



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 06:18 pm GMT

PDB ID : 1A4Y
Title : RIBONUCLEASE INHIBITOR-ANGIOGENIN COMPLEX
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Deposited on : 1998-02-08
Resolution : 2.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

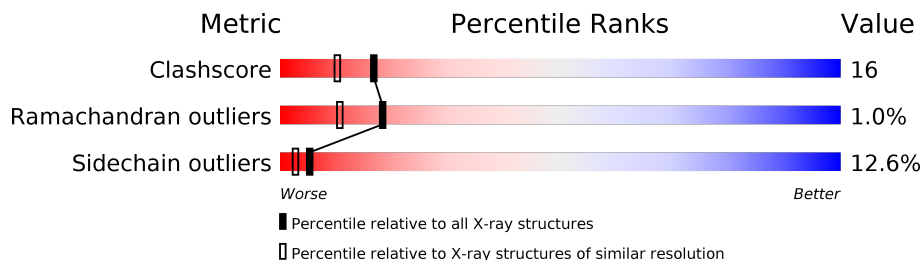
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	460	
1	D	460	
2	B	123	
2	E	123	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8939 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 RIBONUCLEASE INHIBITOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	460	Total	C	N	O	S	3	0	0
			3410	2106	590	680	34			
1	D	460	Total	C	N	O	S	3	0	0
			3410	2106	590	680	34			

- Molecule 2 is a protein called ANGIOGENIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	123	Total	C	N	O	S	0	0	0
			993	610	197	179	7			
2	E	123	Total	C	N	O	S	0	0	0
			993	610	197	179	7			

- Molecule 3 is water.

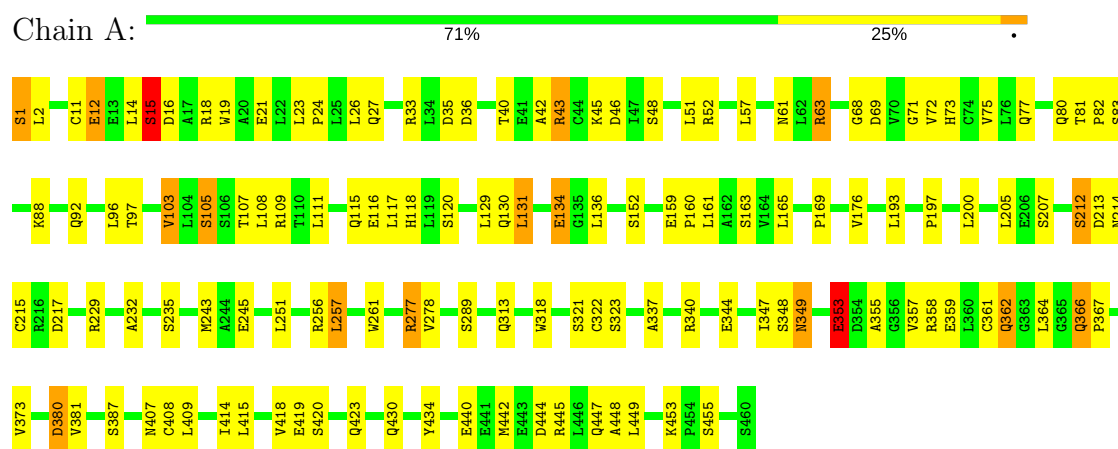
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	56	Total	O	0	0
			56	56		
3	B	18	Total	O	0	0
			18	18		
3	D	51	Total	O	0	0
			51	51		
3	E	8	Total	O	0	0
			8	8		

3 Residue-property plots

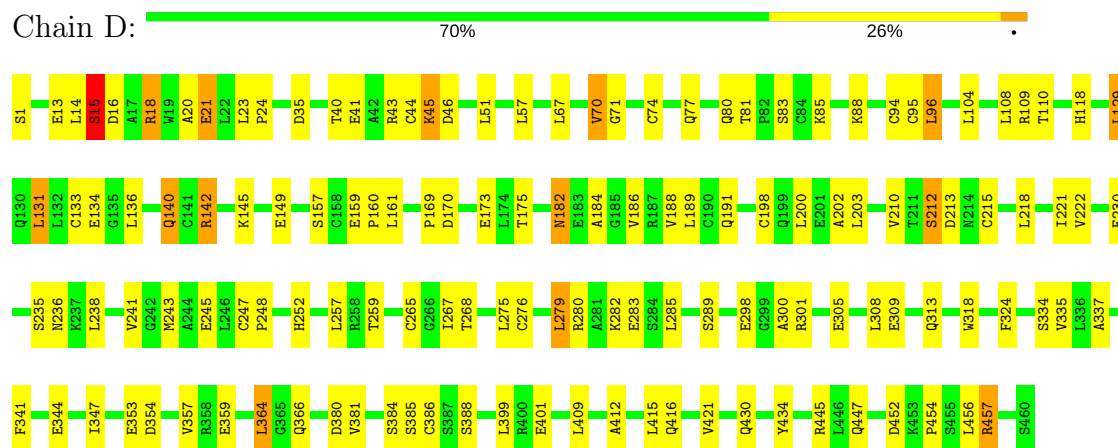
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

