



Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 10:01 pm BST

PDB ID : 6DE1
Title : Crystal structure of the single mutant (D52N) of the full-length NT5C2 in the active state
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Deposited on : 2018-05-10
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 ⓘ symbol.

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)
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

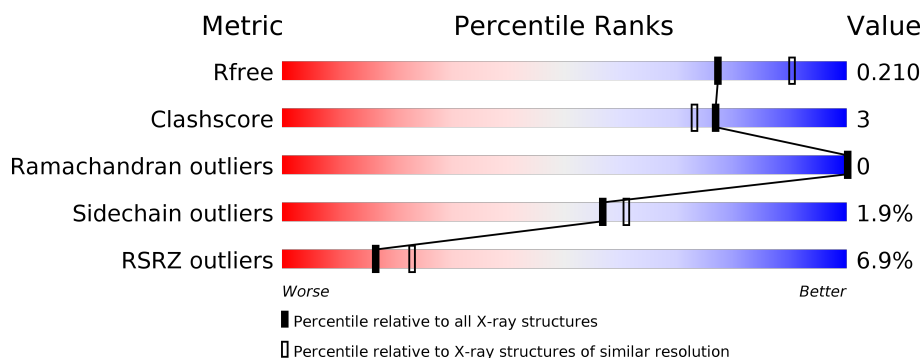
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1479 (2.16-2.16)
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (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 $\leq 5\%$. 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	579	<div> <div>6%</div> <div>73%</div> <div>7%</div> <div>19%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4119 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 Cytosolic purine 5'-nucleotidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	467	Total	C	N	O	S	0	0	0
			3809	2465	633	690	21			

There are 19 discrepancies between the modelled and reference sequences:

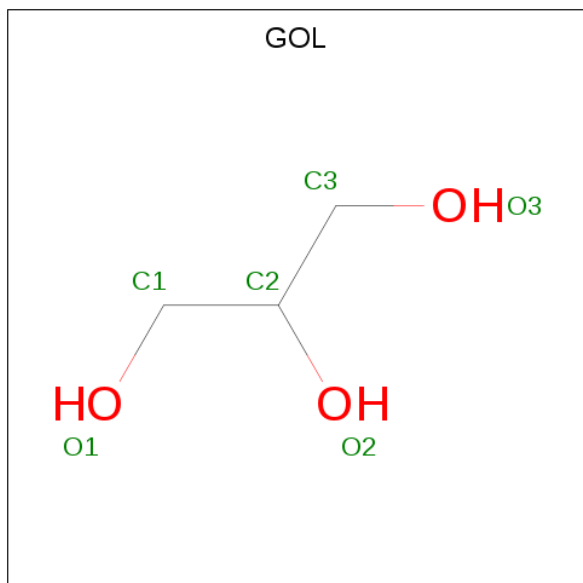
Chain	Residue	Modelled	Actual	Comment	Reference
A	-17	GLY	-	expression tag	UNP P49902
A	-16	SER	-	expression tag	UNP P49902
A	-15	SER	-	expression tag	UNP P49902
A	-14	HIS	-	expression tag	UNP P49902
A	-13	HIS	-	expression tag	UNP P49902
A	-12	HIS	-	expression tag	UNP P49902
A	-11	HIS	-	expression tag	UNP P49902
A	-10	HIS	-	expression tag	UNP P49902
A	-9	HIS	-	expression tag	UNP P49902
A	-8	SER	-	expression tag	UNP P49902
A	-7	SER	-	expression tag	UNP P49902
A	-6	GLY	-	expression tag	UNP P49902
A	-5	LEU	-	expression tag	UNP P49902
A	-4	VAL	-	expression tag	UNP P49902
A	-3	PRO	-	expression tag	UNP P49902
A	-2	ARG	-	expression tag	UNP P49902
A	-1	GLY	-	expression tag	UNP P49902
A	0	SER	-	expression tag	UNP P49902
A	52	ASN	ASP	engineered mutation	UNP P49902

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	284	Total	O	0	0
			284	284		

4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	90.67Å 126.26Å 130.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.88 – 2.15 48.88 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.88-2.15) 99.9 (48.88-2.15)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.59 (at 2.16Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.170 , 0.210 0.171 , 0.210	Depositor DCC
R_{free} test set	4088 reflections (9.97%)	wwPDB-VP
Wilson B-factor (Å ²)	31.6	Xtriage
Anisotropy	0.466	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 52.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.009 for -h,-l,-k	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4119	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.96% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, PO4

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	0/3908	0.51	0/5276

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	A	3809	0	3758	23	0
2	A	20	0	0	1	0
3	A	6	0	8	0	0
4	A	284	0	0	4	0
All	All	4119	0	3766	23	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 3.

