

wwPDB X-ray Structure Validation Summary Report (i)

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PDB ID : 4RJV

Title : Crystal Structure of a De Novo Designed Ferredoxin Fold, Northeast Structural

Genomics Consortium (NESG) Target OR461

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Deposited on : 2014-10-09

Resolution : 1.52 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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:

 $\begin{array}{ccc} \text{MolProbity} & : & 4.02\text{b-}467 \\ \text{Xtriage (Phenix)} & : & 1.13 \end{array}$

EDS : 2.35.1

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

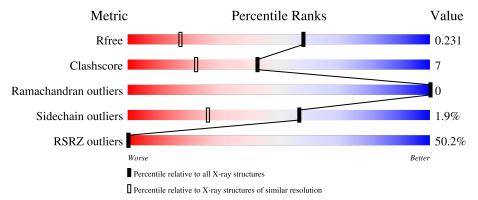
Validation Pipeline (wwPDB-VP) : 2.35.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 1.52 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries},{\rm resolution\ range}(\mathring{\rm A})) \end{array}$
R_{free}	130704	4009 (1.54-1.50)
Clashscore	141614	4249 (1.54-1.50)
Ramachandran outliers	138981	4148 (1.54-1.50)
Sidechain outliers	138945	4146 (1.54-1.50)
RSRZ outliers	127900	3943 (1.54-1.50)

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				
			47%				
1	A	87	72%	22% • 5%			
			46%				
1	В	87	78%	13% • 8%			
			45%				
1	С	87	80%	10% 9%			
			49%				
1	D	87	86%	9% 5%			



2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 2758 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 OR461.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	1 1 1 09	83	Total	С	N	О	S	0	0	0
1	A	0.0	657	408	121	125	3	0	U	U
1	В	80	Total	С	N	О	S	0	0	0
1	Ъ	80	628	391	114	120	3	0	0	U
1	С	79	Total	С	N	О	S	0	0 0 0	0
1		19	620	385	113	119	3	0		U
1	1 D	83	Total	С	N	О	S	0	0	0
1	ש	0.0	657	408	121	125	3	0	U	U

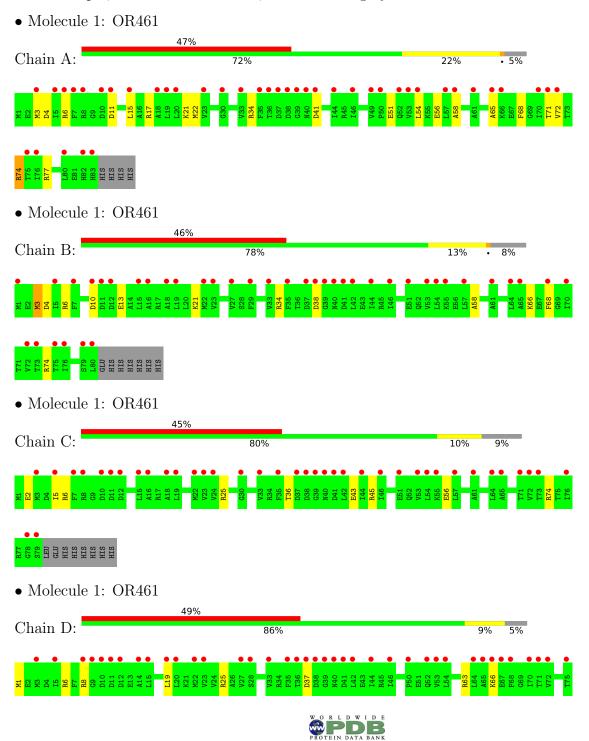
• Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	54	Total O	0	0
			54 54		
2	В	50	Total O	0	0
	D	90	50 - 50		
2	C	45	Total O	0	0
		40	45 45	0	U
2	D	47	Total O	0	0
	ש	41	47 47	0	U



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.







