

Full wwPDB X-ray Structure Validation Report (i)

Oct 14, 2023 – 07:53 PM EDT

PDB ID	:	7STC
Title	:	AQP5 T41H with Ni2+ $$
Authors	:	Kowatz, T.
Deposited on	:	2021-11-12
Resolution	:	2.25 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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

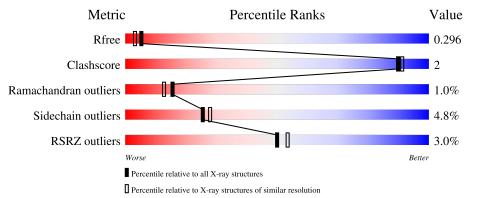
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY\;DIFFRACTION$

The reported resolution of this entry is 2.25 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$	
R_{free}	130704	1377 (2.26-2.26)	
Clashscore	141614	1487 (2.26-2.26)	
Ramachandran outliers	138981	1449 (2.26-2.26)	
Sidechain outliers	138945	1450 (2.26-2.26)	
RSRZ outliers	127900	1356 (2.26-2.26)	

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	А	266	3% 85%	6%	8%
1	В	266	85%	7%	8%
1	С	266	<mark>6%</mark> 82%	9%	8%
1	D	266	% 8 6%	5%	• 8%



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 7412 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.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Λ	244	Total	С	Ν	Ο	\mathbf{S}	0	0	0
	А	244	1810	1196	299	309	6	0	0	U
1	В	244	Total	С	Ν	0	S	0	0	0
	D	244	1810	1196	299	309	6	0	0	0
1	С	244	Total	С	Ν	0	S	0	0	0
	U	244	1810	1196	299	309	6	0	0	0
1	Л	244	Total	С	Ν	0	S	0	0	0
		244	1810	1196	299	309	6		0	0

• Molecule 1 is a protein called Aquaporin-5.

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	0	MET	-	initiating methionine	UNP P55064
А	1	SER	-	expression tag	UNP P55064
A	41	HIS	THR	engineered mutation	UNP P55064
В	0	MET	-	initiating methionine	UNP P55064
В	1	SER	-	expression tag	UNP P55064
В	41	HIS	THR	engineered mutation	UNP P55064
C	0	MET	-	initiating methionine	UNP P55064
С	1	SER	-	expression tag	UNP P55064
С	41	HIS	THR	engineered mutation	UNP P55064
D	0	MET	-	initiating methionine	UNP P55064
D	1	SER	-	expression tag	UNP P55064
D	41	HIS	THR	engineered mutation	UNP P55064

• Molecule 2 is NICKEL (II) ION (three-letter code: NI) (formula: Ni) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	Total Ni 1 1	0	0

• Molecule 3 is water.

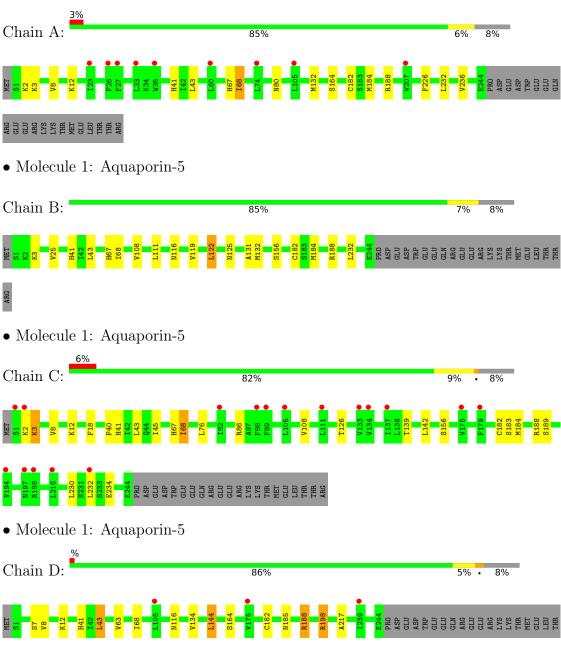


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	42	$\begin{array}{cc} \text{Total} & \text{O} \\ 42 & 42 \end{array}$	0	0
3	В	52	$\begin{array}{cc} \text{Total} & \text{O} \\ 52 & 52 \end{array}$	0	0
3	С	31	Total O 31 31	0	0
3	D	46	Total O 46 46	0	0



