Full wwPDB X-ray Structure Validation Report ⓘ

Apr 21, 2024 – 11:34 am BST

PDB ID	:	6ZI1
Title	:	Crystal structure of the isolated H. influenzae VapD toxin (D7N mutant)
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Deposited on	:	2020-06-24
Resolution	:	2.20 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

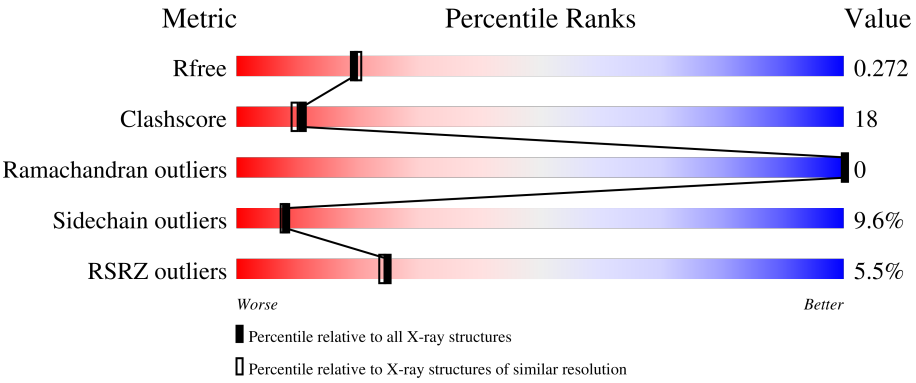
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 2.20 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))
R_{free}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 of 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% 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.

Mol	Chain	Length	Quality of chain
1	AAA	102	3%, 56%, 23%, ·, 19%
1	BBB	102	6%, 62%, 13%, 6%, 20%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 1421 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 Endoribonuclease VapD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	83	Total	C	N	O	S	0	0	0
			672	432	114	122	4			
1	BBB	82	Total	C	N	O	S	0	0	0
			661	425	112	120	4			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	-1	ALA	-	expression tag	UNP Q4QN95
AAA	0	ALA	-	expression tag	UNP Q4QN95
AAA	7	ASN	ASP	engineered mutation	UNP Q4QN95
AAA	93	LEU	-	expression tag	UNP Q4QN95
AAA	94	GLU	-	expression tag	UNP Q4QN95
AAA	95	HIS	-	expression tag	UNP Q4QN95
AAA	96	HIS	-	expression tag	UNP Q4QN95
AAA	97	HIS	-	expression tag	UNP Q4QN95
AAA	98	HIS	-	expression tag	UNP Q4QN95
AAA	99	HIS	-	expression tag	UNP Q4QN95
AAA	100	HIS	-	expression tag	UNP Q4QN95
BBB	-1	ALA	-	expression tag	UNP Q4QN95
BBB	0	ALA	-	expression tag	UNP Q4QN95
BBB	7	ASN	ASP	engineered mutation	UNP Q4QN95
BBB	93	LEU	-	expression tag	UNP Q4QN95
BBB	94	GLU	-	expression tag	UNP Q4QN95
BBB	95	HIS	-	expression tag	UNP Q4QN95
BBB	96	HIS	-	expression tag	UNP Q4QN95
BBB	97	HIS	-	expression tag	UNP Q4QN95
BBB	98	HIS	-	expression tag	UNP Q4QN95
BBB	99	HIS	-	expression tag	UNP Q4QN95
BBB	100	HIS	-	expression tag	UNP Q4QN95

- Molecule 2 is water.

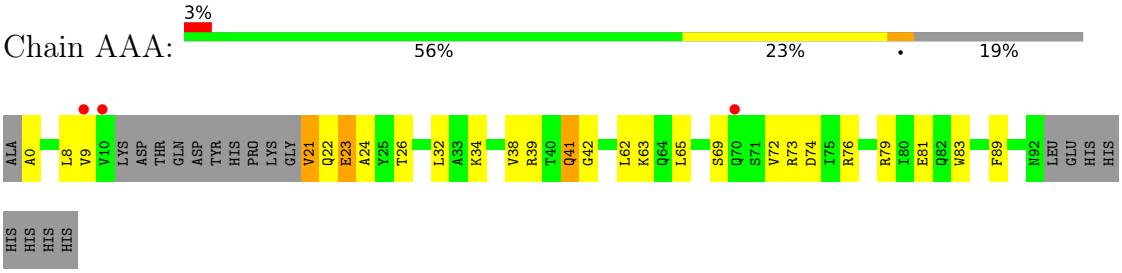
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	AAA	49	Total O 49 49	0	0
2	BBB	39	Total O 39 39	0	0

3 Residue-property plots (i)

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 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.

