



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 18, 2024 – 11:00 AM EDT

PDB ID : 7H3K
Title : Group deposition for crystallographic fragment screening of Coxsackievirus A16 (G-10) 2A protease – Crystal structure of Coxsackievirus A16 (G-10) 2A protease in complex with Z71580604 (A71EV2A-x0416)
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Deposited on : 2024-04-04
Resolution : 1.28 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36.1
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)

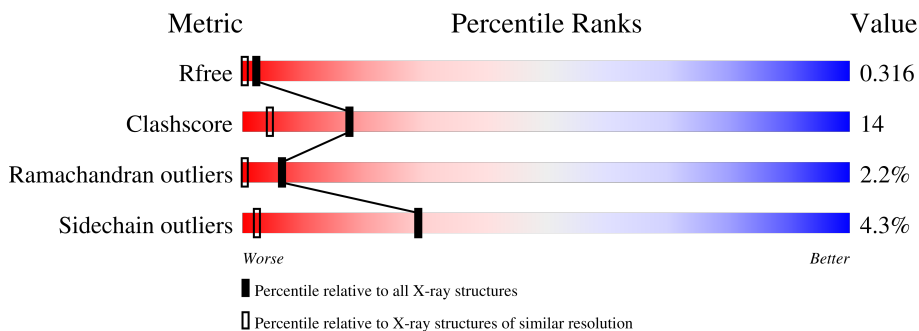
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.28 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	1850 (1.30-1.26)
Clashscore	141614	1926 (1.30-1.26)
Ramachandran outliers	138981	1860 (1.30-1.26)
Sidechain outliers	138945	1859 (1.30-1.26)

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	150	 70% 19% •• 7%

Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.1

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 1337 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.

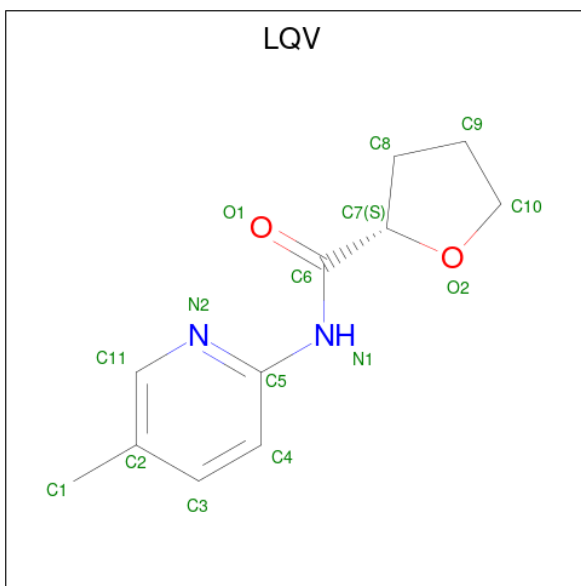
- Molecule 1 is a protein called Protease 2A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	140	1097	683	195	212	7	0	2	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLN	-	expression tag	UNP Q65900
A	2	GLU	-	expression tag	UNP Q65900
A	3	GLN	-	expression tag	UNP Q65900
A	4	THR	-	expression tag	UNP Q65900
A	5	GLY	-	expression tag	UNP Q65900
A	6	GLY	-	expression tag	UNP Q65900

- Molecule 2 is (2S)-N-(5-methylpyridin-2-yl)oxolane-2-carboxamide (three-letter code: LQV) (formula: C₁₁H₁₄N₂O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	15	11	2	2	0	0

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
3	A	1	1	1	0	0

- Molecule 4 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C₂H₆OS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	S		
4	A	1	4	2	1	1	0	0
4	A	1	4	2	1	1	0	0
4	A	1	4	2	1	1	0	0
4	A	1	4	2	1	1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	208	208	208	0	0

3 Residue-property plots [i](#)

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.