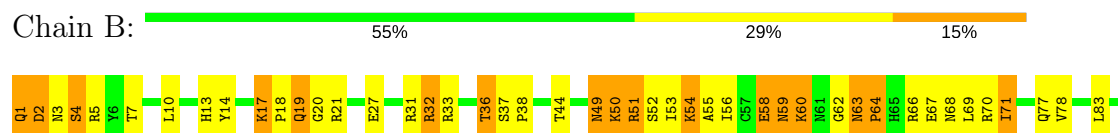
• Molecule 1: RIBONUCLEASE INHIBITOR



• Molecule 1: RIBONUCLEASE INHIBITOR

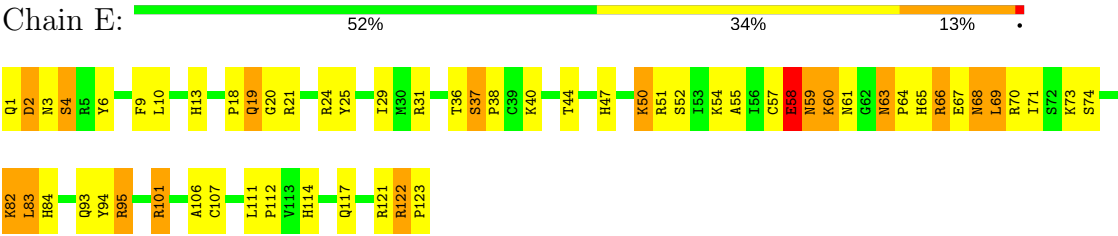


• Molecule 2: ANGIOGENIN





● Molecule 2: ANGIOGENIN



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	66.55Å 105.61Å 93.52Å 90.00° 107.09° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00	Depositor
% Data completeness (in resolution range)	86.9 (20.00-2.00)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.8	Depositor
R, R_{free}	0.193 , 0.286	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	8939	wwPDB-VP
Average B, all atoms (Å ²)	43.0	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	0.46	0/3447	0.75	3/4677 (0.1%)
1	D	0.50	1/3447 (0.0%)	0.69	2/4677 (0.0%)
2	B	0.44	0/1017	0.67	0/1370
2	E	0.45	0/1017	0.70	0/1370
All	All	0.47	1/8928 (0.0%)	0.71	5/12094 (0.0%)

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	1	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	380	ASP	CA-CB	-14.62	1.21	1.53

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	380	ASP	CA-CB-CG	16.59	149.91	113.40
1	A	380	ASP	N-CA-CB	14.37	136.47	110.60
1	D	380	ASP	N-CA-CB	8.01	125.01	110.60
1	D	380	ASP	CA-CB-CG	7.34	129.55	113.40
1	A	43	ARG	NE-CZ-NH2	7.26	123.93	120.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	380	ASP	CA

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	434	TYR	Sidechain

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	3410	0	3389	86	0
1	D	3410	0	3389	83	0
2	B	993	0	965	51	0
2	E	993	0	965	67	0
3	A	56	0	0	1	0
3	B	18	0	0	1	0
3	D	51	0	0	1	0
3	E	8	0	0	0	0
All	All	8939	0	8708	277	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 16.

The worst 5 of 277 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:B:51:ARG:HD2	2:B:51:ARG:H	1.14	1.08
2:E:65:HIS:HE1	2:E:71:ILE:HG22	1.20	1.06
2:E:44:THR:H	2:E:117:GLN:HE22	1.08	0.97
2:E:65:HIS:HB2	2:E:69:LEU:O	1.65	0.97
2:B:44:THR:H	2:B:117:GLN:HE22	1.15	0.93

There are no symmetry-related clashes.

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	458/460 (100%)	437 (95%)	17 (4%)	4 (1%)	20	12
1	D	458/460 (100%)	439 (96%)	17 (4%)	2 (0%)	38	33
2	B	121/123 (98%)	109 (90%)	9 (7%)	3 (2%)	6	2
2	E	121/123 (98%)	109 (90%)	9 (7%)	3 (2%)	6	2
All	All	1158/1166 (99%)	1094 (94%)	52 (4%)	12 (1%)	18	10

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	4	SER
2	E	58	GLU
2	E	59	ASN
1	A	82	PRO
1	D	15	SER

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	382/396 (96%)	344 (90%)	38 (10%)	9	5
1	D	382/396 (96%)	341 (89%)	41 (11%)	8	4
2	B	110/110 (100%)	88 (80%)	22 (20%)	1	0
2	E	110/110 (100%)	87 (79%)	23 (21%)	1	0
All	All	984/1012 (97%)	860 (87%)	124 (13%)	5	3

5 of 124 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	71	ILE
1	D	85	LYS
2	E	63	ASN
2	B	83	LEU
1	D	18	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	117	GLN
1	D	118	HIS
2	E	68	ASN
1	D	10	GLN
1	D	140	GLN

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 carbohydrates 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 ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.