

Full wwPDB X-ray Structure Validation Report (i)

Aug 9, 2020 – 11:03 PM BST

PDB ID	:	2ASI
Title	:	ASPARTIC PROTEINASE
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Deposited on		
$\operatorname{Resolution}$:	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:

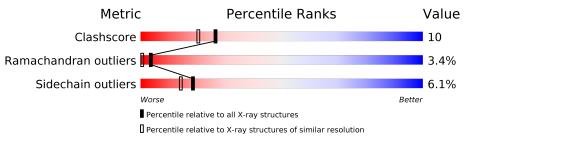
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

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 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries}, { m resolution\ range}({ m \AA}))$	
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	А	361	76%	19%	•••			
2	В	2	100%					



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2822 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 ASPARTIC PROTEINASE.

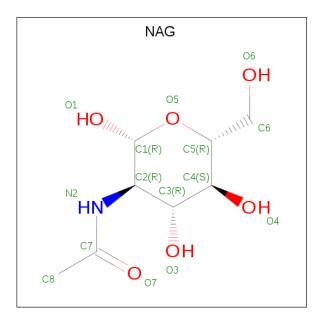
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	А	356	Total 2643	C 1690	N 413	O 529	S 11	0	0	0

• Molecule 2 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-b eta-D-glucopyranose.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
2	В	2	Total C N O 25 14 1 10	0	0	0

• Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	А	1	Total 14	C 8	N 1	O 5	0	0

• Molecule 4 is water.

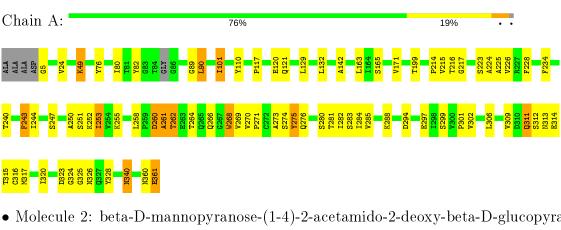
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	140	Total O 140 140	0	0



Residue-property plots (i) 3

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.

Note EDS was not executed.



• Molecule 1: ASPARTIC PROTEINASE

• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B:

100%



4 Data and refinement statistics (i)

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

Property	Value	Source	
Space group	P 21 21 21	Depositor	
Cell constants	41.86Å 51.21 Å 174.24 Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	6.00 - 2.15	Depositor	
% Data completeness	(Not available) (6.00-2.15)	Depositor	
(in resolution range)	(100 available) (0.00 2.10)	-	
R_{merge}	0.06	Depositor	
R _{sym}	(Not available)	Depositor	
Refinement program	X-PLOR	Depositor	
R, R_{free}	0.215 , 0.281	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	2822	wwPDB-VP	
Average B, all atoms $(Å^2)$	39.0	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: BMA, NAG

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	А	0.53	0/2708	0.77	0/3701	

There are no bond length outliers.

There are no bond angle outliers.

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	А	2643	0	2452	52	0
2	В	25	0	22	1	0
3	А	14	0	13	0	0
4	А	140	0	0	0	0
All	All	2822	0	2487	53	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 10.

