Full wwPDB X-ray Structure Validation Report (i)

Jan 27, 2024 – 04:45 PM EST

PDB ID	:	1CXU
Title	:	1.42A RESOLUTION ASV INTEGRASE CORE DOMAIN FROM CITRATE
Authors	:	Lubkowski, J.; Dauter, Z.; Yang, F.; Alexandratos, J.; Wlodawer, A.
Deposited on	:	1999-08-30
Resolution	:	1.42 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 (i) 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 (i)) were used in the production of this report:

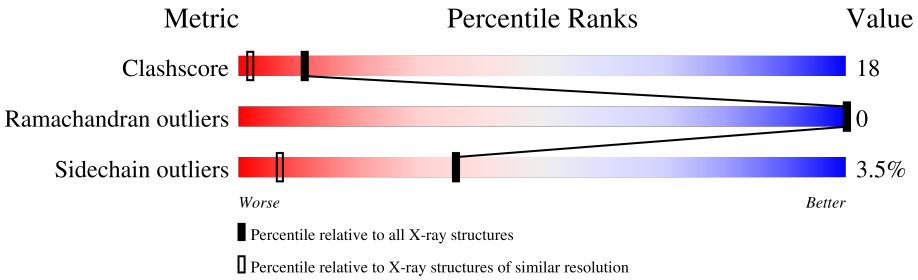
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 1.42 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	141614	2696 (1.44-1.40)
Ramachandran outliers	138981	2632 (1.44-1.40)
Sidechain outliers	138945	2631 (1.44-1.40)

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	162	65% 22% · 12%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 1339 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.

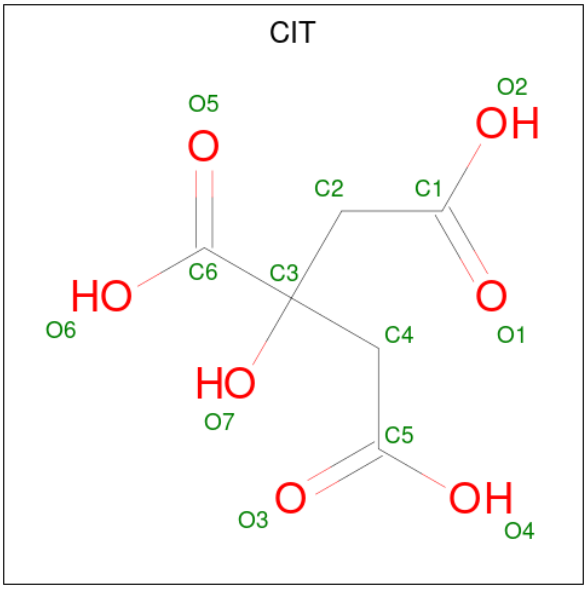
- Molecule 1 is a protein called PROTEIN (AVIAN SARCOMA VIRUS INTEGRASE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	143	1117	704	207	200	6	14	5	0

There are 9 discrepancies between the modelled and reference sequences:

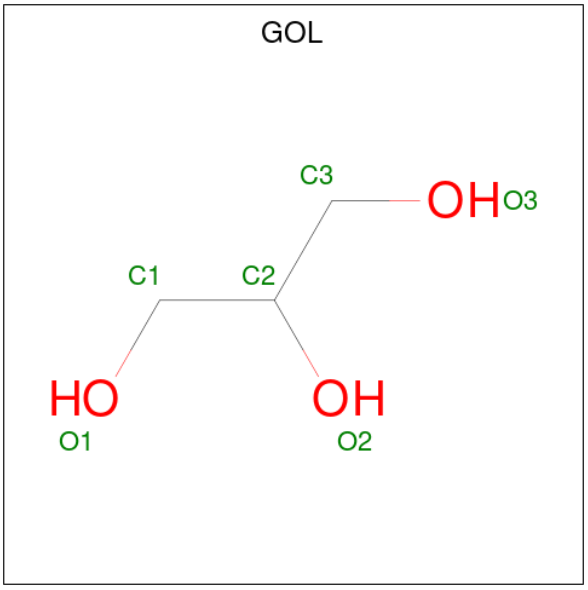
Chain	Residue	Modelled	Actual	Comment	Reference
A	48	PRO	-	insertion	UNP P03354
A	49	LEU	-	insertion	UNP P03354
A	50	ARG	-	insertion	UNP P03354
A	51	GLU	-	insertion	UNP P03354
A	52	GLY	PRO	conflict	UNP P03354
A	101	ALA	VAL	SEE REMARK 999	UNP P03354
A	166	LYS	ARG	SEE REMARK 999	UNP P03354
A	208	ASN	-	insertion	UNP P03354
A	209	LEU	-	insertion	UNP P03354