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: Aquaporin-5



THR ARG



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	89.68Å 90.65 Å 184.77 Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.22 - 2.25	Depositor
Resolution (A)	92.38 - 2.05	EDS
% Data completeness	99.3 (34.22-2.25)	Depositor
(in resolution range)	92.9(92.38-2.05)	EDS
R_{merge}	(Not available)	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.00 (at 2.05 \text{\AA})$	Xtriage
Refinement program	BUSTER 2.10.4	Depositor
R, R_{free}	0.286 , 0.310	Depositor
II, IIfree	0.269 , 0.296	DCC
R_{free} test set	3808 reflections $(4.24%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	35.9	Xtriage
Anisotropy	0.399	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.33 , 58.7	EDS
L-test for $twinning^2$	$< L > = 0.46, < L^2 > = 0.29$	Xtriage
Estimated twinning fraction	0.217 for k,h,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	7412	wwPDB-VP
Average B, all atoms $(Å^2)$	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 15.57% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

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: NI

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	
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.40	0/1854	0.51	0/2532
1	В	0.43	0/1854	0.54	0/2532
1	С	0.37	0/1854	0.52	0/2532
1	D	0.45	0/1854	0.53	0/2532
All	All	0.41	0/7416	0.53	0/10128

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	1810	0	1881	3	0
1	В	1810	0	1881	5	0
1	С	1810	0	1881	13	0
1	D	1810	0	1881	9	0
2	А	1	0	0	0	0
3	А	42	0	0	0	0
3	В	52	0	0	0	0
3	С	31	0	0	0	0
3	D	46	0	0	0	0
All	All	7412	0	7524	27	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 2.

All (27) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:B:108:VAL:HG11	1:D:134:VAL:HG23	1.66	0.78
1:D:116:ASN:HD22	1:D:198:ARG:NH2	1.82	0.77
1:A:41:HIS:HD2	1:A:43:LEU:H	1.36	0.73
1:D:41:HIS:HD2	1:D:43:LEU:H	1.37	0.70
1:B:108:VAL:HG11	1:D:134:VAL:CG2	2.26	0.65
1:C:2:LYS:HB3	1:C:3:LYS:NZ	2.12	0.64
1:C:41:HIS:HD2	1:C:43:LEU:H	1.47	0.60
1:B:122:LEU:HD21	1:B:131:ALA:HB2	1.84	0.57
1:A:8:VAL:HG12	1:A:12:LYS:HE2	1.92	0.51
1:B:41:HIS:HD2	1:B:43:LEU:H	1.59	0.50
1:C:67:HIS:NE2	1:C:76:LEU:CD1	2.76	0.48
1:C:40:PRO:HB2	1:C:45:ILE:HD11	1.97	0.47
1:C:67:HIS:NE2	1:C:76:LEU:HD13	2.30	0.46
1:D:41:HIS:CD2	1:D:43:LEU:HB2	2.52	0.45
1:C:142:LEU:HD22	1:C:184:MET:HE1	1.99	0.44
1:C:8:VAL:HG12	1:C:12:LYS:HE2	2.00	0.44
1:C:230:LEU:HG	1:C:234:GLU:CB	2.48	0.44
1:C:2:LYS:CB	1:C:3:LYS:HZ3	2.31	0.44
1:D:144:LEU:HD23	1:D:217:ALA:HB1	2.00	0.43
1:A:226:PHE:CZ	1:D:63:VAL:HG22	2.54	0.43
1:B:116:ASN:HB3	1:B:119:VAL:HG22	2.01	0.43
1:C:183:SER:HG	1:C:189:SER:HG	1.60	0.42
1:C:41:HIS:CD2	1:C:43:LEU:H	2.34	0.42
1:C:2:LYS:HB3	1:C:3:LYS:HZ3	1.85	0.41
1:D:8:VAL:O	1:D:12:LYS:HD2	2.20	0.41
1:D:185:ASN:HB3	1:D:188:ARG:HB3	2.02	0.41
1:C:183:SER:OG	1:C:189:SER:OG	2.28	0.41

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.



Mol	Chain	Analysed	Analysed Favoured Allowed Outl		Outliers	Percer	ntiles
1	А	242/266~(91%)	234~(97%)	5(2%)	3~(1%)	13	9
1	В	242/266~(91%)	230~(95%)	9~(4%)	3~(1%)	13	9
1	С	242/266~(91%)	232~(96%)	8~(3%)	2(1%)	19	17
1	D	242/266~(91%)	233~(96%)	7 (3%)	2(1%)	19	17
All	All	968/1064~(91%)	929~(96%)	29~(3%)	10 (1%)	15	13

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	182	CYS
1	В	182	CYS
1	В	184	MET
1	С	182	CYS
1	D	182	CYS
1	А	184	MET
1	А	68	ILE
1	В	68	ILE
1	С	68	ILE
1	D	68	ILE

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	187/209~(90%)	177~(95%)	10~(5%)	22 23
1	В	187/209~(90%)	177~(95%)	10~(5%)	22 23
1	С	187/209~(90%)	177~(95%)	10 (5%)	22 23
1	D	187/209~(90%)	181 (97%)	6 (3%)	39 47
All	All	748/836~(90%)	712~(95%)	36~(5%)	25 28