All (53) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



Atom-1	Atom-2	Interatomic	Clash
		distance (Å)	overlap (Å)
1:A:360:ASN:O	1:A:361:GLU:HB2	1.79	0.81
1:A:121:GLN:HE22	1:A:129:LEU:H	1.32	0.78
1:A:171:VAL:HB	1:A:340:ASN:HD21	1.50	0.76
1:A:283:SER:OG	1:A:299:SER:HB3	1.87	0.74
1:A:121:GLN:NE2	1:A:129:LEU:H	1.86	0.74
1:A:244:ILE:HG21	1:A:325:GLY:H	1.56	0.71
1:A:171:VAL:HB	1:A:340:ASN:ND2	2.07	0.69
1:A:273:ALA:O	1:A:275:TYR:N	2.27	0.68
1:A:340:ASN:ND2	1:A:340:ASN:H	1.93	0.66
1:A:49:LYS:HE3	1:A:49:LYS:HA	1.80	0.64
1:A:261:ALA:HA	1:A:270:VAL:HG12	1.83	0.59
1:A:280:SER:O	1:A:302:VAL:HG23	2.03	0.58
1:A:281:THR:HG22	1:A:301:PRO:HA	1.84	0.58
1:A:270:VAL:HG21	1:A:276:GLN:HG3	1.85	0.58
1:A:234:PHE:CE1	1:A:328:TYR:CD2	2.93	0.57
1:A:5:GLY:N	1:A:165:SER:HG	2.03	0.56
1:A:117:PRO:HA	1:A:120:GLU:HG2	1.88	0.56
1:A:309:VAL:CG1	1:A:315:THR:HB	2.35	0.56
1:A:340:ASN:HD22	1:A:340:ASN:H	1.53	0.56
1:A:271:PRO:HA	1:A:314:GLU:O	2.08	0.54
1:A:309:VAL:HG11	1:A:315:THR:HB	1.90	0.53
1:A:244:ILE:HG22	1:A:324:GLY:HA2	1.93	0.51
1:A:284:ILE:O	1:A:297:GLU:HA	2.11	0.51
1:A:252:LYS:HB3	1:A:255:LYS:HE2	1.93	0.51
1:A:340:ASN:HD22	1:A:340:ASN:N	2.09	0.50
1:A:217:GLY:O	1:A:285:VAL:HG23	2.11	0.49
1:A:80:ILE:HD12	1:A:82:TYR:CE2	2.48	0.49
2:B:1:NAG:H61	2:B:2:BMA:H2	1.94	0.49
1:A:269:VAL:HB	1:A:315:THR:HG22	1.96	0.48
1:A:306:LEU:HA	1:A:317:MET:O	2.14	0.48
1:A:269:VAL:HA	1:A:316:CYS:O	2.14	0.47
1:A:269:VAL:HB	1:A:315:THR:CG2	2.44	0.47
1:A:199:THR:OG1	1:A:214:PRO:HD2	2.15	0.47
1:A:216:THR:O	1:A:228:PHE:HD2	1.97	0.47
1:A:261:ALA:CB	1:A:268:TRP:HD1	2.29	0.46
1:A:244:ILE:CG2	1:A:324:GLY:HA2	2.45	0.46
1:A:101:ILE:CD1	1:A:163:LEU:HD13	2.46	0.46
1:A:288:LYS:HD3	1:A:294:ASP:OD1	2.16	0.46
1:A:234:PHE:CZ	1:A:328:TYR:CD2	3.05	0.45
1:A:261:ALA:O	1:A:268:TRP:CD1	2.70	0.44
1:A:76:TYR:O	1:A:90:LEU:HD13	2.19	0.43
1:A:261:ALA:HB1	1:A:268:TRP:HD1	1.83	0.43
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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:80:ILE:HG22	1:A:142:ALA:HB2	2.02	0.42
1:A:282:ILE:O	1:A:299:SER:HA	2.19	0.42
1:A:243:PHE:CE2	1:A:284:ILE:HD11	2.55	0.42
1:A:89:GLY:HA3	1:A:110:TYR:O	2.19	0.42
1:A:253:ILE:HD13	1:A:320:ILE:HD12	2.00	0.42
1:A:324:GLY:C	1:A:326:ASN:H	2.22	0.42
1:A:324:GLY:C	1:A:326:ASN:N	2.73	0.42
1:A:223:SER:O	1:A:225:ALA:N	2.53	0.41
1:A:258:LEU:C	1:A:260:ASP:H	2.24	0.41
1:A:251:SER:O	1:A:253:ILE:HD12	2.21	0.41
1:A:309:VAL:HG12	1:A:315:THR:HB	2.02	0.40

