



Full wwPDB X-ray Structure Validation Report

Feb 21, 2018 – 03:13 pm GMT

PDB ID : 1ELA
Title : Analogous inhibitors of elastase do not always bind analogously
Authors : Mattos, C.; Rasmussen, B.; Ding, X.; Petsko, G.A.; Ringe, D.
Deposited on : 1993-12-07
Resolution : 2.00 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 following versions of software and data (see [references](#) ) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.3 (157068), CSD as539be (2018)
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk30686

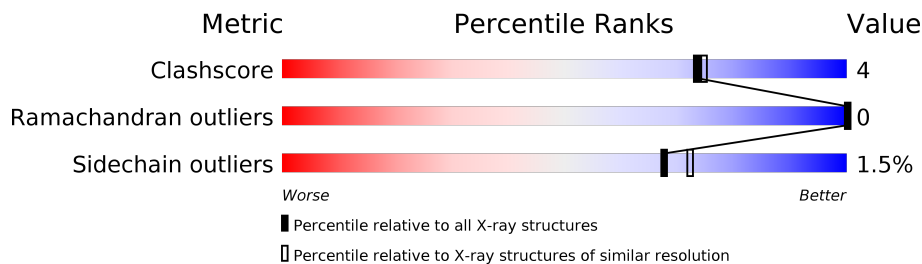
1 Overall quality at a glance

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	122078	8264 (2.00-2.00)
Ramachandran outliers	120005	8163 (2.00-2.00)
Sidechain outliers	119972	8162 (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	240	

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 2030 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.

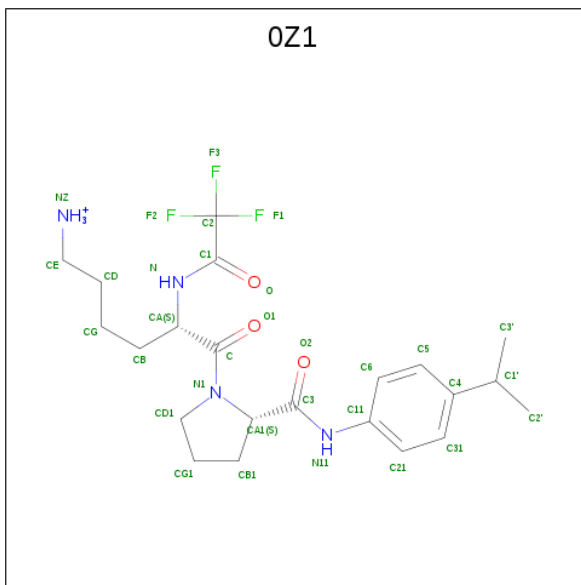
- Molecule 1 is a protein called ELASTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	240	1822	1135	330	347	10	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	81	ASN	ASP	CONFLICT	UNP P00772

- Molecule 2 is 6-ammonio-N-(trifluoroacetyl)-L-norleucyl-N-[4-(1-methylethyl)phenyl]-L-prolinamide (three-letter code: OZ1) (formula: $C_{22}H_{32}F_3N_4O_3$).

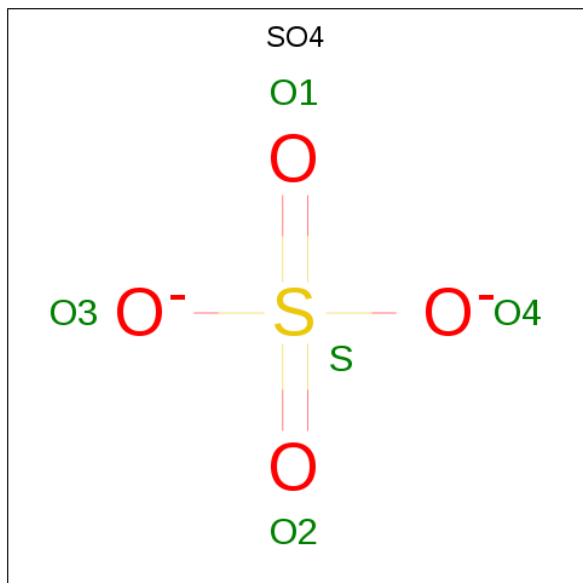


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	F	N	O		
2	A	1	32	22	3	4	3	0	0