- Molecule 2 is CITRIC ACID (three-letter code: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 13 6 7	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 6 3 3	0	0

- Molecule 4 is water.

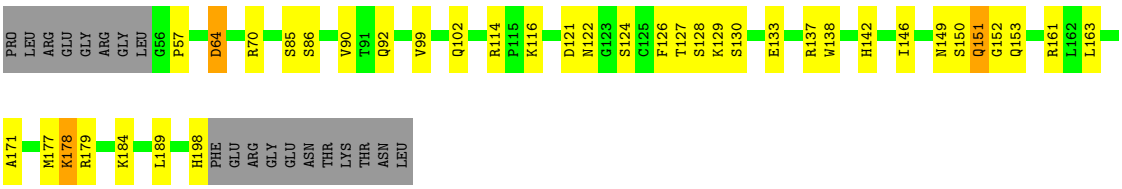
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	203	Total O 203 203	0	0

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: PROTEIN (AVIAN SARCOMA VIRUS INTEGRASE)

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	66.18Å 66.18Å 78.73Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 1.42 12.87 – 1.40	Depositor EDS
% Data completeness (in resolution range)	99.1 (10.00-1.42) 96.2 (12.87-1.40)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.70 (at 1.40Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.187 , 0.221 0.241 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	18.2	Xtriage
Anisotropy	0.222	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.44 , 48.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	1339	wwPDB-VP
Average B, all atoms (Å^2)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.51% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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

Bond lengths and bond angles in the following residue types are not validated in this section: CIT, GOL

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	0.70	0/1162	1.27	6/1576 (0.4%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	179	ARG	NE-CZ-NH1	7.47	124.04	120.30
1	A	64	ASP	CB-CG-OD1	6.75	124.37	118.30
1	A	114	ARG	NE-CZ-NH1	-5.64	117.48	120.30
1	A	114	ARG	CD-NE-CZ	-5.30	116.18	123.60
1	A	171	ALA	O-C-N	5.11	130.88	122.70
1	A	70	ARG	NE-CZ-NH2	5.09	122.84	120.30

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	1117	0	1134	41	0
2	A	13	0	6	0	0
3	A	6	0	8	1	0
4	A	203	0	0	32	4
All	All	1339	0	1148	41	4

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 18.