- Molecule 1: Protease 2A

Chain A:  70% 19% •• 7%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	86.19Å 56.40Å 32.42Å 90.00° 94.87° 90.00°	Depositor
Resolution (Å)	47.14 – 1.28 47.14 – 1.28	Depositor EDS
% Data completeness (in resolution range)	98.1 (47.14-1.28) 98.2 (47.14-1.28)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.04 (at 1.28Å)	Xtrriage
Refinement program	REFMAC 5.8.0267, REFMAC5	Depositor
R, R_{free}	0.202 , 0.238 0.299 , 0.316	Depositor DCC
R_{free} test set	1939 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	16.4	Xtrriage
Anisotropy	0.038	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.21 , 30.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	1337	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.27% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: DMS, LQV, ZN

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	0.73	0/1123	0.92	1/1527 (0.1%)

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
1	A	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	115	ARG	NE-CZ-NH1	5.87	123.23	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	130	GLY	Peptide

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	1097	0	1030	30	0
2	A	15	0	0	0	0
3	A	1	0	0	0	0
4	A	16	0	24	0	0
5	A	208	0	0	7	0
All	All	1337	0	1054	30	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 14.

All (30) 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:50:CYS:O	1:A:51:ASP:OD1	1.86	0.92
1:A:49:GLY:O	5:A:301:HOH:O	2.05	0.75
1:A:81:LEU:HG	1:A:94:TYR:HB3	1.71	0.72
1:A:13:GLY:O	1:A:49:GLY:N	2.23	0.71
1:A:50:CYS:O	1:A:50:CYS:SG	2.54	0.66
1:A:88:GLU:OE1	5:A:302:HOH:O	2.16	0.61
1:A:102:VAL:HG13	1:A:131:LEU:CD1	2.32	0.59
1:A:110:CYS:SG	1:A:125:SER:O	2.62	0.58
1:A:82:ILE:HG22	1:A:83:PHE:O	2.04	0.58
1:A:81:LEU:CG	1:A:94:TYR:HB3	2.35	0.57
1:A:99:MET:O	1:A:133:GLY:HA2	2.07	0.53
1:A:84:VAL:CG2	1:A:95:GLN:HB2	2.38	0.53
1:A:14:ASN:ND2	1:A:47:ALA:O	2.42	0.52
1:A:86:ALA:HB2	5:A:448:HOH:O	2.09	0.51
1:A:92:ALA:O	1:A:93:ARG:O	2.29	0.51
1:A:127:GLY:HA2	1:A:131:LEU:O	2.13	0.48
1:A:81:LEU:CD1	1:A:94:TYR:HB3	2.44	0.48
1:A:48:GLN:NE2	5:A:313:HOH:O	2.47	0.48
1:A:46:THR:O	5:A:303:HOH:O	2.20	0.48
1:A:36[A]:SER:O	1:A:93:ARG:NH2	2.44	0.48
1:A:36[B]:SER:O	1:A:93:ARG:NH2	2.43	0.47
1:A:71:HIS:HE1	5:A:420:HOH:O	1.96	0.47
1:A:21:HIS:HB2	1:A:89:TYR:CD2	2.50	0.46
1:A:130:GLY:O	1:A:131:LEU:HB2	2.17	0.44
1:A:91:PRO:O	1:A:92:ALA:HB2	2.19	0.43
1:A:126:THR:OG1	1:A:133:GLY:HA3	2.19	0.42
1:A:102:VAL:HA	1:A:131:LEU:CD1	2.50	0.42
1:A:82:ILE:HD11	5:A:308:HOH:O	2.19	0.42
1:A:36[B]:SER:C	1:A:93:ARG:HH12	2.23	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:36[A]:SER:C	1:A:93:ARG:HH12	2.24	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	140/150 (93%)	134 (96%)	3 (2%)	3 (2%)	7 0

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	92	ALA
1	A	93	ARG
1	A	131	LEU

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	119/124 (96%)	114 (96%)	5 (4%)	30 2

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	93	ARG
1	A	95	GLN
1	A	125	SER
1	A	129	ASN
1	A	146	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	14	ASN
1	A	71	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	LQV	A	201	-	16,16,16	0.23	0	17,21,21	0.32	0
4	DMS	A	206	-	3,3,3	0.27	0	3,3,3	0.12	0
4	DMS	A	204	-	3,3,3	0.40	0	3,3,3	0.08	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	DMS	A	205	-	3,3,3	0.28	0	3,3,3	0.13	0
4	DMS	A	203	-	3,3,3	0.27	0	3,3,3	0.08	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	LQV	A	201	-	-	3/8/15/15	0/2/2/2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	201	LQV	N1-C6-C7-C8
2	A	201	LQV	O1-C6-C7-C8
2	A	201	LQV	O1-C6-C7-O2

There are no ring outliers.

No monomer is involved in short contacts.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.