



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2018 – 06:02 am GMT

PDB ID : 3D4D
Title : Crystal structure of Staphylococcal nuclease variant Delta+PHS Y91E at cryogenic temperature
Authors : Khangulov, V.S.; Schlessman, J.L.; Garcia-Moreno, E.B.
Deposited on : 2008-05-14
Resolution : 2.10 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)
Xtriage (Phenix) : 1.13
EDS : trunk30967
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk30967

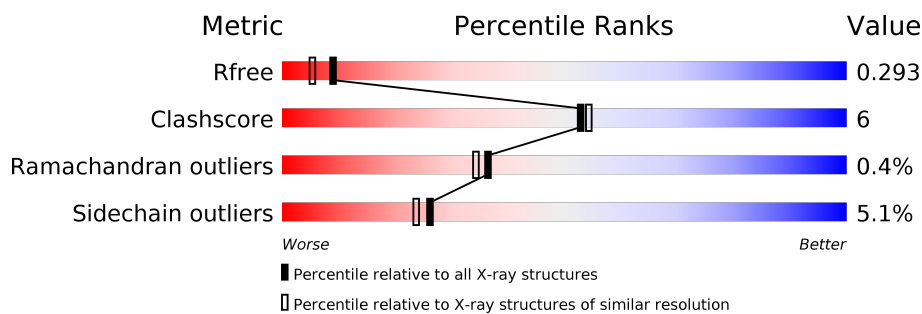
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	111664	4608 (2.10-2.10)
Clashscore	122126	5109 (2.10-2.10)
Ramachandran outliers	120053	5059 (2.10-2.10)
Sidechain outliers	120020	5060 (2.10-2.10)

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	143	 76% 13% • 10%
1	B	143	 75% 14% • 10%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2295 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 Thermonuclease.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	129	Total	C	N	O	S	0	0	0
			1030	657	178	191	4			
1	B	129	Total	C	N	O	S	0	0	0
			1030	657	178	191	4			

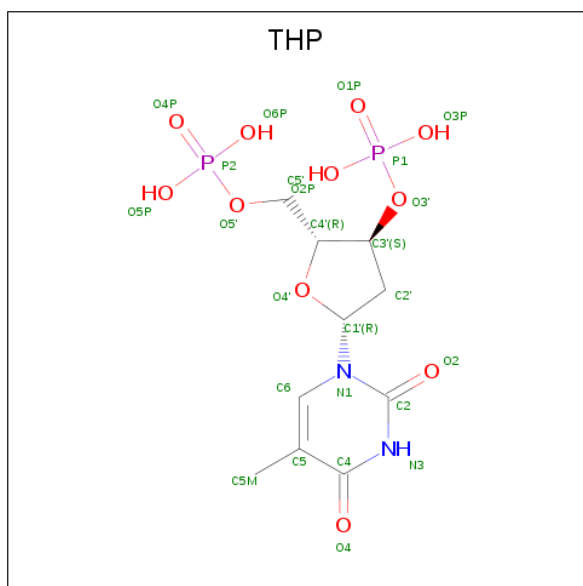
There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	THR	DELETION	UNP P00644
A	?	-	LYS	DELETION	UNP P00644
A	?	-	HIS	DELETION	UNP P00644
A	?	-	PRO	DELETION	UNP P00644
A	?	-	LYS	DELETION	UNP P00644
A	?	-	LYS	DELETION	UNP P00644
A	50	PHE	GLY	ENGINEERED	UNP P00644
A	51	ASN	VAL	ENGINEERED	UNP P00644
A	91	GLU	TYR	ENGINEERED	UNP P00644
A	117	GLY	PRO	ENGINEERED	UNP P00644
A	124	LEU	HIS	ENGINEERED	UNP P00644
A	128	ALA	SER	ENGINEERED	UNP P00644
B	?	-	THR	DELETION	UNP P00644
B	?	-	LYS	DELETION	UNP P00644
B	?	-	HIS	DELETION	UNP P00644
B	?	-	PRO	DELETION	UNP P00644
B	?	-	LYS	DELETION	UNP P00644
B	?	-	LYS	DELETION	UNP P00644
B	50	PHE	GLY	ENGINEERED	UNP P00644
B	51	ASN	VAL	ENGINEERED	UNP P00644
B	91	GLU	TYR	ENGINEERED	UNP P00644
B	117	GLY	PRO	ENGINEERED	UNP P00644
B	124	LEU	HIS	ENGINEERED	UNP P00644
B	128	ALA	SER	ENGINEERED	UNP P00644

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Ca	0	0
			1	1		
2	A	1	Total	Ca	0	0
			1	1		

- Molecule 3 is THYMIDINE-3',5'-DIPHOSPHATE (three-letter code: THP) (formula: C₁₀H₁₆N₂O₁₁P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			25	10	2	11	2		
3	B	1	Total	C	N	O	P	0	0
			25	10	2	11	2		

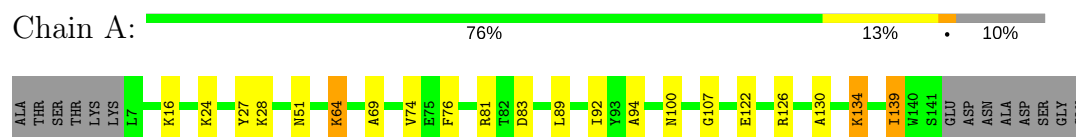
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	81	Total	O	0	0
			81	81		
4	B	102	Total	O	0	0
			102	102		

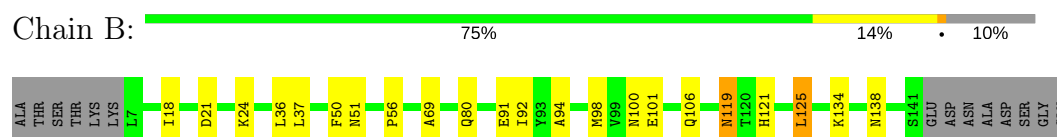
3 Residue-property plots [i](#)

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.

