



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 11:30 PM UTC

PDB ID : 2WVR / pdb_00002wvr
Title : Human Cdt1:Geminin complex
Authors : De Marco, V.; Perrakis, A.
Deposited on : 2009-10-19
Resolution : 3.30 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

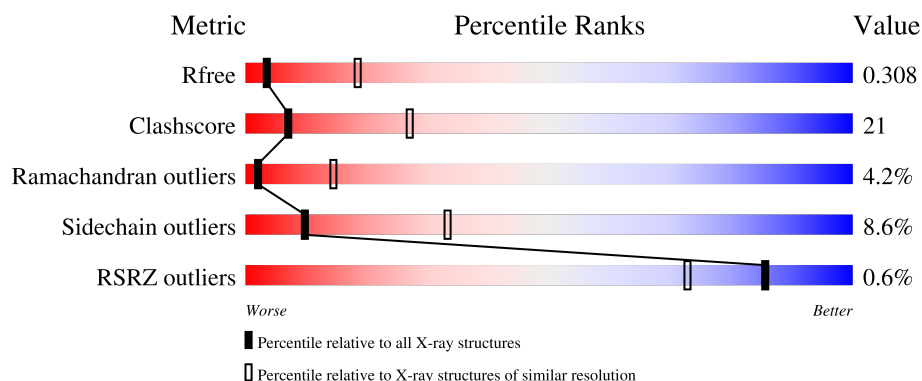
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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	1169 (3.32-3.28)
Clashscore	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)
RSRZ outliers	180081	1169 (3.32-3.28)

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	209	
1	B	209	
2	C	546	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2611 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 GEMININ.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	70	Total	C	N	O	S	0	0	0
			590	368	106	115	1			
1	B	74	Total	C	N	O	S	0	0	0
			629	396	110	121	2			

- Molecule 2 is a protein called DNA REPLICATION FACTOR CDT1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	172	Total	C	N	O	S	0	0	0
			1392	885	254	247	6			



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	92.80Å 92.80Å 164.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.41 – 3.30 19.41 – 3.30	Depositor EDS
% Data completeness (in resolution range)	99.7 (19.41-3.30) 99.1 (19.41-3.30)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.60 (at 3.29Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.240 , 0.301 0.238 , 0.308	Depositor DCC
R_{free} test set	529 reflections (4.68%)	wwPDB-VP
Wilson B-factor (Å ²)	136.5	Xtriage
Anisotropy	0.315	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 94.9	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	0.95	EDS
Total number of atoms	2611	wwPDB-VP
Average B, all atoms (Å ²)	146.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.97% 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

5.1 Standard geometry

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	0.29	0/597	0.73	0/795
1	B	0.30	0/637	0.73	0/849
2	C	0.34	0/1427	0.89	8/1935 (0.4%)
All	All	0.32	0/2661	0.82	8/3579 (0.2%)

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
2	C	0	1

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	178	GLN	CA-C-N	5.86	127.17	119.84
2	C	178	GLN	C-N-CA	5.86	127.17	119.84
2	C	185	VAL	N-CA-C	5.40	116.55	109.21
2	C	332	HIS	CA-C-N	5.39	125.04	119.05
2	C	332	HIS	C-N-CA	5.39	125.04	119.05
2	C	167	ALA	CA-C-N	5.36	126.55	119.84
2	C	167	ALA	C-N-CA	5.36	126.55	119.84
2	C	316	SER	CB-CA-C	-5.11	109.08	116.54

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	167	ALA	Peptide

5.2 Too-close contacts ⓘ

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	590	0	594	20	0
1	B	629	0	635	22	0
2	C	1392	0	1392	78	0
All	All	2611	0	2621	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 21.