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

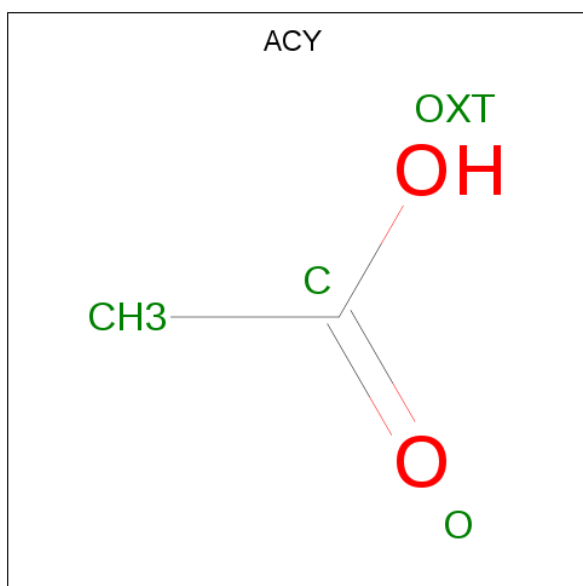
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Ca	0	0
			1	1		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is ACETIC ACID (three-letter code: ACY) (formula: C₂H₄O₂).



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

- Molecule 6 is water.

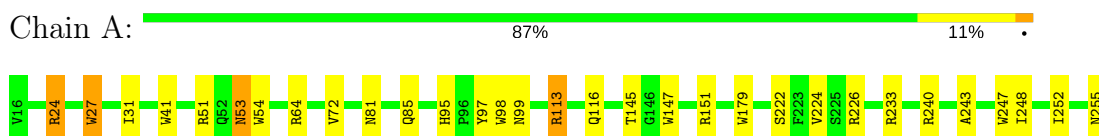
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	166	Total	O	0	0
			166	166		

3 Residue-property plots [i](#)

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: ELASTASE



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	52.37Å 57.71Å 75.43Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.00	Depositor
% Data completeness (in resolution range)	(Not available) (10.00-2.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.185 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	2030	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

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: ACY, OZ1, CA, SO4

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	0.81	0/1862	1.45	36/2543 (1.4%)

There are no bond length outliers.

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	226	ARG	NE-CZ-NH2	-14.30	113.15	120.30
1	A	240	ARG	NE-CZ-NH1	11.43	126.01	120.30
1	A	41	TRP	CD1-CG-CD2	9.48	113.88	106.30
1	A	147	TRP	CD1-CG-CD2	8.45	113.06	106.30
1	A	247	TRP	CD1-CG-CD2	8.06	112.75	106.30
1	A	240	ARG	NE-CZ-NH2	-7.94	116.33	120.30
1	A	27	TRP	CD1-CG-CD2	7.63	112.40	106.30
1	A	147	TRP	CE2-CD2-CG	-7.55	101.26	107.30
1	A	179	TRP	CD1-CG-CD2	7.39	112.21	106.30
1	A	41	TRP	CE2-CD2-CG	-7.29	101.47	107.30
1	A	98	TRP	CD1-CG-CD2	7.10	111.98	106.30
1	A	233	ARG	NE-CZ-NH1	7.02	123.81	120.30
1	A	247	TRP	CE2-CD2-CG	-6.97	101.72	107.30
1	A	24	ARG	NE-CZ-NH2	-6.96	116.82	120.30
1	A	27	TRP	CE2-CD2-CG	-6.87	101.81	107.30
1	A	98	TRP	CE2-CD2-CG	-6.79	101.87	107.30
1	A	54	TRP	CE2-CD2-CG	-6.74	101.91	107.30
1	A	54	TRP	CD1-CG-CD2	6.70	111.66	106.30
1	A	24	ARG	NE-CZ-NH1	6.37	123.48	120.30
1	A	179	TRP	CE2-CD2-CG	-6.36	102.21	107.30
1	A	113	ARG	NE-CZ-NH1	6.12	123.36	120.30
1	A	233	ARG	NE-CZ-NH2	-5.97	117.32	120.30
1	A	41	TRP	CG-CD1-NE1	-5.96	104.14	110.10
1	A	24	ARG	CG-CD-NE	-5.74	99.75	111.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	151	ARG	NE-CZ-NH1	5.72	123.16	120.30
1	A	51	ARG	NE-CZ-NH2	-5.57	117.52	120.30
1	A	27	TRP	CB-CG-CD1	-5.53	119.82	127.00
1	A	27	TRP	CG-CD2-CE3	5.45	138.80	133.90
1	A	98	TRP	CG-CD2-CE3	5.41	138.76	133.90
1	A	147	TRP	CG-CD2-CE3	5.33	138.70	133.90
1	A	64	ARG	NE-CZ-NH1	5.31	122.95	120.30
1	A	51	ARG	NE-CZ-NH1	5.27	122.94	120.30
1	A	247	TRP	CG-CD1-NE1	-5.21	104.89	110.10
1	A	147	TRP	CG-CD1-NE1	-5.18	104.92	110.10
1	A	226	ARG	NH1-CZ-NH2	5.03	124.94	119.40
1	A	27	TRP	CG-CD1-NE1	-5.03	105.07	110.10

