



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 09:56 am BST

PDB ID : 6F5N
Title : Nickel-Bound Crystal Structure of a GB1 Variant
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Deposited on : 2017-12-01
Resolution : 2.20 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 : NOT EXECUTED
Xtriage (Phenix) : 1.13
EDS : NOT EXECUTED
buster-report : NOT EXECUTED
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

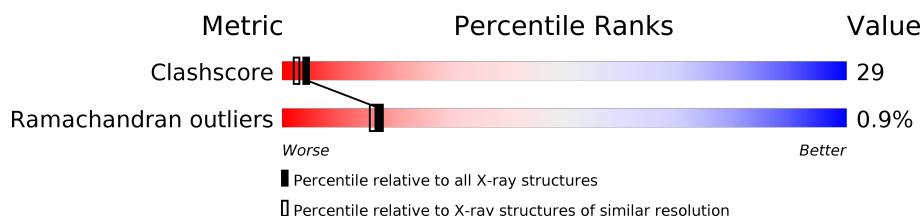
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 Å.


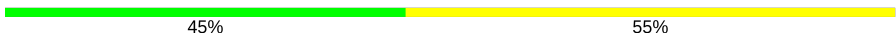
Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	56	 57% 39% .
1	B	56	 45% 55%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 974 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 Nickel-Binding Protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	56	Total	C	N	O	S	0	1	0
			459	293	73	92	1			
1	B	56	Total	C	N	O	S	0	0	0
			450	287	71	91	1			

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

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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	27	Total	O	0	0
			27	27		
3	B	37	Total	O	0	0
			37	37		

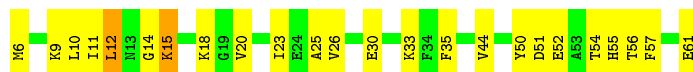
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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. 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. 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.

Note EDS was not executed.

- Molecule 1: Nickel-Binding Protein

Chain A: 



- Molecule 1: Nickel-Binding Protein

Chain B: 



4 Data and refinement statistics

EDS was not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	26.68Å 59.33Å 75.73Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.70 – 2.20	Depositor
% Data completeness (in resolution range)	79.2 (46.70-2.20)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.257 , 0.356	Depositor
Wilson B-factor (Å ²)	(Not available)	Xtriage
Anisotropy	(Not available)	Xtriage
L-test for twinning ¹	$\langle L \rangle =$ (Not available), $\langle L^2 \rangle =$ (Not available)	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	974	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *(Not available)*

¹Theoretical 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: 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	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.47	0/468	0.74	1/630 (0.2%)
1	B	0.44	0/459	0.69	0/619
All	All	0.45	0/927	0.72	1/1249 (0.1%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	12	LEU	CA-CB-CG	5.68	128.36	115.30

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	459	0	437	23	0
1	B	450	0	425	29	0
2	A	1	0	0	0	0
3	A	27	0	0	4	0
3	B	37	0	0	7	0
All	All	974	0	862	52	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 29.