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)
2:C:283:ALA:HB3	2:C:284:PRO:HD3	1.55	0.87
2:C:298:PHE:O	2:C:302:LEU:HD12	1.75	0.86
2:C:215:THR:HG22	2:C:217:ALA:H	1.44	0.83
2:C:200:MET:HE2	2:C:247:TYR:CE1	2.15	0.82
1:B:148:VAL:HG13	1:B:149:GLN:H	1.46	0.81
2:C:290:ARG:O	2:C:294:ARG:HG3	1.94	0.68
1:B:142:ALA:O	1:B:146:GLU:HG3	1.96	0.66
1:A:91:LYS:O	1:A:92:GLU:HB3	1.93	0.66
1:A:148:VAL:HG23	1:B:151:MET:HE2	1.79	0.64
2:C:300:GLN:O	2:C:303:VAL:HG12	1.98	0.64
1:A:155:ILE:HD13	1:B:154:LEU:HD13	1.81	0.63
2:C:209:ASN:HB3	2:C:284:PRO:HB3	1.82	0.62
2:C:316:SER:OG	2:C:317:LEU:HD22	2.00	0.62
2:C:179:PRO:O	2:C:181:LEU:N	2.34	0.61
2:C:215:THR:HG21	2:C:268:GLN:NE2	2.15	0.61
2:C:332:HIS:CD2	2:C:334:ARG:H	2.19	0.60
2:C:167:ALA:HB1	2:C:168:PRO:CD	2.31	0.60
1:B:148:VAL:HG13	1:B:149:GLN:N	2.16	0.60
2:C:277:GLN:HB2	2:C:285:GLN:HE22	1.66	0.60
2:C:232:GLU:H	2:C:235:ASN:HD22	1.50	0.59
2:C:317:LEU:HD22	2:C:317:LEU:H	1.67	0.58
1:A:124:ILE:HG22	1:B:124:ILE:HG12	1.85	0.58
2:C:336:ASN:HD22	2:C:336:ASN:N	2.02	0.58
2:C:167:ALA:CB	2:C:168:PRO:CD	2.81	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:91:LYS:O	1:A:92:GLU:CB	2.52	0.57
2:C:195:GLU:C	2:C:227:MET:HE1	2.29	0.57
2:C:198:ARG:O	2:C:202:THR:HG23	2.04	0.57
2:C:298:PHE:CE2	2:C:302:LEU:HD11	2.39	0.57
2:C:199:SER:HA	2:C:226:MET:HE1	1.87	0.56
2:C:243:TYR:CG	2:C:246:SER:HB3	2.41	0.56
2:C:232:GLU:H	2:C:235:ASN:ND2	2.03	0.56
2:C:318:SER:O	2:C:320:ALA:N	2.39	0.56
1:B:131:ILE:O	1:B:135:LYS:HB2	2.06	0.56
2:C:243:TYR:CD1	2:C:246:SER:HB3	2.42	0.55
1:B:90:ILE:O	2:C:330:ARG:NH2	2.37	0.55
2:C:277:GLN:HG2	2:C:278:GLU:N	2.20	0.54
2:C:215:THR:HG23	2:C:268:GLN:HG2	1.89	0.54
2:C:209:ASN:HA	2:C:284:PRO:HA	1.89	0.54
2:C:201:ASP:OD2	2:C:291:LEU:HD13	2.07	0.54
1:B:97:GLN:HA	1:B:100:LYS:HB3	1.90	0.53
2:C:286:LEU:HD23	2:C:290:ARG:HB2	1.91	0.52
2:C:187:PRO:HD2	2:C:190:TYR:HB2	1.91	0.52
2:C:197:PHE:O	2:C:198:ARG:C	2.53	0.52
1:A:120:LEU:O	1:A:124:ILE:HG23	2.11	0.51
2:C:272:GLU:HG2	2:C:273:PRO:HD2	1.93	0.51
2:C:352:PRO:O	2:C:353:ALA:C	2.53	0.51
2:C:204:VAL:HG11	2:C:247:TYR:HE2	1.76	0.51
2:C:248:ARG:HD3	2:C:250:ARG:NH2	2.26	0.50
2:C:200:MET:HE2	2:C:247:TYR:CZ	2.47	0.50
2:C:277:GLN:HG3	2:C:281:GLY:HA2	1.92	0.50
1:A:145:ALA:O	1:A:149:GLN:HG3	2.11	0.50
2:C:167:ALA:CB	2:C:168:PRO:HD2	2.42	0.49
2:C:277:GLN:HG3	2:C:281:GLY:CA	2.43	0.49
1:B:139:LYS:O	1:B:143:GLU:HB2	2.12	0.49
2:C:194:ALA:HA	2:C:298:PHE:CE2	2.47	0.49
2:C:249:PHE:HB3	2:C:269:LEU:HD21	1.96	0.48
1:B:145:ALA:O	1:B:148:VAL:HG12	2.14	0.48
