

Full wwPDB X-ray Structure Validation Report (i)

Oct 8, 2023 – 11:12 AM EDT

PDB ID : 6EFY

Title : Crystal Structure of DIP-Alpha Ig1-3

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Deposited on : 2018-08-17

Resolution : 2.90 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)

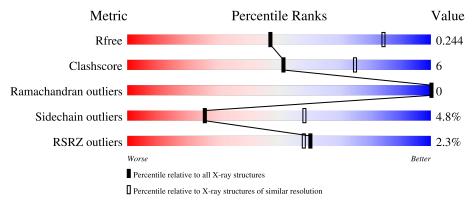
Validation Pipeline (wwPDB-VP) : 2.35.1

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 2.90 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 $(\# \mathrm{Entries})$	Similar resolution $(\#\text{Entries, resolution range}(\mathring{\mathbf{A}}))$
R_{free}	130704	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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	A	308	2%	80%	17%			
2	В	3	33%	67%				



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2420 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 Dpr-interacting protein alpha, isoform A.

Mol	Chain	Residues	${f Atoms}$			ZeroOcc	AltConf	Trace		
1	Δ	303	Total	С	N	О	S	0	0	0
1	11	303	2371	1488	417	453	13			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	342	HIS	-	expression tag	UNP Q9W4R3
A	343	HIS	-	expression tag	UNP Q9W4R3
A	344	HIS	-	expression tag	UNP Q9W4R3
A	345	HIS	-	expression tag	UNP Q9W4R3
A	346	HIS	-	expression tag	UNP Q9W4R3
A	347	HIS	-	expression tag	UNP Q9W4R3

• Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[al pha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace		
2	В	3	Total 38	C 22	N 2	O 14	0	0	0

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





Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
3	A	1	Total 6	C 3	O 3	0	0

• Molecule 4 is water.

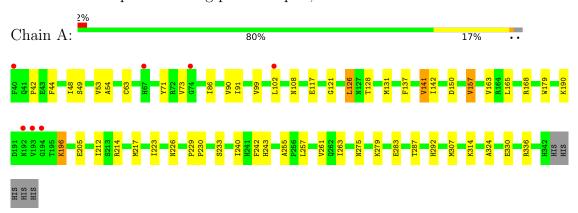
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	5	Total O 5 5	0	0



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: Dpr-interacting protein alpha, isoform A



 \bullet Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B: 33% 67%





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants	104.58Å 104.58Å 102.19Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.94 - 2.90	Depositor
Resolution (A)	19.94 - 2.90	EDS
% Data completeness	99.0 (19.94-2.90)	Depositor
(in resolution range)	99.0 (19.94-2.90)	EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.50 (at 2.88Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
D.D.	0.216 , 0.244	Depositor
R, R_{free}	0.215 , 0.244	DCC
R_{free} test set	725 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	84.3	Xtriage
Anisotropy	0.576	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.29 , 46.8	EDS
L-test for twinning ²	$< L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	0.033 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2420	wwPDB-VP
Average B, all atoms (Å ²)	92.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.61% of the height of the origin peak. No significant pseudotranslation is detected.

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)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, NAG, FUC

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).

Mal	Chain	Bond	lengths	Bond angles		
MOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.26	0/2422	0.48	0/3286	

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	A	2371	0	2344	27	0
2	В	38	0	34	1	0
3	A	6	0	8	0	0
4	A	5	0	0	0	0
All	All	2420	0	2386	27	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 6.