All (41) 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:124:SER:OG	4:A:663:HOH:O	1.59	1.17
1:A:133:GLU:HG3	4:A:422:HOH:O	1.44	1.15
1:A:137:ARG:O	4:A:621:HOH:O	1.74	1.05
1:A:102:GLN:NE2	4:A:410:HOH:O	1.72	1.04
1:A:130:SER:O	4:A:427:HOH:O	1.82	0.97
1:A:122:ASN:O	4:A:657:HOH:O	1.84	0.94
1:A:153:GLN:OE1	4:A:411:HOH:O	1.87	0.91
1:A:133:GLU:CG	4:A:422:HOH:O	2.11	0.88
1:A:127:THR:HA	4:A:620:HOH:O	1.74	0.87
1:A:152:GLY:HA3	4:A:610:HOH:O	1.74	0.86
1:A:129:LYS:HB3	4:A:508:HOH:O	1.80	0.79
1:A:121:ASP:OD2	4:A:489:HOH:O	2.04	0.76
1:A:99:VAL:HG21	4:A:701:HOH:O	1.88	0.73
1:A:128:SER:HB2	4:A:433:HOH:O	1.91	0.70
1:A:151:GLN:OE1	4:A:656:HOH:O	2.11	0.67
1:A:130:SER:OG	4:A:456:HOH:O	2.06	0.65
1:A:177[A]:MET:HB3	1:A:178:LYS:HE2	1.80	0.63
1:A:90:VAL:HG21	1:A:163[A]:LEU:HD21	1.84	0.60
1:A:99:VAL:CG2	4:A:701:HOH:O	2.47	0.59
1:A:126:PHE:O	4:A:620:HOH:O	2.17	0.59
1:A:127:THR:OG1	4:A:647:HOH:O	2.10	0.58
1:A:130:SER:HA	4:A:427:HOH:O	2.05	0.57
1:A:121:ASP:CG	4:A:489:HOH:O	2.43	0.55
1:A:57:PRO:O	1:A:116:LYS:HE2	2.06	0.55
1:A:64:ASP:HB2	4:A:606:HOH:O	2.07	0.55
1:A:151:GLN:NE2	4:A:656:HOH:O	2.40	0.55
1:A:142:HIS:ND1	4:A:490:HOH:O	2.08	0.53
1:A:85:SER:O	1:A:86:SER:HB2	2.09	0.52
1:A:92:GLN:HG3	1:A:189:LEU:HD22	1.91	0.52
1:A:177[B]:MET:HB3	1:A:178:LYS:HE2	1.93	0.51
1:A:161:ARG:HG2	4:A:622:HOH:O	2.11	0.51
1:A:90:VAL:O	3:A:299:GOL:H12	2.12	0.50
1:A:99:VAL:HG21	4:A:639:HOH:O	2.13	0.47
1:A:130:SER:CA	4:A:427:HOH:O	2.63	0.46
1:A:121:ASP:OD1	4:A:489:HOH:O	2.21	0.46
1:A:151:GLN:CD	4:A:656:HOH:O	2.53	0.44
1:A:184:LYS:HE3	4:A:458:HOH:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:149:ASN:OD1	1:A:152:GLY:N	2.51	0.41
1:A:198:HIS:HB3	4:A:643:HOH:O	2.20	0.41
1:A:138:TRP:HA	4:A:621:HOH:O	2.21	0.41

All (4) 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)
4:A:442:HOH:O	4:A:651:HOH:O[3_644]	1.67	0.53
4:A:425:HOH:O	4:A:634:HOH:O[4_565]	1.74	0.46
4:A:480:HOH:O	4:A:601:HOH:O[3_644]	1.81	0.39
4:A:625:HOH:O	4:A:651:HOH:O[3_644]	2.16	0.04

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	146/162 (90%)	144 (99%)	2 (1%)	0	100 100

There are no Ramachandran outliers to report.

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	119/130 (92%)	114 (96%)	5 (4%)	30 4

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

Mol	Chain	Res	Type
1	A	146	ILE
1	A	150[A]	SER
1	A	150[B]	SER
1	A	151	GLN
1	A	178	LYS

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	103	HIS
1	A	160	ASN

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

There are no monosaccharides in this entry.

5.6 Ligand geometry

2 ligands are modelled in this entry.

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	$\#\|Z\|>2$
3	GOL	A	299	-	5,5,5	0.48	0	5,5,5	0.45	0
2	CIT	A	300	-	12,12,12	2.39	5 (41%)	17,17,17	1.72	3 (17%)

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
3	GOL	A	299	-	-	2/4/4/4	-
2	CIT	A	300	-	-	0/16/16/16	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	300	CIT	O1-C1	4.34	1.36	1.22
2	A	300	CIT	O5-C6	3.98	1.35	1.22
2	A	300	CIT	O3-C5	3.24	1.32	1.22
2	A	300	CIT	O4-C5	2.47	1.39	1.30
2	A	300	CIT	C2-C3	2.03	1.56	1.53

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	300	CIT	C3-C2-C1	-3.18	106.11	113.81
2	A	300	CIT	O4-C5-O3	-2.85	116.19	123.30
2	A	300	CIT	O7-C3-C2	2.38	114.96	109.40

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	299	GOL	C1-C2-C3-O3
3	A	299	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	299	GOL	1	0

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.