All (23) 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:202:ARG:HH21	1:A:202:ARG:HA	1.47	0.80
1:A:388:LEU:HD22	1:A:430:MET:HB2	1.89	0.55
1:A:126:ASN:HB3	4:A:932:HOH:O	2.09	0.51
1:A:28:ARG:O	1:A:34:ARG:HG2	2.10	0.51
1:A:59:VAL:HB	1:A:227:VAL:HB	1.91	0.51
1:A:31:ALA:HA	1:A:34:ARG:HG3	1.93	0.50
1:A:28:ARG:HD3	1:A:471:TYR:CE1	2.46	0.50
1:A:349:ILE:HG12	1:A:369:PHE:HB3	1.95	0.48
1:A:229:ASP:OD2	1:A:466:ILE:HD13	2.14	0.48
1:A:228:LYS:HG2	1:A:266:PHE:CZ	2.47	0.48
1:A:202:ARG:NH1	4:A:705:HOH:O	2.41	0.48
1:A:213:SER:O	1:A:217:LYS:HG2	2.13	0.48
1:A:161:GLU:OE2	4:A:701:HOH:O	2.20	0.46
1:A:392:LEU:HD22	1:A:430:MET:HE1	1.98	0.45
1:A:5:TRP:HH2	1:A:55:TYR:HE1	1.65	0.44
1:A:144:ARG:NH1	2:A:602:PO4:O1	2.49	0.44
1:A:321:LEU:HA	1:A:327:TYR:OH	2.18	0.43
1:A:132:GLU:HB2	4:A:890:HOH:O	2.18	0.43
1:A:222:LEU:HD13	1:A:262:TYR:HB2	2.01	0.43
1:A:157:PHE:O	1:A:160:PRO:HD2	2.19	0.42
1:A:442:ARG:HD3	1:A:444:GLY:O	2.18	0.42
1:A:293:PRO:CB	1:A:359:LYS:HG3	2.51	0.41
1:A:422:ARG:O	1:A:426:VAL:HG23	2.22	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	463/579 (80%)	452 (98%)	11 (2%)	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	413/520 (79%)	405 (98%)	8 (2%)	57 61

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	SER
1	A	26	LYS
1	A	30	GLU
1	A	44	GLU
1	A	202	ARG
1	A	220	GLU
1	A	377	GLN
1	A	388	LEU

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

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](#)

5 ligands 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	PO4	A	603	-	4,4,4	0.79	0	6,6,6	0.67	0
2	PO4	A	604	-	4,4,4	0.83	0	6,6,6	0.53	0
2	PO4	A	601	-	4,4,4	1.19	0	6,6,6	0.69	0
2	PO4	A	602	-	4,4,4	0.92	0	6,6,6	0.51	0
3	GOL	A	605	-	5,5,5	0.38	0	5,5,5	0.14	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
3	GOL	A	605	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	605	GOL	O1-C1-C2-C3
3	A	605	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	602	PO4	1	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	467/579 (80%)	0.08	32 (6%) 16 23	21, 34, 87, 126	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	398	PHE	7.7
1	A	399	LEU	7.6
1	A	402	LEU	5.9
1	A	397	ILE	5.8
1	A	395	LEU	4.6
1	A	29	ARG	4.5
1	A	392	LEU	4.5
1	A	394	SER	4.4
1	A	400	ALA	4.3
1	A	401	GLU	4.3
1	A	423	ILE	4.1
1	A	23	ALA	3.9
1	A	426	VAL	3.9
1	A	396	ASP	3.2
1	A	421	ARG	3.1
1	A	27	TYR	2.8
1	A	388	LEU	2.8
1	A	473	PHE	2.8
1	A	26	LYS	2.7
1	A	15	MET	2.7
1	A	25	LYS	2.7
1	A	317	TYR	2.6
1	A	22	HIS	2.5
1	A	422	ARG	2.4
1	A	387	SER	2.4
1	A	393	GLN	2.4
1	A	18	ASN	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	389	PHE	2.3
1	A	390	GLU	2.3
1	A	429	ASP	2.2
1	A	383	THR	2.1
1	A	20	ASP	2.1

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 carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	GOL	A	605	6/6	0.92	0.15	24,49,59,66	0
2	PO4	A	604	5/5	0.94	0.12	67,69,83,85	0
2	PO4	A	602	5/5	0.97	0.14	42,48,55,60	0
2	PO4	A	603	5/5	0.97	0.11	33,40,59,59	0
2	PO4	A	601	5/5	1.00	0.14	26,26,31,39	0

6.5 Other polymers [i](#)

There are no such residues in this entry.