All (27) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



Atom-1	Atom-2	Interatomic	Clash
		${ m distance}({ m \AA})$	overlap (Å)
1:A:54:ALA:HB2	1:A:141:VAL:HG23	1.73	0.70
1:A:86:ILE:HG22	1:A:91:ILE:HD11	1.78	0.66
1:A:168:ARG:NH1	1:A:205:GLU:OE1	2.29	0.65
1:A:279:LYS:HD3	1:A:283:GLU:HB3	1.79	0.63
1:A:287:THR:HG23	1:A:292:HIS:HA	1.88	0.55
1:A:165:LEU:HB3	1:A:179:TRP:CH2	2.43	0.53
1:A:275:ASN:HD22	1:A:324:ALA:HA	1.73	0.52
1:A:117:GLU:N	1:A:117:GLU:OE1	2.44	0.50
1:A:142:ILE:O	1:A:226:ASN:ND2	2.45	0.50
1:A:223:ILE:HG22	1:A:233:SER:HB2	1.94	0.50
1:A:214:ARG:HG2	1:A:242:PHE:CE2	2.47	0.50
1:A:42:PRO:HG2	1:A:71:TYR:CD2	2.48	0.48
1:A:71:TYR:CD2	1:A:128:THR:HG22	2.49	0.48
1:A:257:LEU:HD22	1:A:257:LEU:H	1.78	0.48
1:A:255:ALA:HB2	1:A:261:VAL:HG11	1.96	0.47
1:A:49:SER:HA	2:B:1:NAG:H82	1.97	0.46
1:A:48:ILE:HG21	1:A:63:CYS:SG	2.57	0.45
1:A:157:VAL:HG11	1:A:163:VAL:HG21	1.99	0.45
1:A:217:MET:HB3	1:A:240:ILE:HD12	1.99	0.45
1:A:121:GLY:HA2	1:A:137:PHE:HD1	1.82	0.44
1:A:229:PRO:HA	1:A:230:PRO:HA	1.79	0.44
1:A:73:VAL:HG22	1:A:126:LEU:HD12	2.01	0.43
1:A:190:LYS:HG2	1:A:196:LYS:HB2	2.01	0.43
1:A:53:VAL:O	1:A:54:ALA:HB3	2.19	0.42
1:A:150:ASP:OD2	1:A:168:ARG:HD2	2.20	0.42
1:A:90:VAL:HG22	1:A:99:VAL:HG23	2.02	0.42
1:A:263:ILE:HD11	1:A:307:MET:CE	2.50	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	301/308 (98%)	277 (92%)	24 (8%)	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 side chain 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		Percentiles	
1	A	271/276 (98%)	258 (95%)	13 (5%)	25 58	

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	PHE
1	A	102	LEU
1	A	108	ASN
1	A	126	LEU
1	A	131	MET
1	A	141	VAL
1	A	157	VAL
1	A	196	LYS
1	A	212	ILE
1	A	243	HIS
1	A	314	LYS
1	A	330	GLU
1	A	336	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	\mathbf{Type}
1	A	41	GLN
1	A 64		HIS
1	A	67	HIS
1	A	101	HIS
1	A	125	GLN

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Mol	Chain	Res	Type
1	A	215	ASN
1	A	275	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)

3 monosaccharides 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	Res	Link	Bond lengths			Bond angles		
MIOI	туре	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	В	1	1,2	14,14,15	0.40	0	17,19,21	0.60	0
2	NAG	В	2	2	14,14,15	0.31	0	17,19,21	0.63	1 (5%)
2	FUC	В	3	2	10,10,11	1.05	0	14,14,16	0.89	0

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.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	В	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	В	2	2	-	0/6/23/26	0/1/1/1
2	FUC	В	3	2	-	-	0/1/1/1

There are no bond length outliers.



All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
2	В	2	NAG	C1-O5-C5	2.18	115.14	112.19

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	В	1	NAG	O5-C5-C6-O6
2	В	1	NAG	C4-C5-C6-O6

