



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 25, 2023 – 06:47 PM EDT

PDB ID : 6BIQ
Title : Structure of NlpC2 from Trichomonas vaginalis
Authors : Pinheiro, J.; Simoes-Barbosa, A.; Goldstone, D.C.
Deposited on : 2017-11-02
Resolution : 2.30 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
Xtrriage (Phenix) : 1.13
EDS : 2.35.1
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) : 2.35.1

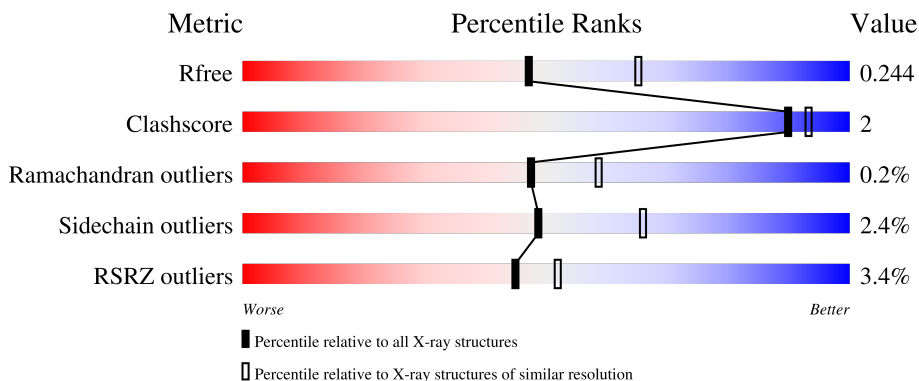
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 $\leq 5\%$. 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	A	278	 90% 5% . .
1	B	278	 2% 90% 6% 5%
1	C	278	 91% 5% 5%
1	D	278	 11% 87% 6% 6%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 16915 atoms, of which 7906 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 Clan CA, family C40, NlpC/P60 superfamily cysteine peptidase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	266	4145	1360	2010	358	408	9	0	0	0
1	B	265	4092	1349	1979	351	404	9	0	0	0
1	C	265	4123	1354	1994	357	409	9	0	0	0
1	D	260	3984	1315	1923	340	397	9	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP A2DC48
A	-1	PRO	-	expression tag	UNP A2DC48
A	0	GLY	-	expression tag	UNP A2DC48
B	-2	GLY	-	expression tag	UNP A2DC48
B	-1	PRO	-	expression tag	UNP A2DC48
B	0	GLY	-	expression tag	UNP A2DC48
C	-2	GLY	-	expression tag	UNP A2DC48
C	-1	PRO	-	expression tag	UNP A2DC48
C	0	GLY	-	expression tag	UNP A2DC48
D	-2	GLY	-	expression tag	UNP A2DC48
D	-1	PRO	-	expression tag	UNP A2DC48
D	0	GLY	-	expression tag	UNP A2DC48

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	179	Total	O	0	0
			179	179		
2	B	154	Total	O	0	0
			154	154		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	138	Total 138	O 138	0	0
2	D	100	Total 100	O 100	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: Clan CA, family C40, NlpC/P60 superfamily cysteine peptidase

Chain A: 



- Molecule 1: Clan CA, family C40, NlpC/P60 superfamily cysteine peptidase

Chain B: 




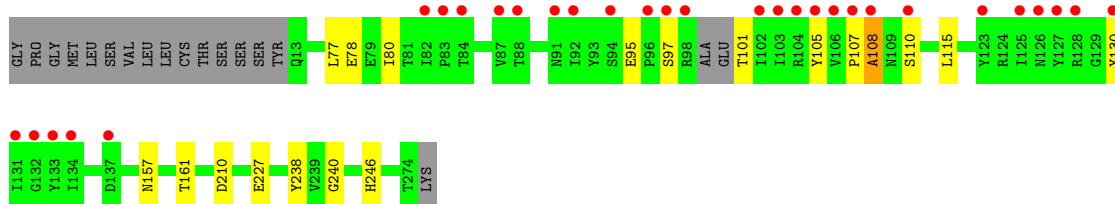
- Molecule 1: Clan CA, family C40, NlpC/P60 superfamily cysteine peptidase