All (52) 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:B:12:LEU:HD11	1:B:44:VAL:HG21	1.57	0.86
1:B:27:ASP:OD2	3:B:101:HOH:O	2.01	0.78
1:B:14:GLY:O	1:B:18:LYS:NZ	2.17	0.76
1:A:55:HIS:O	3:A:201:HOH:O	2.04	0.75
1:A:26:VAL:HG23	1:A:30:GLU:OE1	1.88	0.73
1:A:11:ILE:HG12	1:A:20:VAL:HG22	1.70	0.72
1:B:16:THR:O	3:B:102:HOH:O	2.11	0.66
1:B:9:LYS:HE2	1:B:22:THR:HG22	1.78	0.65
1:B:37:GLN:HA	1:B:40:ASN:OD1	1.97	0.64
1:A:52:GLU:OE1	3:A:202:HOH:O	2.14	0.64
1:A:9:LYS:N	3:A:201:HOH:O	2.30	0.63
1:A:44:VAL:HG23	1:A:61:GLU:HG3	1.81	0.60
1:B:45:ASP:O	1:B:61:GLU:HG2	2.02	0.59
1:A:6:MET:N	1:A:25:ALA:O	2.35	0.58
1:B:61:GLU:OXT	3:B:103:HOH:O	2.17	0.58
1:B:21:ILE:HD11	1:B:38:TYR:CZ	2.41	0.55
1:B:53:ALA:N	3:B:108:HOH:O	2.40	0.54
1:B:12:LEU:CD1	1:B:44:VAL:HG21	2.34	0.54
1:A:10:LEU:HD23	1:A:57:PHE:HB2	1.91	0.53
1:A:10:LEU:HA	1:A:57:PHE:O	2.09	0.52
1:B:10:LEU:HD22	1:B:35:PHE:CD1	2.46	0.51
1:B:40:ASN:ND2	3:B:109:HOH:O	2.41	0.50
1:B:12:LEU:HD11	1:B:44:VAL:HG11	1.94	0.49
1:B:34:PHE:O	1:B:37:GLN:NE2	2.46	0.48
1:B:25:ALA:HB3	1:B:31:ALA:HB2	1.95	0.47
1:B:52:GLU:HG3	1:B:52:GLU:O	2.15	0.47
1:B:48:TRP:CE2	1:B:59:VAL:HB	2.50	0.47
1:A:50:TYR:CE2	1:A:52:GLU:HB2	2.51	0.46
1:A:15[A]:LYS:O	1:A:18:LYS:NZ	2.48	0.46
1:A:26:VAL:N	1:A:30:GLU:OE1	2.33	0.46
1:A:9:LYS:HE3	1:A:9:LYS:HB2	1.57	0.46
1:A:14:GLY:O	1:A:18:LYS:NZ	2.32	0.45
1:A:51:ASP:HB3	1:A:54:THR:OG1	2.17	0.45
1:B:12:LEU:HD21	1:B:44:VAL:HG11	1.97	0.45
1:B:34:PHE:O	1:B:38:TYR:HB2	2.17	0.44
1:A:10:LEU:HB2	1:A:35:PHE:CD2	2.52	0.44
1:B:11:ILE:HD13	1:B:56:THR:HG23	1.98	0.44
1:B:23:ILE:HD13	1:B:34:PHE:HD2	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:58:THR:HG23	3:B:104:HOH:O	2.18	0.43
1:B:13:ASN:CG	1:B:60:THR:HG23	2.39	0.43
1:B:46:GLY:HA3	1:B:61:GLU:HA	2.00	0.43
1:A:15[B]:LYS:O	1:A:18:LYS:NZ	2.51	0.43
1:B:44:VAL:HA	1:B:61:GLU:OE2	2.17	0.43
1:A:33:LYS:HD3	1:A:33:LYS:C	2.39	0.43
1:A:23:ILE:HD12	1:A:25:ALA:HB2	2.01	0.43
1:A:12:LEU:HD22	1:A:44:VAL:HG11	2.01	0.42
1:A:51:ASP:HB3	1:A:54:THR:HG1	1.85	0.42
1:B:56:THR:O	3:B:104:HOH:O	2.22	0.41
1:B:37:GLN:O	1:B:41:ASP:HB2	2.20	0.41
1:A:56:THR:O	3:A:203:HOH:O	2.22	0.41
1:A:54:THR:HB	1:A:56:THR:OG1	2.20	0.41
1:B:34:PHE:HA	1:B:37:GLN:HE21	1.86	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.

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	55/56 (98%)	52 (94%)	1 (2%)	2 (4%)	3	1
1	B	54/56 (96%)	50 (93%)	4 (7%)	0	100	100
All	All	109/112 (97%)	102 (94%)	5 (5%)	2 (2%)	17	5

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	15[A]	LYS
1	A	15[B]	LYS

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

Mogul was not executed - this section is therefore empty.

5.5 Carbohydrates [i](#)

Mogul was not executed - this section is therefore empty.

5.6 Ligand geometry [i](#)

Mogul was not executed - this section is therefore empty.

5.7 Other polymers [i](#)

Mogul was not executed - this section is therefore empty.

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 ⓘ

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.