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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	А	352/361~(98%)	316~(90%)	24 (7%)	12 (3%)	3 0

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	247	SER
1	А	274	SER
1	А	250	ALA
1	А	260	ASP
1	А	262	THR
1	А	275	TYR
1	А	311	GLN
1	А	266	GLN
1	А	312	SER
1	А	224	ALA

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Mol	Chain	Res	Type
1	А	261	ALA
1	А	323	ASP

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	А	277/296~(94%)	260~(94%)	17~(6%)	18 14	

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	24	VAL
1	А	49	LYS
1	А	90	LEU
1	А	101	ILE
1	А	132	LEU
1	А	215	VAL
1	А	226	VAL
1	А	240	THR
1	А	243	PHE
1	А	253	ILE
1	А	262	THR
1	А	264	THR
1	А	268	TRP
1	А	311	GLN
1	А	313	ASN
1	А	340	ASN
1	А	361	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	77	ASN
1	А	121	GLN

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Mol	Chain	Res	Type
1	А	189	ASN
1	А	265	GLN
1	А	276	GLN
1	А	287	GLN
1	А	340	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)

2 monosaccharides 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	Turne	Chain	Res	Link	Bo	ond leng	ths	В	ond ang	les
	Type	Chain	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	В	1	1,2	14,14,15	0.38	0	17,19,21	0.73	0
2	BMA	В	2	2	11,11,12	0.46	0	$15,\!15,\!17$	0.45	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	NAG	В	1	1,2	-	0/6/23/26	0/1/1/1
2	BMA	В	2	2	-	1/2/19/22	0/1/1/1

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	\mathbf{Res}	Type	Atoms
2	В	2	BMA	O5-C5-C6-O6

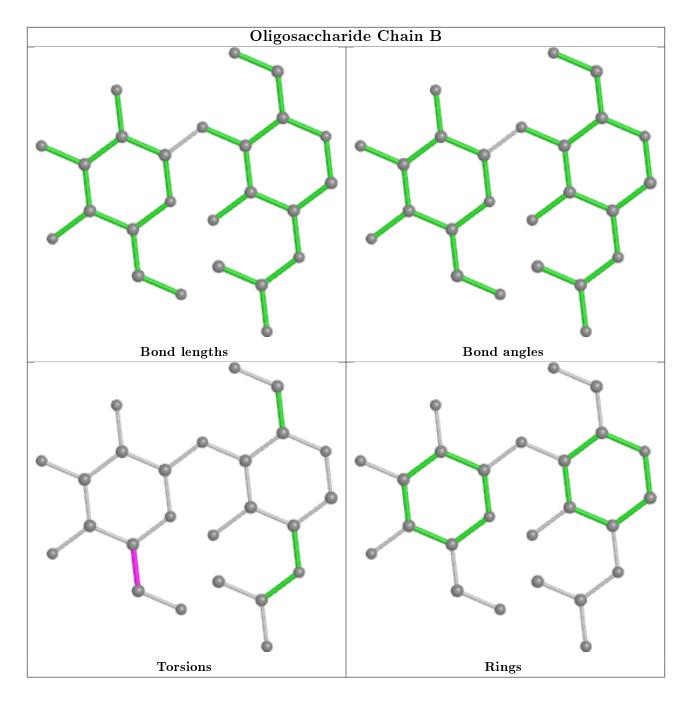
There are no ring outliers.

2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	В	1	NAG	1	0
2	В	2	BMA	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.





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		
	Type				Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	А	600	1	14, 14, 15	0.35	0	$17,\!19,\!21$	0.95	1 (5%)

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	NAG	А	600	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	\mathbf{Res}	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
3	A	600	NAG	C4-C3-C2	-2.87	106.82	111.02

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	А	600	NAG	C3-C2-N2-C7
3	А	600	NAG	C1-C2-N2-C7

There are no ring outliers.

No monomer is involved in short contacts.

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.

