



# Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2020 – 07:38 am BST

PDB ID : 1P04  
Title : STRUCTURE ANALYSIS OF SPECIFICITY. ALPHA-LYTIC PROTEASE  
COMPLEXES WITH ANALOGUES OF REACTION INTERMEDIATES  
Authors : Bone, R.; Agard, D.A.  
Deposited on : 1989-04-24  
Resolution : 2.55 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](mailto: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.

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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)  
Xtrriage (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

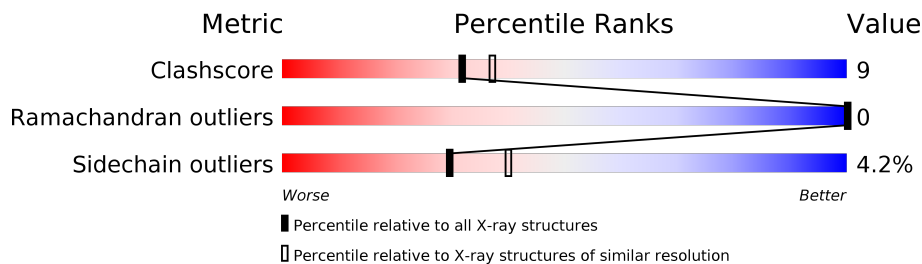
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.55 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	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)

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  $\geq 3$ , 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  $\leq 5\%$ .

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	198	
2	P	5	

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 1563 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.

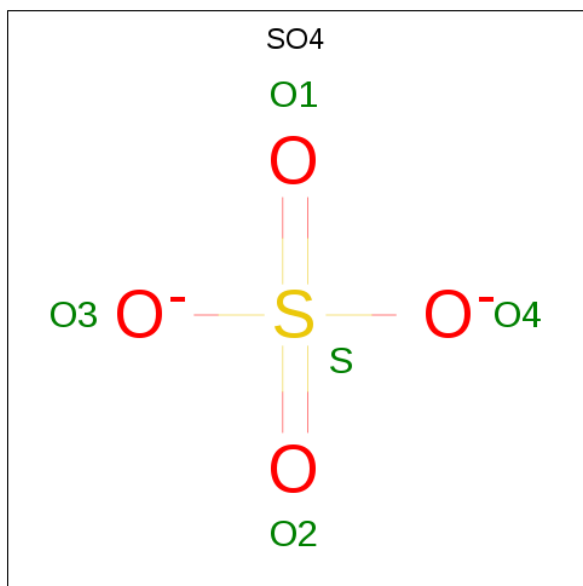
- Molecule 1 is a protein called ALPHA-LYTIC PROTEASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	198	1391	846	262	275	8	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	B	C	N	O			
2	P	4	26	1	16	4	5	0	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

- Molecule 4 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
4	A	136	Total 136	O 136	0	0
4	P	5	Total 5	O 5	0	0

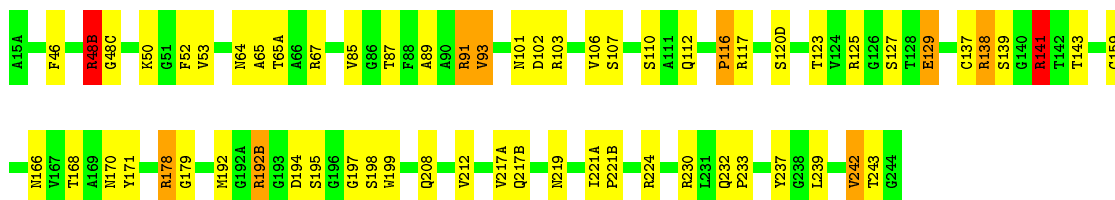
### 3 Residue-property plots [i](#)

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

Chain A: 



- Molecule 2: METHOXYSUCCINYL-ALA-ALA-PRO-ISOLEUCINE BORONIC ACID INHIBITOR

Chain P: 



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	66.30Å 66.30Å 80.31Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	(Not available) – 2.55	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.55)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, $R_{free}$	0.134 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	1563	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	11.0	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: SO4, B2I

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	1.09	0/1409	2.36	65/1909 (3.4%)
2	P	0.61	0/17	1.73	0/23
All	All	1.09	0/1426	2.35	65/1932 (3.4%)

There are no bond length outliers.

