

Full wwPDB X-ray Structure Validation Report (i)

Dec 16, 2023 – 05:28 PM EST

PDB ID	:	2O35
Title	:	Protein of Unknown Function (DUF1244) from Sinorhizobium meliloti
Authors	:	Kim, Y.; Joachimiak, A.; Evdokimova, E.; Kudritska, M.; Edwards, A.;
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Deposited on	:	2006-11-30
Resolution	:	2.12 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:

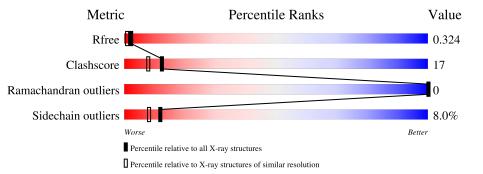
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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 2.12 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R _{free}	130704	6241 (2.14-2.10)
Clashscore	141614	6778 (2.14-2.10)
Ramachandran outliers	138981	6705 (2.14-2.10)
Sidechain outliers	138945	6706 (2.14-2.10)

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%

Mol	Chain	Length	Quality of chain							
1	А	105	54%	18% ·	25%					
1	В	105	58%	25%	7% • 10%					



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 1667 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	А	79	Total 693		N 123			Se 4	0	5	0
1	D	95	Total					Se	0	0	0
	I B	90	855	521	159	170	2	3	0	9	U

• Molecule 1 is a protein called Hypothetical protein DUF1244.

Chain	Residue	Modelled	Actual	Comment	Reference
А	-1	GLY	-	cloning artifact	UNP Q92M60
А	0	HIS	-	cloning artifact	UNP Q92M60
А	1	MSE	MET	modified residue	UNP Q92M60
А	16	VAL	ALA	SEE REMARK 999	UNP Q92M60
А	36	MSE	MET	modified residue	UNP Q92M60
А	61	MSE	MET	modified residue	UNP Q92M60
А	73	MSE	MET	modified residue	UNP Q92M60
А	102	GLY	-	cloning artifact	UNP Q92M60
А	103	SER	-	cloning artifact	UNP Q92M60
В	-1	GLY	-	cloning artifact	UNP Q92M60
В	0	HIS	-	cloning artifact	UNP Q92M60
В	1	MSE	MET	modified residue	UNP Q92M60
В	16	VAL	ALA	SEE REMARK 999	UNP Q92M60
В	36	MSE	MET	modified residue	UNP Q92M60
В	61	MSE	MET	modified residue	UNP Q92M60
В	73	MSE	MET	modified residue	UNP Q92M60
В	102	GLY	-	cloning artifact	UNP Q92M60
В	103	SER	-	cloning artifact	UNP Q92M60

There are 18 discrepancies between the modelled and reference sequences:

• Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	В	1	Total Mg 1 1	0	0

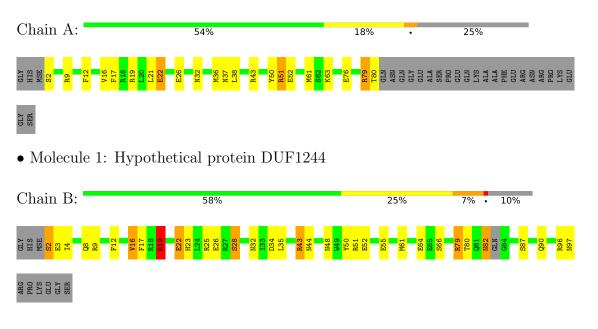
• Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	46	Total O 46 46	0	0
3	В	71	TotalO7171	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. 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.



• Molecule 1: Hypothetical protein DUF1244



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants	80.99Å 80.99 Å 64.71 Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	35.07 - 2.12	Depositor
Resolution (A)	35.07 - 2.12	EDS
% Data completeness	98.1 (35.07 - 2.12)	Depositor
(in resolution range)	98.1 (35.07-2.12)	EDS
R _{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.74 (at 2.12 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.209 , 0.263	Depositor
II, Ilfree	0.284 , 0.324	DCC
R_{free} test set	1382 reflections (9.92%)	wwPDB-VP
Wilson B-factor $(Å^2)$	39.9	Xtriage
Anisotropy	0.539	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.35 , 59.1	EDS
L-test for $twinning^2$	$< L >=0.51, < L^2>=0.34$	Xtriage
Estimated twinning fraction	0.042 for -h,-k,l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	1667	wwPDB-VP
Average B, all atoms $(Å^2)$	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 7.31% 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: MG

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	Bo	nd lengths	Bond angles		
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.86	1/703~(0.1%)	0.83	1/940~(0.1%)	
1	В	1.00	5/866~(0.6%)	0.88	1/1158~(0.1%)	
All	All	0.94	6/1569~(0.4%)	0.86	2/2098~(0.1%)	

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	В	64[A]	GLU	CG-CD	5.98	1.60	1.51
1	В	64[B]	GLU	CG-CD	5.98	1.60	1.51
1	В	64[A]	GLU	CD-OE2	5.55	1.31	1.25
1	В	64[B]	GLU	CD-OE2	5.55	1.31	1.25
1	В	16	VAL	CB-CG2	-5.53	1.41	1.52
1	А	80	THR	CB-OG1	5.01	1.53	1.43

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}(^{o})$
1	А	51	ARG	NE-CZ-NH1	7.82	124.21	120.30
1	В	19	ARG	NE-CZ-NH2	-5.21	117.69	120.30

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	А	693	0	649	17	0
1	В	855	0	791	39	0
2	А	1	0	0	0	0
2	В	1	0	0	0	0
3	А	46	0	0	1	0
3	В	71	0	0	4	0
All	All	1667	0	1440	51	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 17.

