

Full wwPDB X-ray Structure Validation Report (i)

Sep 12, 2023 – 09:58 PM EDT

PDB ID	:	4NWQ
Title	:	Computationally Designed Two-Component Self-Assembling Tetrahedral
		Cage, T33-21, Crystallized in Space Group F4132
Authors	:	McNamara, D.E.; King, N.P.; Bale, J.B.; Sheffler, W.; Baker, D.; Yeates, T.O.
Deposited on	:	2013-12-06
Resolution	:	2.80 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:

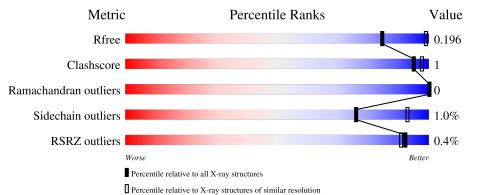
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.80 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	3140 (2.80-2.80)		
Clashscore	141614	3569 (2.80-2.80)		
Ramachandran outliers	138981	3498 (2.80-2.80)		
Sidechain outliers	138945	3500 (2.80-2.80)		
RSRZ outliers	127900	3078 (2.80-2.80)		

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	172	81% 5%	14%
2	В	131	90%	• 8%



4NWQ

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2112 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 Putative uncharacterized protein PH0671.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	А	148	Total 1137	C 729	N 187	0 216	${ m S}{ m 5}$	0	0	0

Chain	Residue	Modelled	Actual	Comment	Reference
А	85	ALA	LYS	engineered mutation	UNP O58404
А	88	LEU	GLU	engineered mutation	UNP O58404
А	89	LYS	GLY	engineered mutation	UNP O58404
A	92	LEU	SER	engineered mutation	UNP O58404
А	95	MET	GLU	engineered mutation	UNP O58404
А	126	LEU	GLU	engineered mutation	UNP O58404
А	130	LEU	ALA	engineered mutation	UNP O58404
А	133	THR	LEU	engineered mutation	UNP O58404
А	140	ALA	LYS	engineered mutation	UNP O58404
А	143	ALA	LEU	engineered mutation	UNP O58404
А	144	ALA	VAL	engineered mutation	UNP O58404
А	147	LEU	ASN	engineered mutation	UNP O58404
А	148	ALA	ARG	engineered mutation	UNP O58404

There are 13 discrepancies between the modelled and reference sequences:

• Molecule 2 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	В	121	Total 904	C 563	N 162	O 176	${ m S} { m 3}$	0	0	0

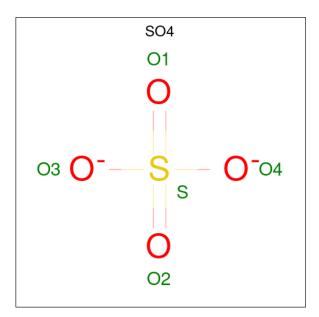
There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
В	27	LYS	ALA	engineered mutation	UNP Q9I2D8
В	74	ILE	ALA	engineered mutation	UNP Q9I2D8
В	78	THR	GLN	engineered mutation	UNP Q9I2D8



Chain	Residue	Modelled	Actual	Comment	Reference
В	79	LEU	ALA	engineered mutation	UNP Q9I2D8
В	82	ALA	GLU	engineered mutation	UNP Q9I2D8
В	86	ALA	GLU	engineered mutation	UNP Q9I2D8
В	90	GLU	GLY	engineered mutation	UNP Q9I2D8
В	112	LEU	ALA	engineered mutation	UNP Q9I2D8
В	124	LEU	-	expression tag	UNP Q9I2D8
В	125	GLU	-	expression tag	UNP Q9I2D8
В	126	HIS	-	expression tag	UNP Q9I2D8
В	127	HIS	-	expression tag	UNP Q9I2D8
В	128	HIS	-	expression tag	UNP Q9I2D8
В	129	HIS	-	expression tag	UNP Q9I2D8
В	130	HIS	-	expression tag	UNP Q9I2D8
В	131	HIS	-	expression tag	UNP Q9I2D8

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	Total O S	0	0
			$\begin{array}{cccc} 5 & 4 & 1 \\ \hline \text{Total} & \text{O} & \text{S} \end{array}$		
3	А	1	5 4 1	0	0
3	А	1	Total O S $\overline{5}$ 4 1	0	0
			$\begin{array}{cccc} 5 & 4 & 1 \\ \hline \text{Total} & \text{O} & \text{S} \end{array}$		
3	А	1	$5 \ 4 \ 1$	0	0
3	А	1	Total O S	0	0
			5 4 1		



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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	В	1	$\begin{array}{c c} \hline Total & O & S \\ \hline 5 & 4 & 1 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0

• Molecule 4 is water.