All (65) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	91	ARG	NE-CZ-NH2	17.85	129.22	120.30
1	A	48(B)	ARG	NE-CZ-NH1	-17.36	111.62	120.30
1	A	67	ARG	NE-CZ-NH1	15.69	128.15	120.30
1	A	230	ARG	NE-CZ-NH1	15.41	128.00	120.30
1	A	91	ARG	NH1-CZ-NH2	-13.57	104.47	119.40
1	A	224	ARG	NE-CZ-NH2	-12.49	114.05	120.30
1	A	48(B)	ARG	NH1-CZ-NH2	12.46	133.10	119.40
1	A	171	TYR	CB-CG-CD2	12.45	128.47	121.00
1	A	91	ARG	NE-CZ-NH1	12.01	126.31	120.30
1	A	171	TYR	CB-CG-CD1	-11.69	113.98	121.00
1	A	230	ARG	NE-CZ-NH2	-10.97	114.82	120.30
1	A	125	ARG	NE-CZ-NH2	-10.65	114.97	120.30
1	A	48(B)	ARG	NE-CZ-NH2	-10.08	115.26	120.30
1	A	224	ARG	CD-NE-CZ	-8.95	111.07	123.60
1	A	48(B)	ARG	CD-NE-CZ	8.83	135.96	123.60
1	A	141	ARG	NE-CZ-NH2	-8.58	116.01	120.30
1	A	125	ARG	NH1-CZ-NH2	8.33	128.56	119.40
1	A	224	ARG	NE-CZ-NH1	8.12	124.36	120.30
1	A	139	SER	N-CA-CB	-8.04	98.44	110.50
1	A	141	ARG	NE-CZ-NH1	8.01	124.30	120.30
1	A	192(B)	ARG	NE-CZ-NH1	-8.00	116.30	120.30
1	A	194	ASP	CB-CG-OD2	7.74	125.26	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	125	ARG	NE-CZ-NH1	-7.71	116.44	120.30
1	A	242	VAL	CG1-CB-CG2	7.47	122.86	110.90
1	A	129	GLU	CG-CD-OE2	-7.17	103.96	118.30
1	A	48(B)	ARG	N-CA-CB	-7.13	97.77	110.60
1	A	138	ARG	NE-CZ-NH2	7.02	123.81	120.30
1	A	85	VAL	CA-CB-CG2	6.94	121.31	110.90
1	A	192(B)	ARG	NE-CZ-NH2	6.90	123.75	120.30
1	A	178	ARG	NE-CZ-NH2	6.85	123.72	120.30
1	A	117	ARG	NE-CZ-NH2	-6.64	116.98	120.30
1	A	102	ASP	CB-CG-OD1	6.59	124.23	118.30
1	A	195	SER	N-CA-CB	6.56	120.34	110.50
1	A	243	THR	CA-CB-CG2	6.52	121.53	112.40
1	A	103	ARG	NE-CZ-NH1	6.49	123.54	120.30
1	A	65(A)	THR	CA-CB-OG1	-6.39	95.57	109.00
1	A	93	VAL	CG1-CB-CG2	6.34	121.04	110.90
1	A	110	SER	CB-CA-C	-6.30	98.13	110.10
1	A	53	VAL	CG1-CB-CG2	-6.11	101.12	110.90
1	A	217(B)	GLN	CG-CD-NE2	6.08	131.30	116.70
1	A	89	ALA	CB-CA-C	-6.05	101.02	110.10
1	A	170	ASN	CA-CB-CG	-5.86	100.50	113.40
1	A	48(B)	ARG	CB-CG-CD	-5.80	96.52	111.60
1	A	143	THR	CA-C-O	-5.78	107.96	120.10
1	A	107	SER	CA-CB-OG	-5.78	95.61	111.20
1	A	194	ASP	OD1-CG-OD2	-5.77	112.34	123.30
1	A	64	ASN	CA-C-O	-5.70	108.12	120.10
1	A	106	VAL	CA-C-O	-5.65	108.24	120.10
1	A	125	ARG	CA-C-N	5.64	127.48	116.20
1	A	103	ARG	NH1-CZ-NH2	-5.61	113.22	119.40
1	A	103	ARG	NE-CZ-NH2	5.53	123.07	120.30
1	A	48(B)	ARG	CG-CD-NE	-5.44	100.38	111.80
1	A	217(B)	GLN	CG-CD-OE1	-5.43	110.73	121.60
1	A	143	THR	CA-C-N	5.39	126.98	116.20
1	A	48(C)	GLY	N-CA-C	-5.34	99.75	113.10
1	A	199	TRP	N-CA-CB	5.31	120.16	110.60
1	A	192(B)	ARG	CD-NE-CZ	-5.31	116.17	123.60
1	A	208	GLN	CG-CD-NE2	-5.29	104.01	116.70
1	A	64	ASN	CA-C-N	5.24	128.73	117.20
1	A	199	TRP	N-CA-C	-5.24	96.86	111.00
1	A	219	ASN	N-CA-CB	5.22	119.99	110.60
1	A	117	ARG	NE-CZ-NH1	5.20	122.90	120.30
1	A	67	ARG	NH1-CZ-NH2	-5.18	113.70	119.40
1	A	91	ARG	CD-NE-CZ	5.10	130.73	123.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	123	THR	O-C-N	5.00	130.70	122.70