All (36) residues with a non-rotameric sidechain are listed below:



Mol	Chain	Res	Type
1	А	2	LYS LYS
1	А	3	LYS
1	А	67	HIS ILE
1	А	68	ILE
1	А	80	ASN
1	A A A A A A	132	MET
1	А	164	SER
1	А	188	ARG
1	A A A A B	232	LEU VAL
1	А	236	VAL
1	В	3	LYS
1	В	25	LYS VAL
1	В	67	HIS
1	В	111	LEU
1	В	122	LEU
1	В	125	ASN
1	В	132	MET
1	В	156	SER
1	В	188	ARG
1	В	232	LEU LYS
1	С	3	LYS
1	С	18	PHE ILE
1	С	68	ILE
1	С	86	ARG
1	B C C C C C C C C C C C	108	ARG VAL
1	С	126	IHK
1	С	139	THR
1	С	156	SER
1	С	188	ARG
1	С	232	LEU
1	D	7	SER
1	D	43	LEU
1	D	144	LEU
1	D	164	SER
1	D	188	ARG
1	D	198	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	41	HIS
1	В	41	HIS
1	D	41	HIS

Continued on next page...



Continued from previous page...

Mol	Chain	Res	Type
1	D	116	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

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)

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	$OWAB(Å^2)$	$\mathbf{Q}{<}0.9$
1	А	244/266~(91%)	0.38	9 (3%) 41 44	42, 57, 78, 88	0
1	В	244/266~(91%)	0.20	0 100 100	39, 52, 75, 88	0
1	С	244/266~(91%)	0.46	17 (6%) 16 17	40, 62, 84, 94	0
1	D	244/266~(91%)	0.21	3 (1%) 79 81	38, 51, 76, 94	0
All	All	976/1064 (91%)	0.31	29 (2%) 50 53	38, 55, 79, 94	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	26	PHE	6.0
1	А	27	PHE	6.0
1	С	137	ILE	4.5
1	А	35	TRP	4.1
1	С	82	ILE	3.9
1	С	1	SER	3.6
1	С	198	ARG	3.5
1	А	23	ILE	3.3
1	А	207	TRP	3.2
1	С	175	VAL	3.2
1	А	33	LEU	3.1
1	С	105	LEU	2.6
1	D	175	VAL	2.6
1	С	133	VAL	2.6
1	С	232	LEU	2.5
1	D	239	ILE	2.4
1	А	105	LEU	2.4
1	С	194	VAL	2.4
1	А	60	LEU	2.4
1	С	88	PHE	2.3
1	С	111	LEU	2.2

Continued on next page...



Mol	Chain	Res	Type	RSRZ
1	С	216	LEU	2.2
1	D	105	LEU	2.2
1	А	74	LEU	2.2
1	С	134	VAL	2.2
1	С	197	ASN	2.1
1	С	2	LYS	2.1
1	С	89	PHE	2.1
1	С	179	PHE	2.0

Continued from previous page...

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.

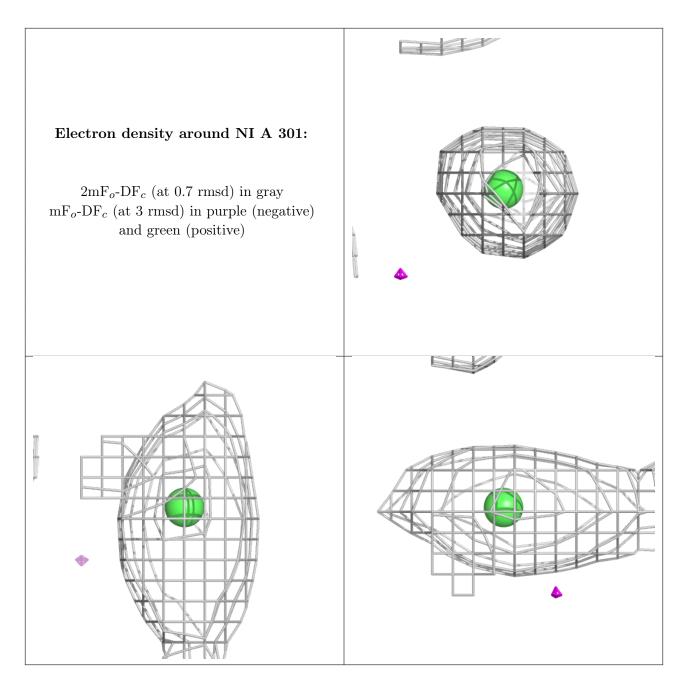
6.4 Ligands (i)

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, 95^{th} 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(Å ²)	Q < 0.9
2	NI	А	301	1/1	0.89	0.20	118,118,118,118	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





6.5 Other polymers (i)

There are no such residues in this entry.