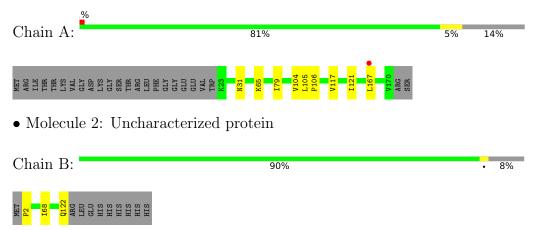
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	3	Total O 3 3	0	0
4	В	13	Total O 13 13	0	0



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: Putative uncharacterized protein PH0671





4 Data and refinement statistics (i)

Property	Value	Source
Space group	F 41 3 2	Depositor
Cell constants	272.18Å 272.18Å 272.18Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	96.23 - 2.80	Depositor
Resolution (A)	96.23 - 2.80	EDS
% Data completeness	100.0 (96.23-2.80)	Depositor
(in resolution range)	$100.0 \ (96.23-2.80)$	EDS
R _{merge}	0.12	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.34 (at 2.82 Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496	Depositor
B B.	0.181 , 0.196	Depositor
R, R_{free}	0.184 , 0.196	DCC
R_{free} test set	2184 reflections (10.00%)	wwPDB-VP
Wilson B-factor $(Å^2)$	69.0	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.35 , 55.7	EDS
L-test for twinning ²	$ \langle L \rangle = 0.49, \langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2112	wwPDB-VP
Average B, all atoms $(Å^2)$	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 2.59% 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: $\mathrm{SO4}$

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		lengths	Bond	Bond angles		
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5		
1	А	0.19	0/1148	0.34	0/1547		
2	В	0.20	0/913	0.34	0/1233		
All	All	0.20	0/2061	0.34	0/2780		

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	1137	0	1166	4	0
2	В	904	0	911	1	0
3	А	25	0	0	0	0
3	В	30	0	0	0	0
4	А	3	0	0	0	0
4	В	13	0	0	0	0
All	All	2112	0	2077	5	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 1.

All (5) close contacts within the same asymmetric unit are listed below, sorted by their clash



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:117:VAL:O	1:A:121:ILE:HG12	2.13	0.47
1:A:104:VAL:HG11	1:A:167:LEU:HD12	1.96	0.47
1:A:65:LYS:HD2	1:A:79:ILE:HA	1.97	0.46
1:A:105:LEU:HA	1:A:106:PRO:HD3	1.91	0.44
2:B:2:PRO:HB3	2:B:68:ILE:HG22	2.03	0.40

magnitude.

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	Perce	ntiles
1	А	146/172~(85%)	145 (99%)	1 (1%)	0	100	100
2	В	119/131 (91%)	118 (99%)	1 (1%)	0	100	100
All	All	265/303~(88%)	263 (99%)	2 (1%)	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	Analysed Rotameric Outliers		Percentiles		
1	А	117/145~(81%)	116~(99%)	1 (1%)	78 94		
2	В	91/102~(89%)	90 (99%)	1 (1%)	73 92		



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Mol	Chain	Analysed Rotameric (Outliers	Percentiles	
All	All	208/247~(84%)	206~(99%)	2(1%)	76 93	

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	31	ASN
2	В	122	GLN

Sometimes 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 monosaccharides in this entry.

5.6 Ligand geometry (i)

11 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	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain Res	Link	B	Bond lengths			Bond angles		
	туре		nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2							
3	SO4	А	203	-	4,4,4	0.14	0	$6,\!6,\!6$	0.05	0							
3	SO4	В	201	-	4,4,4	0.14	0	$6,\!6,\!6$	0.05	0							
3	SO4	А	205	-	4,4,4	0.14	0	$6,\!6,\!6$	0.05	0							



Mol	Turne	Chain	Dec	Res Link		ond leng	gths	В	Bond angles		
IVIOI	Type	Unam			Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2	
3	SO4	А	204	-	4,4,4	0.14	0	$6,\!6,\!6$	0.05	0	
3	SO4	В	202	-	4,4,4	0.14	0	$6,\!6,\!6$	0.05	0	
3	SO4	В	205	-	4,4,4	0.14	0	$6,\!6,\!6$	0.04	0	
3	SO4	В	206	-	4,4,4	0.14	0	$6,\!6,\!6$	0.05	0	
3	SO4	В	203	-	4,4,4	0.14	0	$6,\!6,\!6$	0.04	0	
3	SO4	А	202	-	4,4,4	0.14	0	$6,\!6,\!6$	0.05	0	
3	SO4	А	201	-	4,4,4	0.14	0	$6,\!6,\!6$	0.05	0	
3	SO4	В	204	-	4,4,4	0.14	0	$6,\!6,\!6$	0.05	0	

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	$\langle RSRZ \rangle$	#RSRZ>2	$\mathbf{OWAB}(\mathrm{\AA}^2)$	Q < 0.9
1	А	148/172~(86%)	0.26	1 (0%) 87 84	44, 73, 124, 145	0
2	В	$121/131 \ (92\%)$	0.12	0 100 100	47, 62, 85, 107	0
All	All	269/303~(88%)	0.19	1 (0%) 92 91	44, 66, 114, 145	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ	
1	А	167	LEU	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)

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
3	SO4	В	206	5/5	0.78	0.38	160, 160, 160, 160	5
3	SO4	А	204	5/5	0.87	0.18	139,148,154,158	0
3	SO4	В	204	5/5	0.88	0.17	98,101,129,145	0
3	SO4	А	203	5/5	0.92	0.20	113,115,123,135	0



Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} extsf{-}\mathbf{factors}(\mathbf{\AA}^2)$	Q<0.9
3	SO4	В	205	5/5	0.94	0.25	71,99,126,134	0
3	SO4	А	202	5/5	0.96	0.20	$60,\!62,\!76,\!80$	5
3	SO4	А	205	5/5	0.96	0.23	101,101,101,101	5
3	SO4	В	203	5/5	0.96	0.15	75,82,86,88	5
3	SO4	А	201	5/5	0.99	0.24	$52,\!55,\!55,\!59$	5
3	SO4	В	202	5/5	0.99	0.18	51,60,71,91	0
3	SO4	В	201	5/5	1.00	0.16	39,42,42,50	5

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6.5 Other polymers (i)

There are no such residues in this entry.