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	1391	0	1360	25	0
2	P	26	0	28	5	0
3	A	5	0	0	1	0
4	A	136	0	0	3	1
4	P	5	0	0	0	0
All	All	1563	0	1388	25	1

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 9.

All (25) 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:217(A):VAL:HG11	2:P:1:B2I:HD11	1.45	0.95
1:A:93:VAL:HG11	1:A:101:ASN:HD22	1.66	0.60
1:A:192(B):ARG:HA	2:P:1:B2I:HD13	1.89	0.55
1:A:197:GLY:O	1:A:212:VAL:HA	2.07	0.54
1:A:129:GLU:HG3	4:A:361:HOH:O	2.08	0.54
1:A:221(A):ILE:HB	1:A:221(B):PRO:HD2	1.89	0.54
1:A:217(A):VAL:CG1	2:P:1:B2I:HD11	2.28	0.52
1:A:116:PRO:HB3	1:A:242:VAL:HG12	1.91	0.51
1:A:48(B):ARG:HG3	1:A:239:LEU:HD23	1.93	0.49
1:A:127:SER:O	1:A:232:GLN:NE2	2.44	0.49
1:A:217(A):VAL:HG11	2:P:1:B2I:CD1	2.30	0.48
1:A:166:ASN:HD22	1:A:179:GLY:HA2	1.78	0.48
1:A:48(B):ARG:CZ	4:A:377:HOH:O	2.62	0.48
1:A:46:PHE:O	1:A:52:PHE:HA	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:168:THR:HG23	1:A:178:ARG:HG2	1.98	0.46
1:A:192(B):ARG:CA	2:P:1:B2I:HD13	2.45	0.46
1:A:50:LYS:NZ	1:A:112:GLN:O	2.38	0.46
1:A:138:ARG:HA	1:A:198:SER:O	2.17	0.44
1:A:232:GLN:N	1:A:233:PRO:HD2	2.33	0.44
1:A:65:ALA:O	1:A:87:THR:HA	2.18	0.43
1:A:137:CYS:HA	1:A:159:CYS:HA	2.00	0.42
1:A:233:PRO:HB3	3:A:1:SO4:O4	2.20	0.42
1:A:141:ARG:C	1:A:141:ARG:HD3	2.41	0.41
1:A:237:TYR:HB2	1:A:239:LEU:HG	2.03	0.41
1:A:48(B):ARG:HD2	4:A:352:HOH:O	2.21	0.40

All (1) 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:254:HOH:O	4:A:347:HOH:O[5_665]	0.41	1.79

## 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	196/198 (99%)	187 (95%)	9 (5%)	0	100	100
2	P	2/5 (40%)	2 (100%)	0	0	100	100
All	All	198/203 (98%)	189 (96%)	9 (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	Outliers	Percentiles	
1	A	142/142 (100%)	136 (96%)	6 (4%)	30	40
2	P	1/1 (100%)	1 (100%)	0	100	100
All	All	143/143 (100%)	137 (96%)	6 (4%)	30	40

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48(B)	ARG
1	A	91	ARG
1	A	116	PRO
1	A	120(D)	SER
1	A	141	ARG
1	A	192	MET

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		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	B2I	P	1	1,2	3,8,8	0.36	0	2,10,10	1.50	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	B2I	P	1	1,2	-	1/3/10/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	P	1	B2I	CG2-CB-CG1-CD1

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	P	1	B2I	5	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		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
3	SO4	A	1	-	4,4,4	0.67	0	6,6,6	0.38	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

### 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.