



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 06:19 PM UTC

PDB ID : 1IEF / pdb_00001ief
Title : CRYSTAL STRUCTURE OF THE CATALYTIC SITE MUTANT S134A OF
THE HUMAN CYTOMEGALOVIRUS PROTEASE
Authors : Khayat, R.; Batra, R.; Massariol, M.J.; Lagace, L.; Tong, L.
Deposited on : 2001-04-09
Resolution : 2.30 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)	:	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

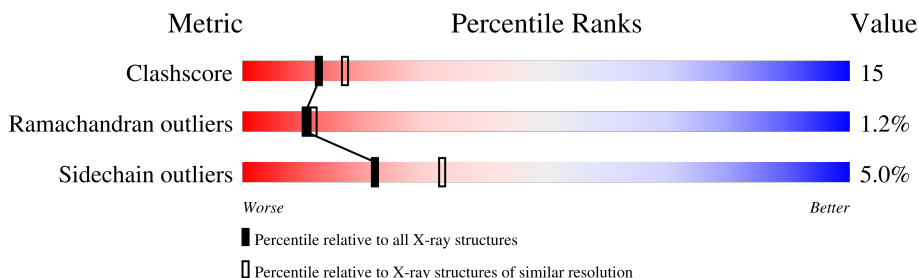
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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))
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)

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 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	256	
1	B	256	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3584 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 CAPSID PROTEIN P40: ASSEMBLIN PROTEASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	208	Total	C	N	O	S	0	0	0
			1628	1028	294	302	4			
1	B	220	Total	C	N	O	S	0	0	0
			1715	1078	308	325	4			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	134	ALA	SER	engineered mutation	UNP P16753
A	143	GLN	ALA	engineered mutation	UNP P16753
B	434	ALA	SER	engineered mutation	UNP P16753
B	443	GLN	ALA	engineered mutation	UNP P16753

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	95	Total	O	0	0
			95	95		
2	B	146	Total	O	0	0
			146	146		

4 Data and refinement statistics

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

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	76.40 Å 76.40 Å 171.80 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.34 – 2.30	Depositor
% Data completeness (in resolution range)	97.3 (29.34-2.30)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.229 , 0.270	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3584	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

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	0.39	0/1660	0.89	4/2248 (0.2%)
1	B	0.41	0/1747	0.90	6/2366 (0.3%)
All	All	0.40	0/3407	0.89	10/4614 (0.2%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	413	SER	N-CA-C	7.27	125.88	109.81
1	B	484	PHE	CA-C-N	5.72	125.57	119.28
1	B	484	PHE	C-N-CA	5.72	125.57	119.28
1	B	380	ASP	N-CA-C	5.55	120.05	113.28
1	A	160	LEU	N-CA-C	-5.46	100.40	109.46
1	A	34	LEU	CA-C-N	5.21	125.21	119.89
1	A	34	LEU	C-N-CA	5.21	125.21	119.89
1	B	476	ASP	CA-C-N	5.10	124.71	119.05
1	B	476	ASP	C-N-CA	5.10	124.71	119.05
1	A	66	THR	N-CA-C	-5.05	106.70	112.92

There are no chirality outliers.

There are no planarity outliers.

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	1628	0	1615	65	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1715	0	1690	40	1
2	A	95	0	0	2	0
2	B	146	0	0	4	0
All	All	3584	0	3305	102	1

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 15.