2:C:199:SER:O	2:C:200:MET:C	2.56	0.48
2:C:249:PHE:CE2	2:C:271:ILE:HG23	2.48	0.47
2:C:287:THR:H	2:C:290:ARG:HG3	1.78	0.47
1:B:93:ASN:HA	1:B:94:PRO:HD3	1.71	0.47
2:C:248:ARG:HB2	2:C:274:LEU:HD21	1.97	0.47
2:C:277:GLN:HG3	2:C:285:GLN:HE22	1.80	0.46
1:B:147:HIS:O	1:B:149:GLN:N	2.49	0.46
2:C:314:LEU:HD22	2:C:321:MET:HE3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:145:ALA:HA	1:A:148:VAL:CG1	2.46	0.46
2:C:178:GLN:HA	2:C:179:PRO:HD3	1.64	0.46
1:A:95:SER:O	1:A:96:SER:C	2.59	0.46
1:A:114:LEU:HD11	2:C:173:PHE:HB2	1.97	0.46
2:C:277:GLN:CB	2:C:285:GLN:HE22	2.29	0.46
2:C:202:THR:HA	2:C:291:LEU:HD21	1.98	0.46
2:C:194:ALA:HA	2:C:298:PHE:HE2	1.80	0.46
2:C:272:GLU:HG2	2:C:273:PRO:CD	2.46	0.45
2:C:199:SER:OG	2:C:227:MET:HE3	2.16	0.45
1:A:121:HIS:O	1:A:124:ILE:HG12	2.17	0.45
1:B:101:GLU:OE2	2:C:334:ARG:HD3	2.16	0.45
2:C:215:THR:HG22	2:C:217:ALA:N	2.23	0.45
2:C:296:GLN:O	2:C:300:GLN:HG3	2.16	0.45
2:C:182:PRO:HB2	2:C:183:GLY:H	1.67	0.45
2:C:196:MET:N	2:C:227:MET:HE1	2.30	0.44
2:C:195:GLU:HB3	2:C:227:MET:CE	2.48	0.44
2:C:199:SER:HA	2:C:226:MET:CE	2.47	0.44
1:A:111:TYR:C	1:A:111:TYR:CD1	2.96	0.44
2:C:167:ALA:HB1	2:C:168:PRO:HD3	2.00	0.44
2:C:201:ASP:HA	2:C:247:TYR:OH	2.17	0.44
1:A:98:TYR:O	1:A:102:VAL:HG23	2.18	0.43
1:A:123:GLU:O	1:A:127:LYS:HG2	2.18	0.43
2:C:243:TYR:HB2	2:C:298:PHE:HD1	1.83	0.43
2:C:314:LEU:C	2:C:316:SER:H	2.25	0.43
2:C:224:GLN:HE21	2:C:231:PHE:H	1.67	0.43
1:B:101:GLU:CD	2:C:334:ARG:HD3	2.44	0.43
1:B:110:LEU:O	1:B:114:LEU:HD13	2.18	0.43
2:C:213:THR:HA	2:C:214:PRO:HD3	1.76	0.43
1:A:124:ILE:HG22	1:B:124:ILE:CG1	2.47	0.42
1:A:138:ASN:HD22	1:A:138:ASN:HA	1.59	0.42
2:C:180:GLY:O	2:C:181:LEU:C	2.61	0.42
2:C:283:ALA:CB	2:C:284:PRO:HD3	2.35	0.42
1:B:86:PHE:N	1:B:89:MET:HE2	2.34	0.42
1:A:100:LYS:HE3	1:B:99:TRP:CZ2	2.55	0.42
1:B:147:HIS:O	1:B:148:VAL:C	2.63	0.42
2:C:246:SER:O	2:C:294:ARG:NH2	2.53	0.41
2:C:282:ALA:O	2:C:285:GLN:HG3	2.20	0.41
1:B:116:GLU:OE2	2:C:172:ARG:NH1	2.54	0.41
1:A:111:TYR:C	1:A:111:TYR:HD1	2.27	0.41
1:A:98:TYR:CE2	1:A:102:VAL:HG21	2.55	0.40
2:C:170:TYR:CD2	2:C:170:TYR:C	2.98	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:136:LYS:O	1:A:140:GLU:HG3	2.20	0.40
1:B:91:LYS:HG3	1:B:92:GLU:HG3	2.02	0.40
2:C:208:HIS:CG	2:C:273:PRO:HG2	2.57	0.40
2:C:308:GLU:OE2	2:C:308:GLU:HA	2.20	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	68/209 (32%)	62 (91%)	4 (6%)	2 (3%)	3	21
1	B	72/209 (34%)	66 (92%)	4 (6%)	2 (3%)	4	21
2	C	168/546 (31%)	141 (84%)	18 (11%)	9 (5%)	1	10
All	All	308/964 (32%)	269 (87%)	26 (8%)	13 (4%)	2	14