4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants	37.67Å 46.69Å 48.07Å	Depositor
a, b, c, α , β , γ	86.49° 72.89° 72.33°	Depositor
Resolution (Å)	30.17 - 1.52	Depositor
rtesolution (A)	30.17 - 1.52	EDS
% Data completeness	93.2 (30.17-1.52)	Depositor
(in resolution range)	93.5 (30.17-1.52)	EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.72 (at 1.52Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
P. P.	0.199 , 0.231	Depositor
R, R_{free}	0.199 , 0.231	DCC
R_{free} test set	2012 reflections (4.62%)	wwPDB-VP
Wilson B-factor (Å ²)	18.2	Xtriage
Anisotropy	0.438	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.34, 58.4	EDS
L-test for twinning ²	$< L > = 0.48, < L^2> = 0.31$	Xtriage
Estimated twinning fraction	0.030 for -h,-l,-k	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	2758	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The analyses of the Patterson function reveals a significant off-origin peak that is 38.67 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.5610e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

²Theoretical values of <|L|>, $<L^2>$ 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)

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		
Moi Chain	RMSZ	# Z > 5	RMSZ	# Z > 5		
1	A	0.35	0/663	0.52	0/888	
1	В	0.38	0/632	0.63	1/846 (0.1%)	
1	С	0.37	0/624	0.53	0/835	
1	D	0.34	0/663	0.53	0/888	
All	All	0.36	0/2582	0.55	1/3457 (0.0%)	

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}({}^{o})$
1	В	3	MET	CG-SD-CE	-9.54	84.94	100.20

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	657	0	668	15	0
1	В	628	0	648	10	0
1	С	620	0	637	7	0
1	D	657	0	668	6	0
2	A	54	0	0	5	1
2	В	50	0	0	1	1
2	С	45	0	0	2	0
2	D	47	0	0	4	2

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	2758	0	2621	35	2

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 7.

The worst 5 of 35 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:D:25:ARG:NH1	2:D:144:HOH:O	1.98	0.92
1:A:22:MET:SD	2:A:142:HOH:O	2.31	0.88
1:A:34:ARG:HG2	1:B:34:ARG:HG2	1.54	0.88
1:C:45:ARG:NH1	2:C:127:HOH:O	2.18	0.76
1:C:25:ARG:NH2	1:C:56:GLU:OE1	2.28	0.67

All (2) 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	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
2:A:145:HOH:O	2:D:143:HOH:O[1_644]	1.84	0.36
2:B:118:HOH:O	2:D:107:HOH:O[1_554]	2.13	0.07

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	A	81/87 (93%)	79 (98%)	2 (2%)	0	100	100
1	В	78/87 (90%)	78 (100%)	0	0	100	100
1	С	77/87 (88%)	76 (99%)	1 (1%)	0	100	100
1	D	81/87 (93%)	81 (100%)	0	0	100	100
All	All	317/348 (91%)	314 (99%)	3 (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	Rotameric	Outliers	Perce	ntiles
1	A	$69/73 \; (94\%)$	68 (99%)	1 (1%)	67	41
1	В	$66/73 \; (90\%)$	64 (97%)	2 (3%)	41	12
1	\mathbf{C}	65/73~(89%)	65 (100%)	0	100	100
1	D	69/73 (94%)	67 (97%)	2 (3%)	42	13
All	All	$269/292 \ (92\%)$	264 (98%)	5 (2%)	57	26

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	74	ARG
1	В	10	ASP
1	В	74	ARG
1	D	1	MET
1	D	19	LEU

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)

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 (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 $>$	$\#\mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q < 0.9
1	A	83/87 (95%)	2.59	41 (49%) 0 0	20, 37, 64, 89	0
1	В	80/87 (91%)	2.24	40 (50%) 0 0	17, 29, 57, 79	0
1	С	79/87 (90%)	2.34	39 (49%) 0 0	20, 32, 59, 77	0
1	D	83/87 (95%)	2.63	43 (51%) 0 0	17, 35, 66, 84	0
All	All	325/348 (93%)	2.46	163 (50%) 0 0	17, 34, 64, 89	0

The worst 5 of 163 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	40	ASN	12.7
1	A	39	GLY	11.9
1	D	40	ASN	11.3
1	D	38	ASP	11.0
1	A	83	HIS	10.3

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.