All (102) 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:248:THR:HG22	1:A:250:ARG:H	1.33	0.93
1:B:542:LYS:HE3	1:B:548:THR:HG22	1.59	0.84
1:A:163:VAL:HG11	1:A:234:ARG:HG3	1.62	0.80
1:A:163:VAL:HG12	1:A:238:LEU:HD13	1.66	0.78
1:A:29:GLU:HB3	1:A:31:GLU:HG2	1.66	0.76
1:B:483:ARG:HA	1:B:550:ARG:HG2	1.67	0.76
1:B:373:ALA:HB3	1:B:385:LEU:HD12	1.69	0.74
1:A:223:GLY:O	1:A:226:VAL:HG12	1.88	0.73
1:A:163:VAL:HG12	1:A:238:LEU:CD1	2.21	0.71
1:B:545:VAL:HG23	1:B:547:VAL:HG23	1.73	0.70
1:B:431:LEU:HD13	1:B:471:ALA:HB2	1.75	0.68
1:B:361:ILE:HD13	1:B:521:LEU:HD21	1.76	0.67
1:A:27:PRO:HB2	1:A:32:LEU:HB2	1.78	0.65
1:B:523:GLY:O	1:B:526:VAL:HG12	1.98	0.63
1:A:131:LEU:HD13	1:A:171:ALA:HB2	1.80	0.62
1:A:58:PRO:HG2	1:A:157:HIS:HB3	1.82	0.62
1:A:23:TYR:CE2	1:A:81:GLY:HA2	2.35	0.62
1:A:245:VAL:HG23	1:A:247:VAL:HG23	1.81	0.61
1:A:163:VAL:CG1	1:A:234:ARG:HG3	2.29	0.61
1:A:111:PRO:HD3	1:A:122:GLU:OE2	2.00	0.61
1:A:57:LEU:HD21	1:A:155:PHE:HB2	1.83	0.61
1:A:233:GLU:C	1:A:236:PRO:HD2	2.26	0.60
1:A:90:SER:O	1:A:94:LEU:HD23	2.02	0.59
1:B:361:ILE:HD12	1:B:367:ALA:HB1	1.83	0.58
1:A:229:LEU:HD23	1:B:529:LEU:HD23	1.84	0.58
1:B:463:VAL:HG23	1:B:538:LEU:HD13	1.87	0.56
1:A:162:SER:O	1:A:163:VAL:HG13	2.06	0.56
1:A:113:SER:HB3	1:A:114:PRO:CD	2.36	0.56
1:A:178:GLU:O	1:A:182:GLN:HG2	2.06	0.56
1:A:35:PRO:O	1:A:39:VAL:HG23	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:361:ILE:HD11	1:B:393:PHE:CE1	2.42	0.55
1:A:61:ILE:HD11	1:A:93:PHE:CE1	2.43	0.54
1:B:339:VAL:O	1:B:343:LEU:HB2	2.07	0.54
1:A:88:VAL:HG12	1:A:94:LEU:HD21	1.90	0.54
1:B:535:LEU:O	1:B:539:ARG:HG3	2.07	0.54
1:A:180:VAL:O	1:A:183:ARG:HB2	2.08	0.53
1:A:162:SER:OG	1:A:234:ARG:NE	2.38	0.53
1:A:75:MET:CE	1:A:82:LEU:HD21	2.39	0.53
1:B:315:TYR:CD2	1:B:477:PRO:HG3	2.44	0.53
1:B:479:TRP:O	1:B:483:ARG:HD2	2.09	0.52
1:A:96:ILE:HD13	2:B:58:HOH:O	2.09	0.52
1:B:533:GLU:C	1:B:536:PRO:HD2	2.34	0.52
1:B:329:GLU:OE2	1:B:465:ARG:NH1	2.43	0.52
1:A:58:PRO:O	1:A:157:HIS:HB2	2.10	0.51
1:A:35:PRO:O	1:A:38:VAL:HG22	2.10	0.51
1:B:361:ILE:HD13	1:B:521:LEU:CD2	2.41	0.51
1:B:357:LEU:HD22	1:B:456:LYS:O	2.10	0.51
1:A:30:ALA:HA	1:A:33:LEU:HD23	1.93	0.50
1:A:27:PRO:HG2	1:A:33:LEU:HD22	1.92	0.50
1:A:58:PRO:HG2	1:A:157:HIS:CB	2.42	0.49
1:B:505:THR:C	1:B:507:VAL:H	2.20	0.49
1:A:182:GLN:HG3	2:A:306:HOH:O	2.13	0.49
1:A:96:ILE:CD1	1:B:519:TYR:HE1	2.26	0.49
1:B:315:TYR:CE2	1:B:477:PRO:HG3	2.48	0.49
1:A:113:SER:HB3	1:A:114:PRO:HD3	1.95	0.48
1:A:241:ASP:O	1:A:245:VAL:HG22	2.14	0.48
1:B:480:VAL:O	1:B:483:ARG:HB2	2.14	0.48
1:B:496:ARG:HG3	1:B:499:TRP:CZ2	2.49	0.48
1:B:435:SER:C	1:B:456:LYS:HD3	2.39	0.47
1:B:496:ARG:HA	1:B:499:TRP:NE1	2.29	0.47
1:A:30:ALA:HA	1:A:33:LEU:CD2	2.44	0.47
1:A:178:GLU:OE1	1:A:196:ARG:NE	2.45	0.47
1:A:27:PRO:HG3	1:A:33:LEU:HA	1.97	0.47
1:A:27:PRO:CG	1:A:33:LEU:HD22	2.44	0.47
1:A:15:TYR:HD2	1:A:85:LEU:HD11	1.79	0.47
1:A:35:PRO:HD2	1:A:38:VAL:HG21	1.98	0.46
1:A:61:ILE:HD11	1:A:69:VAL:HG11	1.97	0.46
1:A:63:HIS:CE1	1:A:134:ALA:HB2	2.51	0.46
1:B:496:ARG:O	1:B:500:GLN:HG3	2.15	0.46
1:B:534:ARG:NE	2:B:60:HOH:O	2.49	0.46
1:A:95:GLU:OE2	1:A:98:ARG:NH1	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:62:ASN:O	1:A:63:HIS:HB2	2.16	0.45
1:B:402:GLU:OE2	1:B:419:LYS:HD3	2.17	0.45
1:A:20:LEU:HD12	1:A:75:MET:HE3	1.99	0.45
1:A:179:TRP:O	1:A:183:ARG:HD2	2.17	0.45
1:A:29:GLU:C	1:A:31:GLU:H	2.25	0.44
1:A:96:ILE:HD12	1:B:519:TYR:HE1	1.82	0.44
1:A:156:LYS:O	1:A:157:HIS:HB3	2.18	0.44
1:A:27:PRO:CB	1:A:32:LEU:HB2	2.46	0.43
1:B:403:LYS:NZ	1:B:403:LYS:HB3	2.34	0.43
1:A:76:GLN:OE1	1:A:194:GLY:HA3	2.19	0.43
1:B:483:ARG:O	1:B:485:PRO:HD3	2.19	0.43
1:A:62:ASN:HD22	1:A:62:ASN:HA	1.66	0.42
1:B:392:ARG:O	1:B:396:ILE:HG13	2.18	0.42
1:B:549:GLU:O	1:B:550:ARG:C	2.61	0.42
1:A:27:PRO:CG	1:A:33:LEU:HD13	2.49	0.42
1:B:467:ARG:NE	1:B:467:ARG:HA	2.34	0.42
1:A:238:LEU:HB3	1:A:256:ALA:HB1	2.02	0.42
1:A:23:TYR:CD2	1:A:81:GLY:HA2	2.55	0.41
1:A:34:LEU:HG	1:A:39:VAL:CG2	2.49	0.41
1:A:162:SER:O	1:A:163:VAL:CG1	2.68	0.41
1:A:179:TRP:NE1	1:A:183:ARG:NH1	2.68	0.41
1:B:492:ARG:HD2	2:B:47:HOH:O	2.19	0.41
1:B:511:GLY:N	2:B:131:HOH:O	2.54	0.41
1:A:183:ARG:HA	1:A:183:ARG:NE	2.35	0.41
1:A:212:ASP:HB3	2:A:282:HOH:O	2.20	0.41
1:B:484:PHE:HA	1:B:485:PRO:HD3	1.86	0.41
1:A:113:SER:CB	1:A:114:PRO:CD	2.99	0.41
1:B:385:LEU:C	1:B:385:LEU:HD13	2.46	0.41
1:A:167:ARG:NE	1:A:167:ARG:HA	2.35	0.41
1:A:15:TYR:CD2	1:A:85:LEU:HD11	2.56	0.40
1:B:323:TYR:CD2	1:B:381:GLY:HA2	2.57	0.40

