

Full wwPDB X-ray Structure Validation Report (i)

May 23, 2020 – 07:34 am BST

PDB ID : 3LPR

Title : STRUCTURAL BASIS FOR BROAD SPECIFICITY IN ALPHA-LYTIC

PROTEASE MUTANTS

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Deposited on : 1991-08-05

Resolution : 2.15 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 following versions of software and data (see references (1)) were used in the production of this report:

MolProbity : 4.02b-467

Mogul : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : NOT EXECUTED EDS : NOT EXECUTED

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

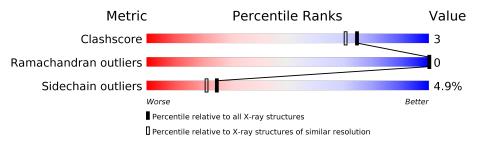
Validation Pipeline (wwPDB-VP) : 2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY\ DIFFRACTION$

The reported resolution of this entry is 2.15 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	Similar resolution		
Medic	$(\# {\rm Entries})$	$(\# ext{Entries}, ext{resolution range}(ext{Å}))$		
Clashscore	141614	1585 (2.16-2.16)		
Ramachandran outliers	138981	1560 (2.16-2.16)		
Sidechain outliers	138945	1559 (2.16-2.16)		

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 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%

Note EDS was not executed.

Mol	Chain	Length		Quality of chain	
1	A	198		79%	18% • •
2	Р	5	20%	60%	20%



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 1607 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 ALPHA-LYTIC PROTEASE.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	198	Total	С	N	0	S	0	1	0
			1395	849	263	276	7			

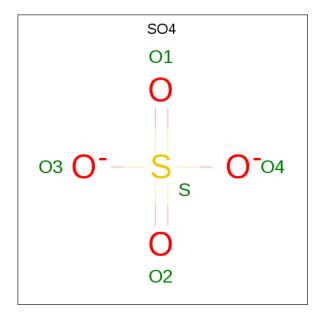
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Residue Modelled		Comment	Reference	
A	192	ALA	MET	CONFLICT	UNP P00778	

• Molecule 2 is a protein called METHOXYSUCCINYL-ALA-ALA-PRO-NORLEUCINE BORONIC ACID INHIBITOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	4	Total	В	С	Ν	О	0	0	0
	Γ	4	26	1	16	4	5	U	U	U

• Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).





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

• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	177	Total O 177 177	0	0
4	Р	4	$\begin{array}{cc} \text{Total} & \text{O} \\ 4 & 4 \end{array}$	0	0

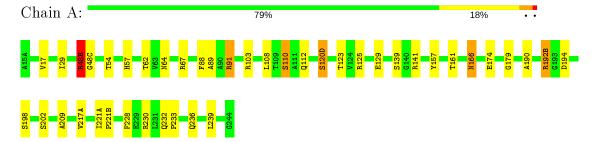


3 Residue-property plots (i)

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. 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.

Note EDS was not executed.

• Molecule 1: ALPHA-LYTIC PROTEASE



• Molecule 2: METHOXYSUCCINYL-ALA-ALA-PRO-NORLEUCINE BORONIC ACID INHIBITOR

Chain P: 20% 60% 20%



4 Data and refinement statistics (i)

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

Property	Value	Source	
Space group	P 32 2 1	Depositor	
Cell constants	66.37Å $66.37Å$ $80.10Å$	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor	
Resolution (Å)	(Not available) – 2.15	Depositor	
% Data completeness	(Not available) ((Not available)-2.15)	Depositor	
(in resolution range)		•	
R_{merge}	(Not available)	Depositor	
R_{sym}	(Not available)	Depositor	
Refinement program	PROLSQ	Depositor	
R, R_{free}	0.138 , (Not available)	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	1607	wwPDB-VP	
Average B, all atoms (Å ²)	13.0	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: BNO, 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		
MIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z >5	
1	A	1.09	0/1413	2.32	40/1916 (2.1%)	
2	Р	0.81	0/17	1.81	0/23	
All	All	1.09	0/1430	2.32	40/1939 (2.1%)	

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	Α	0	1

There are no bond length outliers.

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^o)$
1	A	48(B)	ARG	NE-CZ-NH2	-32.35	104.13	120.30
1	A	48(B)	ARG	NE-CZ-NH1	22.07	131.33	120.30
1	A	67	ARG	NE-CZ-NH1	20.09	130.34	120.30
1	A	192(B)	ARG	NE-CZ-NH2	-19.99	110.31	120.30
1	A	91	ARG	NE-CZ-NH1	17.86	129.23	120.30
1	A	192(B)	ARG	NE-CZ-NH1	12.91	126.76	120.30
1	A	67	ARG	NE-CZ-NH2	-12.81	113.89	120.30
1	A	230	ARG	NE-CZ-NH1	11.36	125.98	120.30
1	A	125	ARG	NE-CZ-NH1	-11.31	114.64	120.30
1	A	103	ARG	NE-CZ-NH2	8.69	124.64	120.30
1	A	120(D)	SER	N-CA-CB	-8.26	98.11	110.50
1	A	110	SER	CA-CB-OG	-7.59	90.71	111.20
1	A	174	GLU	CG-CD-OE2	-7.54	103.23	118.30
1	A	139	SER	N-CA-CB	-6.89	100.16	110.50