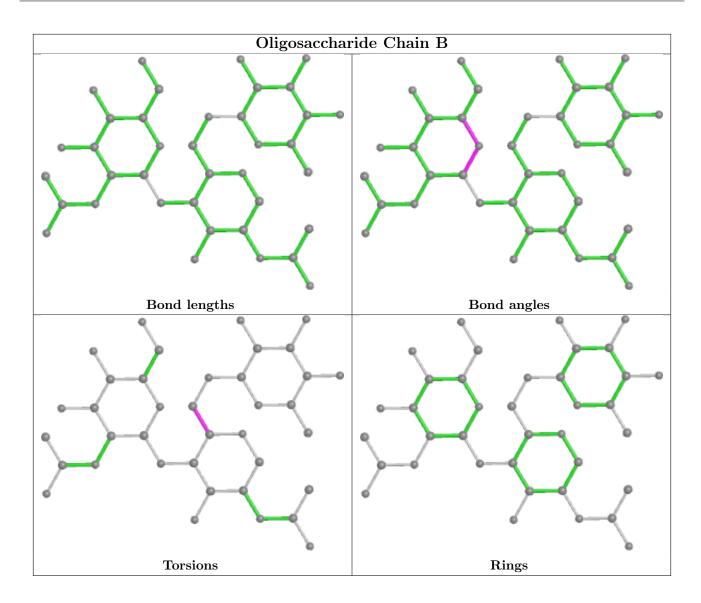
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	В	1	NAG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.





5.6 Ligand geometry (i)

1 ligand is 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	Res	Link	В	Bond lengths			Bond angles		
WIOI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2	
3	GOL	A	404	-	5,5,5	0.57	0	5,5,5	0.16	0	

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.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	A	404	-	-	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	A	404	GOL	C1-C2-C3-O3
3	A	404	GOL	O2-C2-C3-O3

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.

M	ol	Chain	Analysed	<RSRZ $>$	# RSRZ > 2		$OWAB(Å^2)$	Q<0.9
]	-	A	303/308 (98%)	0.01	7 (2%) 60	58	56, 87, 138, 174	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	193	VAL	5.8
1	A	40	PHE	4.3
1	A	102	LEU	4.0
1	A	192	ASN	3.9
1	A	74	GLY	3.4
1	A	194	GLY	3.3
1	A	67	HIS	2.2

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)

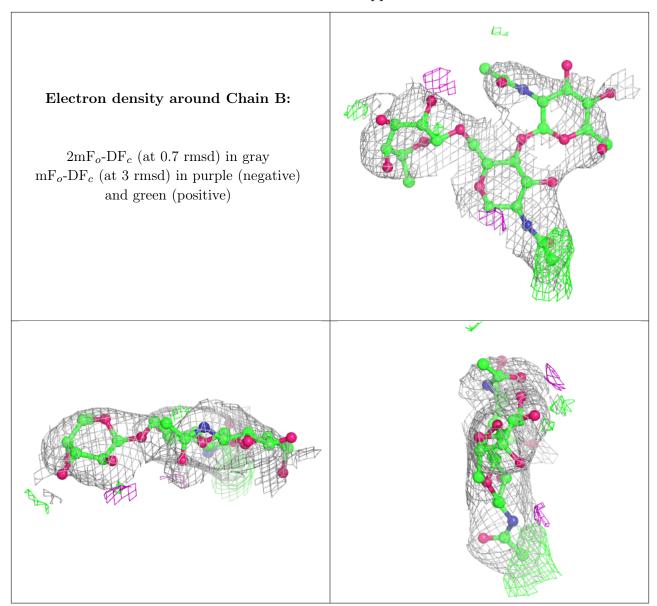
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\operatorname{B-factors}(\mathring{\mathbf{A}}^2)$	Q<0.9
2	NAG	В	2	14/15	0.77	0.40	105,144,168,168	0
2	NAG	В	1	14/15	0.93	0.14	95,110,125,135	0
2	FUC	В	3	10/11	0.94	0.18	94,105,124,134	0

The following is a graphical depiction of the model fit to experimental electron density for oligosac-



charide. Each fit is shown from different orientation to approximate a three-dimensional view.



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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
3	GOL	A	404	6/6	0.92	0.18	67,80,82,88	0



6.5 Other polymers (i)

There are no such residues in this entry.