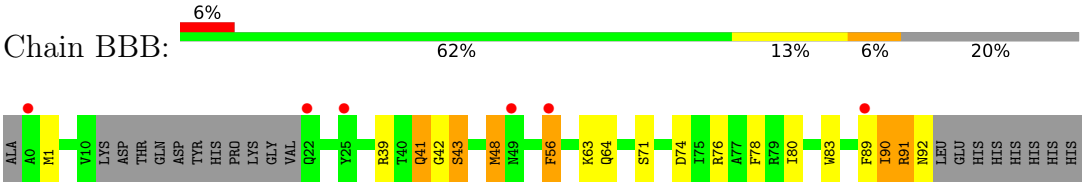
• Molecule 1: Endoribonuclease VapD

Chain AAA:



• Molecule 1: Endoribonuclease VapD

Chain BBB:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants a, b, c, α, β, γ	84.38Å 84.38Å 49.48Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	42.23 – 2.20 42.19 – 2.20	Depositor EDS
% Data completeness (in resolution range)	97.2 (42.23-2.20) 97.2 (42.19-2.20)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.63 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.8.0253	Depositor
R, R_{free}	0.214 , 0.267 0.221 , 0.272	Depositor DCC
R_{free} test set	1028 reflections (9.97%)	wwPDB-VP
Wilson B-factor (Å^2)	47.3	Xtriage
Anisotropy	0.285	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 42.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.35$	Xtriage
Estimated twinning fraction	0.487 for -h,-k,l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	1421	wwPDB-VP
Average B, all atoms (Å^2)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.74% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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	AAA	0.66	0/684	0.83	0/923
1	BBB	0.64	0/673	0.84	0/908
All	All	0.65	0/1357	0.83	0/1831

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

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	AAA	672	0	658	26	0
1	BBB	661	0	643	26	0
2	AAA	49	0	0	16	0
2	BBB	39	0	0	11	0
All	All	1421	0	1301	48	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 18.