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Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^o)$
1	A	91	ARG	CD-NE-CZ	6.77	133.08	123.60
1	A	230	ARG	NE-CZ-NH2	-6.65	116.98	120.30
1	A	110	SER	N-CA-CB	-6.38	100.93	110.50
1	A	161	THR	CA-CB-CG2	6.29	121.21	112.40
1	A	112	GLN	CG-CD-OE1	6.21	134.01	121.60
1	A	174	GLU	OE1-CD-OE2	6.21	130.75	123.30
1	A	129	GLU	OE1-CD-OE2	5.91	130.39	123.30
1	A	91	ARG	NH1-CZ-NH2	-5.81	113.01	119.40
1	A	54	THR	CA-CB-CG2	5.79	120.51	112.40
1	A	209	ALA	N-CA-CB	-5.71	102.11	110.10
1	A	64	ASN	CA-C-O	-5.64	108.25	120.10
1	A	48(C)	GLY	N-CA-C	-5.52	99.31	113.10
1	A	89	ALA	N-CA-CB	-5.47	102.44	110.10
1	A	228	PHE	O-C-N	5.46	131.44	122.70
1	A	91	ARG	NE-CZ-NH2	-5.44	117.58	120.30
1	A	190	ALA	N-CA-CB	-5.36	102.60	110.10
1	A	57	HIS	CA-C-O	-5.30	108.96	120.10
1	A	192(B)	ARG	CD-NE-CZ	-5.30	116.19	123.60
1	A	62	THR	CA-CB-CG2	-5.28	105.00	112.40
1	A	194	ASP	CB-CG-OD1	5.24	123.02	118.30
1	A	236	GLN	CG-CD-OE1	5.17	131.95	121.60
1	A	108	LEU	N-CA-CB	-5.08	100.23	110.40
1	A	157	TYR	N-CA-CB	-5.07	101.47	110.60
1	A	202	SER	O-C-N	5.05	130.78	122.70
1	A	123	THR	O-C-N	5.04	130.76	122.70
1	A	88	PHE	O-C-N	5.03	130.75	122.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	192(B)	ARG	Sidechain

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	1395	0	1364	8	0
2	Р	26	0	28	2	0
3	A	5	0	0	1	0
4	A	177	0	0	1	0
4	Р	4	0	0	0	0
All	All	1607	0	1392	9	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 3.

All (9) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$egin{array}{c} ext{Clash} \ ext{overlap } (ext{Å}) \end{array}$
1:A:48(B):ARG:HD2	4:A:353:HOH:O	1.91	0.70
1:A:221(A):ILE:HB	1:A:221(B):PRO:HD2	1.80	0.63
1:A:166:ASN:HD22	1:A:179:GLY:HA2	1.62	0.63
1:A:17:VAL:O	1:A:29:ILE:HG12	2.08	0.54
1:A:217(A)[A]:VAL:HG12	2:P:1:BNO:HE3	1.92	0.51
1:A:232:GLN:N	1:A:233:PRO:HD2	2.29	0.48
1:A:48(B):ARG:HG3	1:A:239:LEU:HD23	2.00	0.41
2:P:3:ALA:HA	2:P:2:PRO:HD3	1.95	0.41
1:A:233:PRO:HB3	3:A:1:SO4:O4	2.21	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	${f Analysed}$	Favoured	Allowed	Outliers	Perce	${f ntiles}$
1	A	$197/198 \; (100\%)$	190 (96%)	7 (4%)	0	100	100
2	Р	$2/5 \; (40\%)$	2 (100%)	0	0	100	100
All	All	$199/203\ (98\%)$	192 (96%)	7 (4%)	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	Rotameric Outliers		Percentiles		
1	A	142/141 (101%)	135 (95%)	7 (5%)	25	21		
2	Р	1/1 (100%)	1 (100%)	0	100	100		
All	All	143/142 (101%)	136 (95%)	7 (5%)	25	21		

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48(B)	ARG
1	A	91	ARG
1	A	110	SER
1	A	120(D)	SER
1	A	141	ARG
1	A	166	ASN
1	A	198	SER

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

Mol	Chain	Res	Type
1	A	101	ASN
1	A	166	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)

1 non-standard protein/DNA/RNA residue is 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		
	MIOI	туре	Chain	res	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
Ī	2	BNO	Р	1	1,2	3,8,8	0.47	0	3,9,9	0.67	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.

\mathbf{Mol}	Type	Chain	${f Res}$	Link	Chirals	Torsions	\mathbf{Rings}
2	BNO	Р	1	1,2	-	0/4/8/8	_

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	Р	1	BNO	1	0

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

1 ligand is 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		
10101	туре	Chain	ites	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
3	SO4	A	1	_	4,4,4	0.56	0	6,6,6	1.13	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1	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 (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.

