:364:GLN:H	1.28	0.81
2:B:48:VAL:O	2:B:52:LEU:HB2	1.81	0.79
1:A:364:GLN:H	1:A:364:GLN:NE2	1.80	0.79
1:A:508:LYS:HE3	1:A:568:GLU:OE1	1.87	0.75
1:A:447:LEU:O	1:A:450:THR:HG22	1.90	0.70
1:A:612:ARG:NH1	2:B:62:GLN:HA	2.07	0.69
2:B:34:THR:HG23	2:B:37:GLU:H	1.59	0.67
1:A:185:ARG:HH11	1:A:224:HIS:CE1	2.15	0.65
1:A:263:LEU:HD21	1:A:273:VAL:HG21	1.78	0.65
2:B:5:GLY:N	2:B:50:SER:HG	1.95	0.64
1:A:490:GLY:O	1:A:494:VAL:HG23	1.97	0.64
1:A:164:ASP:O	1:A:167:VAL:HG22	1.97	0.64
1:A:515:ARG:HD3	1:A:515:ARG:C	2.22	0.64
1:A:653:THR:CB	2:B:29:MET:HE1	2.29	0.63
2:B:21:ARG:HB2	2:B:51:GLN:NE2	2.13	0.63
1:A:564:VAL:HG13	1:A:564:VAL:O	1.98	0.63
1:A:176:HIS:O	1:A:179:SER:HB3	1.99	0.62
2:B:68:VAL:HG13	2:B:68:VAL:O	1.98	0.62
1:A:653:THR:HG21	2:B:29:MET:CE	2.30	0.62
1:A:510:THR:O	1:A:514:ILE:HG12	1.99	0.62
1:A:625:LYS:O	1:A:629:GLU:HG3	2.00	0.62
1:A:478:ALA:O	1:A:482:GLN:HG3	2.00	0.62
1:A:225:ARG:NH1	1:A:266:GLN:OE1	2.32	0.61
1:A:515:ARG:HH11	1:A:516:ASN:ND2	1.99	0.61
1:A:612:ARG:HH12	2:B:62:GLN:HA	1.66	0.61
1:A:653:THR:HG21	2:B:29:MET:HE1	1.84	0.59
2:B:34:THR:HG22	2:B:37:GLU:CD	2.29	0.58
2:B:21:ARG:HB2	2:B:51:GLN:HE22	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:207:ASP:OD2	1:A:210:THR:HG23	2.04	0.57
1:A:490:GLY:O	1:A:493:VAL:HG12	2.03	0.57
1:A:185:ARG:NH1	1:A:224:HIS:CE1	2.73	0.56
1:A:202:MET:HB2	1:A:214:THR:OG1	2.05	0.56
1:A:354:LYS:HB3	1:A:355:PRO:HD3	1.88	0.56
1:A:454:ALA:O	1:A:457:ARG:HB2	2.06	0.56
1:A:460:ILE:O	1:A:463:PRO:HD2	2.05	0.56
1:A:349:VAL:HG11	2:B:74:SER:H	1.72	0.55
1:A:320:GLY:N	1:A:321:PRO:HD2	2.22	0.55
1:A:634:GLU:O	1:A:634:GLU:HG3	2.08	0.54
1:A:237:ILE:O	1:A:241:VAL:HG23	2.08	0.54
1:A:429:CYS:SG	2:B:67:VAL:C	2.92	0.53
1:A:458:GLU:OE2	1:A:502:SER:HA	2.09	0.53
1:A:280:GLN:NE2	1:A:314:ILE:HG21	2.24	0.52
1:A:491:LEU:HD22	1:A:527:LEU:HD21	1.91	0.52
1:A:515:ARG:HH11	1:A:516:ASN:HD22	1.57	0.52
1:A:447:LEU:HA	1:A:450:THR:HG22	1.91	0.51
1:A:302:GLN:HB2	1:A:343:VAL:HG22	1.91	0.51
1:A:236:GLY:O	1:A:239:ALA:HB3	2.11	0.51
1:A:279:LEU:HB2	1:A:280:GLN:NE2	2.27	0.50
1:A:658:VAL:HG12	1:A:662:MET:HE2	1.93	0.50
2:B:34:THR:HG22	2:B:37:GLU:CG	2.42	0.49
1:A:237:ILE:HB	1:A:238:PRO:HD3	1.94	0.49
2:B:29:MET:HG2	2:B:60:ILE:H	1.78	0.49
1:A:653:THR:CG2	2:B:29:MET:HE1	2.42	0.48
1:A:513:LEU:O	1:A:517:LEU:HG	2.13	0.48
2:B:7:PRO:O	2:B:8:ALA:HB2	2.13	0.48
1:A:525:ALA:HB3	1:A:526:PRO:HD3	1.95	0.48
1:A:153:ILE:N	1:A:154:PRO:HD2	2.30	0.47
1:A:185:ARG:HD2	1:A:224:HIS:HE1	1.79	0.47
1:A:414:ILE:HG23	1:A:460:ILE:HD11	1.96	0.47
1:A:202:MET:HB2	1:A:214:THR:CB	2.45	0.47
1:A:287:ASN:HD22	1:A:287:ASN:H	1.63	0.47
1:A:320:GLY:O	1:A:324:LEU:HG	2.14	0.47
1:A:584:VAL:HG13	1:A:585:HIS:N	2.29	0.47
1:A:208:VAL:HG23	1:A:209:GLU:N	2.30	0.47
1:A:228:LEU:HD22	1:A:262:LEU:HD23	1.96	0.47
1:A:491:LEU:HB2	1:A:492:PRO:HD3	1.96	0.47
1:A:495:VAL:HG21	1:A:530:GLN:HB3	1.96	0.47