All (1) 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:B:550:ARG:NH1	1:B:550:ARG:NH1[7_646]	1.66	0.54

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	200/256 (78%)	182 (91%)	15 (8%)	3 (2%)	8	8
1	B	210/256 (82%)	197 (94%)	11 (5%)	2 (1%)	12	15
All	All	410/512 (80%)	379 (92%)	26 (6%)	5 (1%)	10	12

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	113	SER
1	B	413	SER
1	A	135	SER
1	B	549	GLU
1	A	11	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	173/214 (81%)	165 (95%)	8 (5%)	24	36
1	B	184/214 (86%)	174 (95%)	10 (5%)	20	29
All	All	357/428 (83%)	339 (95%)	18 (5%)	22	33

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

Mol	Chain	Res	Type
1	A	24	ASP

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Mol	Chain	Res	Type
1	A	25	GLN
1	A	29	GLU
1	A	62	ASN
1	A	99	ARG
1	A	131	LEU
1	A	183	ARG
1	A	238	LEU
1	B	322	ARG
1	B	324	ASP
1	B	362	ASN
1	B	394	LEU
1	B	403	LYS
1	B	411	PRO
1	B	431	LEU
1	B	483	ARG
1	B	538	LEU
1	B	548	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	62	ASN
1	A	116	GLN
1	A	182	GLN
1	A	224	ASN
1	A	243	GLN
1	B	306	GLN
1	B	362	ASN
1	B	482	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 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.