All (51) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

A	A.L. 0	Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
1:B:61:MSE:HE3	1:B:66:SER:HB3	1.13	1.08
1:B:51:ARG:HA	1:B:61:MSE:HE2	1.36	1.07
1:B:43[A]:ARG:HH21	1:B:43[A]:ARG:HG3	1.27	0.97
1:B:87:SER:H	1:B:90[B]:GLN:HE21	0.94	0.91
1:B:61:MSE:HE3	1:B:66:SER:CB	2.00	0.91
1:B:12:PHE:O	1:B:16:VAL:HG23	1.70	0.89
1:B:87:SER:H	1:B:90[B]:GLN:NE2	1.70	0.89
1:B:51:ARG:HA	1:B:61:MSE:CE	2.05	0.86
1:A:12:PHE:O	1:A:16:VAL:HG23	1.78	0.82
1:B:87:SER:N	1:B:90[B]:GLN:HE21	1.78	0.78
1:A:51:ARG:HD2	1:A:61:MSE:O	1.85	0.77
1:A:79:ARG:HH11	1:A:79:ARG:CG	1.98	0.76
1:B:43[A]:ARG:HH21	1:B:43[A]:ARG:CG	2.04	0.70
1:A:79:ARG:HH11	1:A:79:ARG:HG2	1.57	0.69
1:B:4[B]:ILE:HG22	1:B:9[B]:ARG:HD2	1.74	0.68
1:A:52:GLU:OE2	1:B:19:ARG:NH1	2.28	0.67
1:A:76[B]:GLU:CD	1:A:76[B]:GLU:H	1.96	0.67
1:B:44[B]:ASN:O	1:B:48[B]:ASN:ND2	2.29	0.65
1:B:87:SER:OG	1:B:90[B]:GLN:HG3	1.97	0.64
1:B:43[B]:ARG:NH2	3:B:218:HOH:O	2.31	0.62
1:B:51:ARG:O	1:B:55:GLU:HG3	2.00	0.62
1:B:51:ARG:CA	1:B:61:MSE:HE2	2.22	0.61
1:B:4[B]:ILE:CG2	1:B:9[B]:ARG:HD2	2.31	0.61
3:A:204:HOH:O	1:B:19:ARG:HG3	2.01	0.60
1:B:51:ARG:CA	1:B:61:MSE:CE	2.79	0.60
1:A:79:ARG:HG2	1:A:79:ARG:NH1	2.15	0.60
1:B:22[A]:GLU:HG2	1:B:23:HIS:N	2.10	0.59
1:B:43[A]:ARG:HG3	1:B:43[A]:ARG:NH2	2.03	0.58

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Atom 1	A + a	Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (\AA)
1:B:50:TYR:HD2	1:B:61:MSE:HE1	1.71	0.54
1:B:28:SER:HB3	3:B:240:HOH:O	2.07	0.53
1:A:38:LEU:HD11	1:B:34:ASP:HB3	1.89	0.53
1:A:17:PHE:HB2	1:B:17:PHE:HB2	1.90	0.52
1:B:32:ASN:OD1	1:B:43[B]:ARG:HG3	2.10	0.52
1:B:97:ASN:HB2	3:B:233:HOH:O	2.11	0.51
1:B:32:ASN:OD1	1:B:43[A]:ARG:HG3	2.10	0.51
1:A:22[B]:GLU:O	1:A:26[B]:GLU:HG3	2.11	0.51
1:A:36[B]:MSE:HE2	1:A:37:ASN:OD1	2.14	0.48
1:A:2:SER:N	1:A:9:ARG:HH21	2.11	0.47
1:A:50:TYR:HA	1:B:16:VAL:CG2	2.44	0.47
1:A:51:ARG:CZ	1:A:63[A]:LYS:HG3	2.45	0.47
1:A:32:ASN:HD21	1:A:43:ARG:HB2	1.81	0.46
1:B:4[B]:ILE:HG23	1:B:8:GLN:HB2	1.98	0.46
1:B:26[A]:GLU:HG3	3:B:264:HOH:O	2.16	0.45
1:B:79:ARG:O	1:B:82:ASN:HB2	2.18	0.44
1:B:96:ARG:HG3	1:B:97:ASN:N	2.33	0.43
1:B:48[B]:ASN:O	1:B:52:GLU:HG3	2.19	0.43
1:B:2:SER:OG	1:B:3:GLU:N	2.52	0.42
1:A:16:VAL:CG2	1:B:50:TYR:HA	2.49	0.42
1:B:80:THR:C	1:B:82:ASN:H	2.23	0.41
1:A:32:ASN:ND2	1:A:43:ARG:HH11	2.19	0.40
1:B:22[B]:GLU:OE2	1:B:25:ARG:NH1	2.55	0.40

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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	82/105~(78%)	79~(96%)	3~(4%)	0	100	100
1	В	100/105~(95%)	94 (94%)	6 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	182/210~(87%)	173~(95%)	9~(5%)	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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	А	74/85~(87%)	69~(93%)	5(7%)	16 12
1	В	90/85~(106%)	80 (89%)	10 (11%)	6 3
All	All	164/170~(96%)	149~(91%)	15~(9%)	12 6

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	19	ARG
1	А	21	LEU
1	А	22[A]	GLU
1	А	22[B]	GLU
1	А	79	ARG
1	В	2	SER
1	В	19	ARG
1	В	22[A]	GLU
1	В	22[B]	GLU
1	В	28	SER
1	В	35	LEU
1	В	43[A]	ARG
1	В	43[B]	ARG
1	В	79	ARG
1	В	82	ASN

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such side chains are listed below:



Mol	Chain	Res	Type
1	А	32	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 2 ligands modelled in this entry, 2 are 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)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