1:A:462:GLU:HB3	1:A:463:PRO:HD3	1.96	0.47
1:A:523:ASN:C	1:A:526:PRO:HD2	2.40	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:179:SER:HB2	1:A:217:THR:HG23	1.96	0.46
1:A:157:THR:HG21	1:A:193:GLN:HG2	1.98	0.46
1:A:217:THR:O	1:A:221:LEU:HG	2.16	0.46
1:A:447:LEU:C	1:A:450:THR:HG22	2.40	0.46
1:A:169:ASN:HA	1:A:210:THR:HG22	1.98	0.46
1:A:395:GLN:HE21	1:A:395:GLN:HB3	1.60	0.46
1:A:507:ILE:O	1:A:511:VAL:HG23	2.16	0.46
1:A:653:THR:HG21	2:B:29:MET:HE3	1.98	0.46
1:A:308:ASN:O	1:A:312:LYS:HG3	2.16	0.46
1:A:171:ALA:O	1:A:175:VAL:HG23	2.16	0.45
1:A:287:ASN:HD22	1:A:287:ASN:N	2.15	0.45
1:A:346:VAL:O	1:A:349:VAL:HG22	2.17	0.44
2:B:29:MET:HA	2:B:59:SER:CB	2.48	0.44
1:A:493:VAL:O	1:A:497:LEU:HG	2.18	0.44
2:B:21:ARG:CZ	2:B:51:GLN:NE2	2.80	0.44
1:A:541:VAL:O	1:A:545:GLN:HG3	2.18	0.43
1:A:566:MET:O	1:A:570:VAL:HG23	2.18	0.43
1:A:386:ARG:HG2	2:B:71:PHE:CD2	2.53	0.43
1:A:185:ARG:HH11	1:A:185:ARG:HG2	1.84	0.42
1:A:571:GLU:HB2	1:A:610:ILE:CD1	2.50	0.42
1:A:248:VAL:HG12	1:A:250:SER:HB3	2.02	0.42
1:A:316:LEU:HD12	1:A:316:LEU:O	2.20	0.42
1:A:162:ASP:CG	1:A:163:GLU:H	2.28	0.41
1:A:520:CYS:HA	1:A:521:PRO:HD2	1.88	0.41
1:A:202:MET:HB2	1:A:214:THR:HB	2.02	0.41
1:A:256:ILE:HG23	1:A:296:ILE:HG21	2.02	0.41
1:A:491:LEU:HD23	1:A:491:LEU:HA	1.89	0.41
1:A:370:LEU:HB2	1:A:404:THR:HG21	2.02	0.41
1:A:162:ASP:CG	1:A:163:GLU:N	2.79	0.41
1:A:195:VAL:O	1:A:199:VAL:HG23	2.21	0.41
1:A:474:ARG:HH12	2:B:66:ASP:CG	2.28	0.41
1:A:571:GLU:HB2	1:A:610:ILE:HD11	2.03	0.41
1:A:571:GLU:CD	1:A:609:ASN:HB3	2.45	0.41
1:A:280:GLN:NE2	1:A:280:GLN:N	2.68	0.40
1:A:456:ASP:OD2	1:A:456:ASP:C	2.65	0.40
1:A:661:ARG:C	1:A:663:SER:H	2.29	0.40
2:B:68:VAL:O	2:B:68:VAL:CG1	2.69	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	497/514 (97%)	481 (97%)	14 (3%)	2 (0%)	30	49
2	B	69/75 (92%)	55 (80%)	9 (13%)	5 (7%)	1	1
All	All	566/589 (96%)	536 (95%)	23 (4%)	7 (1%)	10	20

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	60	ILE
2	B	65	GLU
1	A	250	SER
2	B	61	ASP
1	A	351	SER
2	B	7	PRO
2	B	8	ALA

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	386/426 (91%)	377 (98%)	9 (2%)	44	72
2	B	49/65 (75%)	45 (92%)	4 (8%)	10	23
All	All	435/491 (89%)	422 (97%)	13 (3%)	36	64

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	252	LEU
1	A	275	LEU
1	A	287	ASN
1	A	342	ARG
1	A	364	GLN
1	A	393	THR
1	A	477	GLU
1	A	602	LEU
1	A	647	ARG
2	B	26	LEU
2	B	38	GLU
2	B	41	LEU
2	B	65	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	161	ASN
1	A	165	GLN
1	A	223	HIS
1	A	224	HIS
1	A	261	ASN
1	A	265	HIS
1	A	280	GLN
1	A	287	ASN
1	A	302	GLN
1	A	364	GLN
1	A	395	GLN
1	A	503	HIS
1	A	516	ASN
1	A	544	HIS
1	A	548	GLN
1	A	585	HIS
1	A	611	GLN
2	B	17	GLN
2	B	51	GLN

5.3.3 RNA ⓘ

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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.