

wwPDB X-ray Structure Validation Summary Report (i)

May 13, 2020 - 06:32 am BST

PDB ID	:	2P12
Title	:	Crystal structure of protein of unknown function DUF402 from Rhodococcus
		sp. RHA1
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Deposited on		
Resolution	:	1.63 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 following versions of software and data (see references (1)) were used in the production of this report:

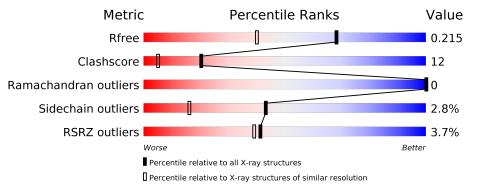
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 1.63 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries},{ m resolution\ range}({ m \AA}))$
R_{free}	130704	3122(1.66-1.62)
Clashscore	141614	3268 (1.66-1.62)
Ramachandran outliers	138981	3215(1.66-1.62)
Sidechain outliers	138945	3215(1.66-1.62)
RSRZ outliers	127900	3079 (1.66-1.62)

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 <=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	176	76%	17%	• 6%
1	В	176	76%	15%	• 6%



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 3493 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	Δ	166	Total	С	Ν	Ο	Se	0	12	0
	л	100	1470	922	264	281	3	0	10	0
1	р	165	Total	С	Ν	Ο	Se	0	15	0
	D	105	1481	935	265	278	3	0	10	0

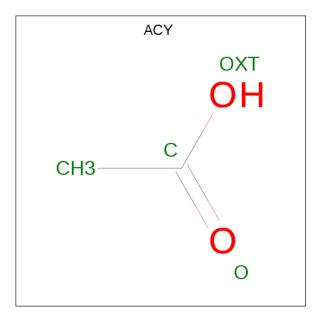
• Molecule 1 is a protein called Hypothetical protein DUF402.

Chain	Residue	Modelled	Actual	Comment	Reference
А	-1	GLY	-	CLONING ARTIFACT	UNP Q0SI31
А	0	HIS	-	CLONING ARTIFACT	UNP Q0SI31
A	1	MSE	MET	MODIFIED RESIDUE	UNP Q0SI31
А	45	MSE	MET	MODIFIED RESIDUE	UNP Q0SI31
А	124	MSE	MET	MODIFIED RESIDUE	UNP Q0SI31
А	167	MSE	MET	MODIFIED RESIDUE	UNP Q0SI31
А	173	GLY	-	CLONING ARTIFACT	UNP Q0SI31
А	174	SER	-	CLONING ARTIFACT	UNP Q0SI31
В	-1	GLY	-	CLONING ARTIFACT	UNP Q0SI31
В	0	HIS	-	CLONING ARTIFACT	UNP Q0SI31
В	1	MSE	MET	MODIFIED RESIDUE	UNP Q0SI31
В	45	MSE	MET	MODIFIED RESIDUE	UNP Q0SI31
В	124	MSE	MET	MODIFIED RESIDUE	UNP Q0SI31
В	167	MSE	MET	MODIFIED RESIDUE	UNP Q0SI31
В	173	GLY	-	CLONING ARTIFACT	UNP Q0SI31
В	174	SER	-	CLONING ARTIFACT	UNP Q0SI31

There are 16 discrepancies between the modelled and reference sequences:

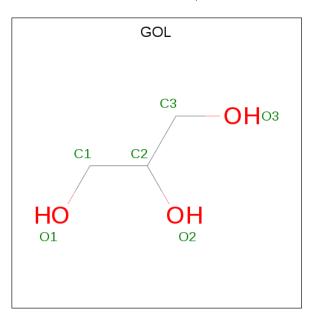
• Molecule 2 is ACETIC ACID (three-letter code: ACY) (formula: $C_2H_4O_2$).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
2	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0

• Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	А	1	$\begin{array}{ccc} {\rm Total} & {\rm C} \\ 6 & 3 \end{array}$	O 3	0	0

• Molecule 4 is water.

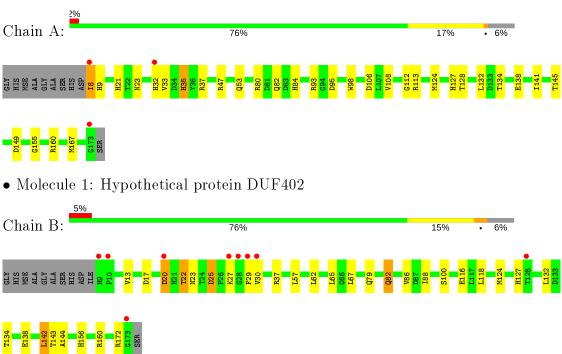


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	271	Total O 271 271	0	0
4	В	257	$\begin{array}{cc} {\rm Total} & {\rm O} \\ 257 & 257 \end{array}$	0	0



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 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: Hypothetical protein DUF402