- Molecule 1: Thermonuclease



- Molecule 1: Thermonuclease



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	31.02Å 81.29Å 60.38Å 90.00° 90.05° 90.00°	Depositor
Resolution (Å)	60.38 – 2.10 60.38 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.9 (60.38-2.10) 99.7 (60.38-2.10)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.02	Depositor
$\langle I/\sigma(I) \rangle$ ¹	14.03 (at 2.10Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.233 , 0.290 0.235 , 0.293	Depositor DCC
R_{free} test set	1781 reflections (10.15%)	wwPDB-VP
Wilson B-factor (Å ²)	10.4	Xtriage
Anisotropy	0.174	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 15.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.21$	Xtriage
Estimated twinning fraction	0.480 for h,-k,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	2295	wwPDB-VP
Average B, all atoms (Å ²)	8.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.42% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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

Bond lengths and bond angles in the following residue types are not validated in this section: CA, THP

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	0.45	0/1047	0.61	0/1403
1	B	0.48	0/1047	0.62	0/1403
All	All	0.46	0/2094	0.61	0/2806

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	A	1030	0	1058	14	0
1	B	1030	0	1058	14	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	25	0	12	0	0
3	B	25	0	12	0	0
4	A	81	0	0	0	0
4	B	102	0	0	1	0
All	All	2295	0	2140	25	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 6.

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:130:ALA:O	1:A:134:LYS:HE2	1.73	0.89
1:A:64:LYS:NZ	1:A:64:LYS:HB2	1.92	0.84
1:A:64:LYS:HE2	1:B:50:PHE:O	1.91	0.69
1:A:74:VAL:HG12	1:A:92:ILE:HD12	1.77	0.67
1:A:64:LYS:HZ2	1:A:64:LYS:HB2	1.64	0.62
1:A:76:PHE:HB3	1:A:81:ARG:HE	1.65	0.62
1:B:18:ILE:HD11	1:B:24:LYS:HB2	1.85	0.59
1:A:83:ASP:HB3	1:A:89:LEU:HD21	1.86	0.57
1:A:69:ALA:HB2	1:A:94:ALA:HB1	1.87	0.57
1:A:27:TYR:CE2	1:A:28:LYS:HD2	2.41	0.56
1:A:107:GLY:O	1:A:139:ILE:HB	2.08	0.54
1:B:119:ASN:HD22	1:B:119:ASN:H	1.57	0.50
1:B:21:ASP:HA	1:B:36:LEU:HD22	1.94	0.49
1:B:69:ALA:HB2	1:B:94:ALA:HB1	1.96	0.47
1:A:122:GLU:O	1:A:126:ARG:HG3	2.15	0.46
1:B:106:GLN:HG2	4:B:241:HOH:O	2.18	0.43
1:B:98:MET:SD	1:B:100:ASN:HB2	2.61	0.41
1:B:134:LYS:HE2	1:B:134:LYS:HB3	1.94	0.41
1:A:64:LYS:CE	1:B:50:PHE:O	2.64	0.41
1:A:76:PHE:CB	1:A:81:ARG:HE	2.31	0.41
1:B:101:GLU:HA	1:B:125:LEU:HD13	2.02	0.41
1:A:64:LYS:HD2	1:B:56:PRO:CG	2.51	0.41
1:B:37:LEU:HD12	1:B:91:GLU:OE1	2.21	0.41
1:B:91:GLU:C	1:B:92:ILE:HD12	2.41	0.41
1:B:121:HIS:O	1:B:125:LEU:HD23	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	127/143 (89%)	123 (97%)	4 (3%)	0	100	100
1	B	127/143 (89%)	123 (97%)	3 (2%)	1 (1%)	21	16
All	All	254/286 (89%)	246 (97%)	7 (3%)	1 (0%)	36	34

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	138	ASN

5.3.2 Protein sidechains ⓘ

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	107/118 (91%)	100 (94%)	7 (6%)	19	16
1	B	107/118 (91%)	103 (96%)	4 (4%)	37	38
All	All	214/236 (91%)	203 (95%)	11 (5%)	26	24

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	LYS
1	A	24	LYS
1	A	51	ASN
1	A	64	LYS
1	A	100	ASN
1	A	134	LYS
1	A	139	ILE
1	B	51	ASN
1	B	80	GLN
1	B	119	ASN
1	B	125	LEU

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

Mol	Chain	Res	Type
1	A	123	GLN
1	A	138	ASN
1	B	30	GLN
1	B	51	ASN
1	B	80	GLN
1	B	119	ASN
1	B	138	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, 2 are monoatomic - leaving 2 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	$\# Z > 2$
3	THP	A	151	-	21,26,26	0.74	0	29,40,40	1.69	2 (6%)
3	THP	B	151	-	21,26,26	0.80	0	29,40,40	1.60	2 (6%)

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	THP	A	151	-	-	0/11/27/27	0/2/2/2
3	THP	B	151	-	-	0/11/27/27	0/2/2/2

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	B	151	THP	C5-C6-N1	-2.15	119.82	122.15
3	A	151	THP	O3'-P1-O1P	-2.04	101.50	109.39
3	B	151	THP	C4-N3-C2	6.24	120.45	115.14
3	A	151	THP	C4-N3-C2	6.77	120.90	115.14

There are no chirality outliers.

There are no torsion outliers.

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](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.