Chain C: 



- Molecule 1: Clan CA, family C40, NlpC/P60 superfamily cysteine peptidase

Chain D: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	36.82Å 99.03Å 102.84Å 115.02° 96.28° 94.28°	Depositor
Resolution (Å)	35.70 – 2.30 50.90 – 2.30	Depositor EDS
% Data completeness (in resolution range)	89.2 (35.70-2.30) 88.3 (50.90-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.62 (at 2.29Å)	Xtrriage
Refinement program	PHENIX (1.10_2155: ???)	Depositor
R, R_{free}	0.199 , 0.241 0.201 , 0.244	Depositor DCC
R_{free} test set	2397 reflections (4.72%)	wwPDB-VP
Wilson B-factor (Å ²)	23.6	Xtrriage
Anisotropy	0.451	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 38.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.020 for -h,-l,-k	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	16915	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.16% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.38	0/2194	0.55	0/2989
1	B	0.35	0/2172	0.55	0/2962
1	C	0.38	1/2188 (0.0%)	0.55	1/2983 (0.0%)
1	D	0.35	0/2117	0.55	0/2889
All	All	0.37	1/8671 (0.0%)	0.55	1/11823 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	179	CYS	CB-SG	5.30	1.91	1.82

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	179	CYS	CA-CB-SG	6.90	126.42	114.00

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	2135	2010	2009	8	0
1	B	2113	1979	1978	7	0
1	C	2129	1994	1995	8	0
1	D	2061	1923	1923	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	179	0	0	1	0
2	B	154	0	0	2	1
2	C	138	0	0	6	0
2	D	100	0	0	2	1
All	All	9009	7906	7905	30	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 2.

All (30) 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:77:LEU:O	2:A:301:HOH:O	2.05	0.74
1:D:227:GLU:OE2	2:D:301:HOH:O	2.07	0.71
1:B:179:CYS:HB3	1:B:234:HIS:CE1	2.27	0.69
1:C:39:ASN:ND2	2:C:304:HOH:O	2.26	0.69
1:C:21:THR:O	2:C:302:HOH:O	2.13	0.67
1:C:95:GLU:OE2	2:C:301:HOH:O	2.12	0.66
1:B:48:ASP:OD2	2:B:301:HOH:O	2.15	0.65
1:C:11:SER:N	2:C:305:HOH:O	2.29	0.64
1:A:179:CYS:HB3	1:A:234:HIS:CE1	2.35	0.62
1:C:209:GLU:OE2	2:C:303:HOH:O	2.19	0.53
1:A:95:GLU:HB2	1:A:100:GLU:HG3	1.92	0.51
1:A:103:ILE:O	1:A:104:ARG:HG2	2.11	0.51
1:B:95:GLU:O	1:B:97:SER:N	2.45	0.48
1:D:78:GLU:HG3	1:D:80:ILE:HG23	1.98	0.46
1:B:87:VAL:HG12	1:B:87:VAL:O	2.16	0.46
1:A:95:GLU:O	1:A:97:SER:N	2.49	0.45
1:D:107:PRO:O	1:D:108:ALA:C	2.56	0.45
1:B:106:VAL:HG13	2:B:306:HOH:O	2.19	0.43
1:B:180:SER:HB2	1:B:196:ARG:O	2.19	0.43
1:D:157:ASN:O	2:D:302:HOH:O	2.21	0.43
1:A:37:ASP:HB3	1:A:40:ARG:HG3	1.99	0.43
1:B:167:TYR:HA	1:B:177:PHE:O	2.19	0.43
1:D:238:TYR:CE2	1:D:240:GLY:HA2	2.53	0.42
1:A:275:LYS:C	1:A:275:LYS:HD2	2.40	0.42
1:D:95:GLU:O	1:D:97:SER:N	2.48	0.42
1:D:157:ASN:O	1:D:161:THR:HG23	2.19	0.42
1:A:21:THR:O	1:A:22:THR:C	2.58	0.41
1:C:95:GLU:O	1:C:97:SER:N	2.49	0.41
1:C:136:GLU:HG2	2:C:343:HOH:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:62:HIS:HB2	1:C:71:TRP:CZ3	2.55	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)
2:B:449:HOH:O	2:D:366:HOH:O[1_655]	2.01	0.19