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	132.20Å 38.98Å 70.72Å	Depositor
a, b, c, α , β , γ	90.00° 107.69° 90.00°	Depositor
Resolution (Å)	40.30 - 1.63	Depositor
Resolution (A)	40.30 - 1.62	EDS
% Data completeness	93.5 (40.30-1.63)	Depositor
(in resolution range)	92.5(40.30 - 1.62)	EDS
R _{merge}	0.07	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$3.22 (at 1.63 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
D D	0.171 , 0.216	Depositor
R, R_{free}	0.170 , 0.215	DCC
R_{free} test set	4037 reflections $(9.93%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	18.6	Xtriage
Anisotropy	0.661	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.31 , 43.1	EDS
L-test for twinning ²	$ \langle L \rangle = 0.48, \langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3493	wwPDB-VP
Average B, all atoms $(Å^2)$	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.56% 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: GOL, ACY

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	0.78	0/1511	0.86	4/2052~(0.2%)	
1	В	0.73	0/1522	0.87	2/2065~(0.1%)	
All	All	0.76	0/3033	0.87	6/4117~(0.1%)	

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	В	0	1

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
1	В	23	ASN	N-CA-CB	-6.74	98.48	110.60
1	А	35	HIS	N-CA-CB	-6.48	98.93	110.60
1	А	37	ARG	NE-CZ-NH1	6.12	123.36	120.30
1	А	113	ARG	NE-CZ-NH2	-5.42	117.59	120.30
1	В	20	ASP	CB-CG-OD2	-5.33	113.51	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	В	22	THR	Peptide



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	1470	0	1346	32	0
1	В	1481	0	1372	44	0
2	А	4	0	3	0	0
2	В	4	0	3	0	0
3	А	6	0	8	2	0
4	А	271	0	0	13	1
4	В	257	0	0	11	1
All	All	3493	0	2732	71	1

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 12.

The worst 5 of 71 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic}\\ {\rm distance}~({\rm \AA}) \end{array}$	Clash overlap (Å)
1:B:62:LEU:HD12	1:B:67[B]:LEU:CD2	1.50	1.40
1:B:62:LEU:HD12	1:B:67[B]:LEU:HD21	1.30	1.09
1:B:67[B]:LEU:HD12	1:B:86:VAL:HG11	1.45	0.95
1:B:62:LEU:CD1	1:B:67[B]:LEU:CD2	2.44	0.94
1:B:27[A]:LYS:HD3	1:B:29[A]:PHE:CZ	2.03	0.94

All (1) 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	Interatomic distance (Å)	Clash overlap (Å)
4:A:865:HOH:	$D = 4:B:624:HOH:O[3_445]$	1.95	0.25

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	Favoured Allowed		Outliers	Percentiles		
1	А	176/176~(100%)	173~(98%)	3 (2%)	0	100	100	
1	В	177/176~(101%)	174 (98%)	3 (2%)	0	100	100	
All	All	353/352~(100%)	347~(98%)	6 (2%)	0	100	100	

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

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		Percentiles		
1	А	155/145~(107%)	152 (98%)	3(2%)	57 32		
1	В	156/145~(108%)	148 (95%)	8 (5%)	24 4		
All	All	311/290~(107%)	300~(96%)	11 (4%)	43 10		

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	79[A]	GLN
1	В	79[B]	GLN
1	В	132	LEU
1	В	25	ASP
1	В	82[B]	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	А	84	HIS
1	В	156	HIS
1	В	78	HIS
1	А	78	HIS
1	А	127	HIS



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 carbohydrates in this entry.

5.6 Ligand geometry (i)

3 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	Chain	Chain	Chain	Chain	Chain Res	Link	B	Bond lengths			Bond angles		
	Type	Chain	nes	1165	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2											
3	GOL	А	603	-	5, 5, 5	0.40	0	5,5,5	0.30	0													
2	ACY	А	601	-	1,3,3	1.57	0	$_{0,3,3}$	0.00	-													
2	ACY	В	602	-	1,3,3	1.33	0	$_{0,3,3}$	0.00	-													

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

\mathbb{N}	/lol	Type	Chain	Res	Link	Chirals	Torsions	Rings
	3	GOL	А	603	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:



Mol	Chain	Res	Type	Atoms
3	А	603	GOL	O2-C2-C3-O3
3	A	603	GOL	C1-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	603	GOL	2	0

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 $>$	$\# RSRZ {>}2$	$OWAB(Å^2)$	Q<0.9
1	А	163/176~(92%)	-0.27	3 (1%) 68 69	16, 21, 29, 38	0
1	В	162/176~(92%)	0.11	9 (5%) 24 22	14, 23, 32, 46	0
All	All	325/352~(92%)	-0.08	12 (3%) 41 39	14, 22, 31, 46	0

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	29[A]	PHE	6.7
1	В	173[A]	GLY	5.6
1	В	9	HIS	4.4
1	А	8	ILE	3.1
1	В	30	VAL	3.0

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 carbohydrates 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	$\mathbf{B} ext{-factors}(\mathbf{A}^2)$	$Q{<}0.9$
3	GOL	А	603	6/6	0.75	0.12	$51,\!54,\!55,\!55$	0
2	ACY	В	602	4/4	0.88	0.21	39,41,41,41	0
2	ACY	А	601	4/4	0.93	0.15	$29,\!29,\!30,\!31$	0

6.5 Other polymers (i)

There are no such residues in this entry.