All (48) 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:BBB:1:MET:HE3	2:BBB:229:HOH:O	1.54	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BBB:48:MET:HG3	2:BBB:229:HOH:O	1.59	0.99
1:AAA:63:LYS:HG3	2:AAA:215:HOH:O	1.64	0.97
1:BBB:39:ARG:HD2	1:BBB:42:GLY:O	1.78	0.83
1:AAA:9:VAL:HG11	1:AAA:73:ARG:CZ	2.11	0.81
1:BBB:1:MET:SD	2:BBB:229:HOH:O	2.39	0.79
2:AAA:215:HOH:O	1:BBB:89:PHE:CD2	2.38	0.76
1:BBB:1:MET:CE	2:BBB:229:HOH:O	2.20	0.72
1:BBB:48:MET:CG	2:BBB:229:HOH:O	2.28	0.69
1:BBB:56:PHE:HD1	1:BBB:56:PHE:O	1.78	0.66
1:AAA:38:VAL:HG12	2:AAA:211:HOH:O	1.97	0.63
2:AAA:215:HOH:O	1:BBB:89:PHE:CE2	2.50	0.62
1:AAA:9:VAL:CG1	1:AAA:73:ARG:HG2	2.31	0.60
2:AAA:215:HOH:O	1:BBB:90:ILE:CD1	2.54	0.55
1:AAA:9:VAL:CG1	1:AAA:73:ARG:CG	2.85	0.55
1:AAA:74:ASP:HA	2:BBB:202:HOH:O	2.08	0.54
1:AAA:72:VAL:HG23	2:AAA:205:HOH:O	2.09	0.53
1:BBB:1:MET:HG3	2:BBB:229:HOH:O	2.09	0.53
2:AAA:229:HOH:O	1:BBB:63:LYS:HB2	2.10	0.52
1:BBB:91:ARG:HG3	1:BBB:91:ARG:HH11	1.74	0.52
1:AAA:65:LEU:HD23	2:AAA:236:HOH:O	2.10	0.52
1:BBB:1:MET:CG	2:BBB:229:HOH:O	2.56	0.51
1:AAA:79:ARG:NH2	1:AAA:81:GLU:OE2	2.44	0.51
1:AAA:0:ALA:HB1	1:AAA:79:ARG:HD2	1.95	0.49
1:AAA:32:LEU:HD21	1:AAA:62:LEU:HD11	1.95	0.48
1:AAA:39:ARG:HD2	1:AAA:42:GLY:O	2.13	0.48
1:AAA:23:GLU:O	1:AAA:26:THR:HB	2.13	0.48
1:BBB:78:PHE:N	2:BBB:203:HOH:O	2.46	0.47
2:AAA:215:HOH:O	1:BBB:89:PHE:HD2	1.88	0.47
1:AAA:26:THR:HG22	2:AAA:201:HOH:O	2.14	0.47
1:AAA:63:LYS:HB3	2:AAA:240:HOH:O	2.14	0.47
1:AAA:41:GLN:HG2	2:BBB:206:HOH:O	2.14	0.46
1:AAA:89:PHE:HD1	2:AAA:229:HOH:O	1.98	0.46
1:BBB:43:SER:O	1:BBB:43:SER:OG	2.17	0.46
1:AAA:24:ALA:HB1	2:AAA:237:HOH:O	2.14	0.46
1:AAA:8:LEU:HD21	2:AAA:237:HOH:O	2.17	0.45
1:AAA:74:ASP:OD2	1:BBB:41:GLN:NE2	2.50	0.44
1:BBB:39:ARG:CD	1:BBB:42:GLY:O	2.60	0.44
1:BBB:1:MET:HG2	1:BBB:80:ILE:HB	2.01	0.43
1:BBB:56:PHE:C	1:BBB:56:PHE:CD1	2.92	0.43
1:AAA:9:VAL:HG11	1:AAA:73:ARG:HG2	2.00	0.42
1:AAA:41:GLN:NE2	1:BBB:74:ASP:OD2	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AAA:215:HOH:O	1:BBB:90:ILE:HD13	2.18	0.41
1:AAA:76:ARG:HG3	1:BBB:83:TRP:CH2	2.56	0.41
1:AAA:21:VAL:HG13	1:AAA:22:GLN:N	2.36	0.41
1:AAA:63:LYS:HD2	2:AAA:240:HOH:O	2.20	0.41
1:BBB:92:ASN:C	2:BBB:226:HOH:O	2.59	0.40
1:AAA:83:TRP:CH2	1:BBB:76:ARG:HG3	2.57	0.40

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	AAA	79/102 (78%)	74 (94%)	5 (6%)	0	100	100
1	BBB	78/102 (76%)	70 (90%)	8 (10%)	0	100	100
All	All	157/204 (77%)	144 (92%)	13 (8%)	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	AAA	69/86 (80%)	64 (93%)	5 (7%)	14	15
1	BBB	67/86 (78%)	59 (88%)	8 (12%)	5	4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	136/172 (79%)	123 (90%)	13 (10%)	8 8

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	21	VAL
1	AAA	23	GLU
1	AAA	34	LYS
1	AAA	41	GLN
1	AAA	69	SER
1	BBB	41	GLN
1	BBB	43	SER
1	BBB	48	MET
1	BBB	56	PHE
1	BBB	64	GLN
1	BBB	71	SER
1	BBB	90	ILE
1	BBB	91	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

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 (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	AAA	83/102 (81%)	0.19	3 (3%)	42	41	36, 56, 108, 131	0
1	BBB	82/102 (80%)	0.16	6 (7%)	15	14	35, 59, 103, 122	0
All	All	165/204 (80%)	0.17	9 (5%)	25	24	35, 58, 108, 131	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	10	VAL	6.5
1	BBB	22	GLN	5.5
1	BBB	0	ALA	4.6
1	AAA	70	GLN	4.3
1	BBB	89	PHE	3.1
1	BBB	56	PHE	3.0
1	AAA	9	VAL	2.8
1	BBB	25	TYR	2.7
1	BBB	49	ASN	2.1

6.2 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.