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	264/278 (95%)	254 (96%)	10 (4%)	0	100	100
1	B	263/278 (95%)	252 (96%)	10 (4%)	1 (0%)	34	42
1	C	263/278 (95%)	253 (96%)	10 (4%)	0	100	100
1	D	256/278 (92%)	244 (95%)	11 (4%)	1 (0%)	34	42
All	All	1046/1112 (94%)	1003 (96%)	41 (4%)	2 (0%)	47	58

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	108	ALA
1	B	43	TYR

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	226/241 (94%)	220 (97%)	6 (3%)	44	61
1	B	222/241 (92%)	218 (98%)	4 (2%)	59	75
1	C	226/241 (94%)	223 (99%)	3 (1%)	69	82
1	D	218/241 (90%)	210 (96%)	8 (4%)	34	48
All	All	892/964 (92%)	871 (98%)	21 (2%)	49	66

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	SER
1	A	27	LEU
1	A	40	ARG
1	A	98	ARG
1	A	246	HIS
1	A	275	LYS
1	B	73	SER
1	B	88	THR
1	B	246	HIS
1	B	275	LYS
1	C	88	THR
1	C	246	HIS
1	C	274	THR
1	D	77	LEU
1	D	101	THR
1	D	105	TYR
1	D	110	SER
1	D	115	LEU
1	D	130	TYR
1	D	210	ASP
1	D	246	HIS

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 [i](#)

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

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, 95th 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	A	266/278 (95%)	-0.18	0 100 100	12, 22, 43, 66	0
1	B	265/278 (95%)	-0.02	5 (1%) 66 73	15, 26, 56, 69	0
1	C	265/278 (95%)	-0.00	1 (0%) 92 95	14, 27, 49, 74	0
1	D	260/278 (93%)	0.40	30 (11%) 4 7	16, 31, 77, 104	0
All	All	1056/1112 (94%)	0.05	36 (3%) 45 52	12, 26, 66, 104	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	127	TYR	7.3
1	D	98	ARG	5.3
1	D	130	TYR	5.1
1	D	92	ILE	5.1
1	D	102	ILE	4.3
1	D	91	ASN	4.2
1	D	108	ALA	4.0
1	D	137	ASP	4.0
1	D	106	VAL	3.7
1	D	125	ILE	3.4
1	D	134	ILE	3.3
1	D	133	TYR	3.2
1	D	107	PRO	3.2
1	D	84	THR	3.1
1	D	132	GLY	3.1
1	D	96	PRO	3.0
1	D	97	SER	3.0
1	D	103	ILE	3.0
1	D	88	THR	2.9
1	D	82	ILE	2.9
1	B	101	THR	2.8

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Mol	Chain	Res	Type	RSRZ
1	D	110	SER	2.8
1	D	128	ARG	2.7
1	D	87	VAL	2.7
1	B	127	TYR	2.6
1	D	131	ILE	2.5
1	B	90	ALA	2.4
1	D	105	TYR	2.4
1	B	106	VAL	2.3
1	D	126	ASN	2.3
1	D	94	SER	2.3
1	B	130	TYR	2.2
1	C	88	THR	2.2
1	D	104	ARG	2.1
1	D	83	PRO	2.1
1	D	123	TYR	2.0

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.