There are no chirality outliers.

There are no planarity outliers.

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	1822	0	1759	13	0
2	A	32	0	32	2	0
3	A	1	0	0	0	0
4	A	5	0	0	1	0
5	A	4	0	3	0	0
6	A	166	0	0	0	0
All	All	2030	0	1794	13	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 4.

All (13) 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:53:ASN:HD22	1:A:53:ASN:H	1.50	0.60
1:A:95:HIS:HD2	1:A:97:TYR:H	1.55	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:248:ILE:O	1:A:252:ILE:HG12	2.13	0.49
1:A:24:ARG:HH12	1:A:81:ASN:ND2	2.10	0.49
1:A:113:ARG:HH11	1:A:255:ASN:HB3	1.78	0.48
1:A:95:HIS:CD2	1:A:97:TYR:H	2.31	0.48
1:A:31:ILE:HG22	1:A:72:VAL:HG12	1.96	0.48
1:A:222:SER:O	2:A:256:OZ1:HB2	2.16	0.46
1:A:224:VAL:O	2:A:256:OZ1:H6	2.18	0.43
1:A:24:ARG:HH12	1:A:81:ASN:HD22	1.66	0.42
1:A:243:ALA:HA	4:A:290:SO4:O4	2.20	0.42
1:A:27:TRP:CD1	1:A:145:THR:HG21	2.55	0.42
1:A:72:VAL:CG2	1:A:85:GLN:HB2	2.50	0.41

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	238/240 (99%)	234 (98%)	4 (2%)	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	198/198 (100%)	195 (98%)	3 (2%)	67 72

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53	ASN
1	A	99	ASN
1	A	116	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	53	ASN
1	A	78	ASN
1	A	95	HIS
1	A	99	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 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	0Z1	A	256	-	33,33,33	0.88	2 (6%)	46,46,46	1.41	9 (19%)
4	SO4	A	290	-	4,4,4	0.44	0	6,6,6	0.18	0
5	ACY	A	300	-	1,3,3	3.89	1 (100%)	0,3,3	0.00	-

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	0Z1	A	256	-	-	0/35/45/45	0/2/2/2
4	SO4	A	290	-	-	0/0/0/0	0/0/0/0
5	ACY	A	300	-	-	0/0/0/0	0/0/0/0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	256	0Z1	C11-N11	-2.52	1.36	1.41
2	A	256	0Z1	C2-C1	2.09	1.58	1.53
5	A	300	ACY	CH3-C	3.89	1.53	1.48

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	256	0Z1	CA1-C3-N11	-3.58	107.46	114.37
2	A	256	0Z1	CB-CA-N	-3.10	104.57	110.88
2	A	256	0Z1	O1-C-N1	-2.43	117.33	121.39
2	A	256	0Z1	C3'-C1'-C4	-2.03	106.18	112.11
2	A	256	0Z1	CB1-CA1-C3	2.23	115.51	111.25
2	A	256	0Z1	CA-N-C1	2.24	125.84	121.50
2	A	256	0Z1	C2-C1-N	2.39	118.27	115.17
2	A	256	0Z1	O2-C3-N11	2.78	128.84	123.91
2	A	256	0Z1	CA-C-N1	3.53	124.50	118.62

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	256	OZ1	2	0
4	A	290	SO4	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

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.