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	96	SER
1	B	147	HIS
1	B	148	VAL
2	C	168	PRO
2	C	180	GLY
2	C	182	PRO
1	A	92	GLU
2	C	319	PRO
2	C	320	ALA
2	C	199	SER
2	C	198	ARG
2	C	181	LEU
2	C	352	PRO

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	62/189 (33%)	58 (94%)	4 (6%)	15	43
1	B	67/189 (35%)	62 (92%)	5 (8%)	12	38
2	C	149/456 (33%)	134 (90%)	15 (10%)	7	26
All	All	278/834 (33%)	254 (91%)	24 (9%)	10	33

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	131	ILE
1	A	138	ASN
1	A	148	VAL
1	A	156	GLU
1	B	90	ILE
1	B	93	ASN
1	B	137	GLU
1	B	154	LEU
1	B	159	ASN
2	C	189	LYS
2	C	210	ARG
2	C	241	THR
2	C	269	LEU
2	C	276	GLU
2	C	277	GLN
2	C	278	GLU
2	C	286	LEU
2	C	287	THR
2	C	291	LEU
2	C	292	LEU
2	C	296	GLN
2	C	302	LEU
2	C	317	LEU
2	C	336	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13)

such sidechains are listed below:

Mol	Chain	Res	Type
1	A	138	ASN
1	B	129	ASN
1	B	147	HIS
1	B	159	ASN
2	C	191	GLN
2	C	220	GLN
2	C	224	GLN
2	C	235	ASN
2	C	268	GLN
2	C	277	GLN
2	C	285	GLN
2	C	310	HIS
2	C	336	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 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](#)

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	70/209 (33%)	-0.39	0 100 100	119, 149, 166, 172	0
1	B	74/209 (35%)	-0.20	1 (1%) 73 55	116, 153, 178, 183	0
2	C	172/546 (31%)	-0.27	1 (0%) 85 73	106, 137, 208, 243	0
All	All	316/964 (32%)	-0.28	2 (0%) 85 73	106, 144, 181, 243	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	86	PHE	3.8
2	C	181	LEU	3.0

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.