

wwPDB X-ray Structure Validation Summary Report (i)

Nov 2, 2023 – 09:08 AM EDT

PDB ID : 3HQR

Title : PHD2:Mn:NOG:HIF1-alpha substrate complex Authors : Chowdhury, R.; McDonough, M.A.; Schofield, C.J.

Deposited on : 2009-06-08

Resolution : 2.00 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:

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)

 $Refmac \quad : \quad 5.8.0158$

 $\begin{array}{cccc} & CCP4 & : & 7.0.044 \; (Gargrove) \\ Ideal \; geometry \; (proteins) & : & Engh \; \& \; Huber \; (2001) \end{array}$

Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

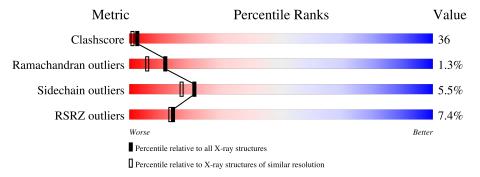
 $Validation\ Pipeline\ (wwPDB-VP) \quad : \quad 2.36$

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 2.00 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	Similar resolution
TVICTIC	$(\# ext{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	246	5% 43%	44%	• 9%			
2	S	17	29% 29%	65%	6%			



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 2075 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 Egl nine homolog 1.

Mol	Chain	Residues		Atoms				ZeroOcc	AltConf	Trace
1	Λ	225	Total	С	N	О	S	0	2	0
1	Λ	229	1768	1121	307	327	13		9	

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	398	ALA	ARG	engineered mutation	UNP Q9GZT9

• Molecule 2 is a protein called Hypoxia-inducible factor 1 alpha.

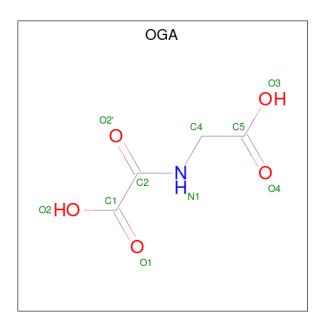
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
9	C	17	Total	С	N	О	S	0	1	0
	S	11	145	94	18	30	3	U	1	U

• Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mn 1 1	0	0

• Molecule 4 is N-OXALYLGLYCINE (three-letter code: OGA) (formula: C₄H₅NO₅).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total 10	C 4	N 1	O 5	0	0

• Molecule 5 is water.

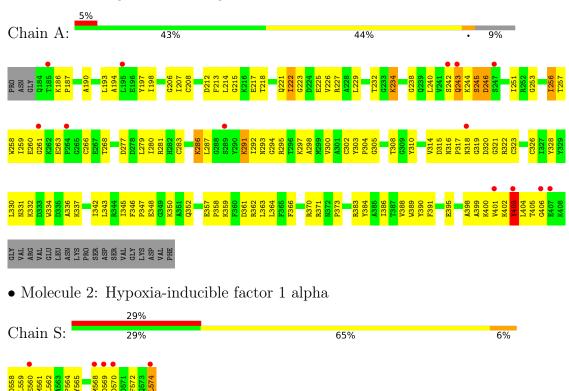
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	151	Total O 151 151	0	0



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: Egl nine homolog 1





4 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 21 21 21	Depositor	
Cell constants	39.38Å 68.80Å 72.22Å	Denogitor	
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	34.18 - 2.00	Depositor	
Resolution (A)	34.18 - 2.00	EDS	
% Data completeness	97.6 (34.18-2.00)	Depositor	
(in resolution range)	97.6 (34.18-2.00)	EDS	
R_{merge}	0.16	Depositor	
R_{sym}	(Not available)	Depositor	
$< I/\sigma(I) > 1$	2.99 (at 2.00Å)	Xtriage	
Refinement program	CNS 1.1	Depositor	
D D.	0.234 , 0.248	Depositor	
R, R_{free}	0.221 , (Not available)	DCC	
R_{free} test set	No test flags present.	wwPDB-VP	
Wilson B-factor (Å ²)	19.8	Xtriage	
Anisotropy	0.405	Xtriage	
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.38 , 51.7	EDS	
L-test for twinning ²	$< L >=0.45, < L^2>=0.28$	Xtriage	
Estimated twinning fraction	0.037 for -h,l,k	Xtriage	
F_o, F_c correlation	0.92	EDS	
Total number of atoms	2075	wwPDB-VP	
Average B, all atoms (Å ²)	25.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 7.76% 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: OGA, MN

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		
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.44	0/1823	0.75	1/2463 (0.0%)	
2	S	0.44	0/152	0.77	0/204	
All	All	0.44	0/1975	0.75	1/2667 (0.0%)	

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	A	0	2

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	A	406	GLY	N-CA-C	-7.57	94.18	113.10

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	403[A]	TYR	Sidechain
1	A	403[B]	TYR	Sidechain

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	1768	0	1727	134	0
2	S	145	0	133	24	0
3	A	1	0	0	0	0
4	A	10	0	3	0	0
5	A	151	0	0	8	0
All	All	2075	0	1863	138	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 36.

The worst 5 of 138 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:A:222:ILE:HD11	1:A:330:LEU:HD21	1.38	1.04
1:A:244:LYS:HG2	1:A:245:SER:H	1.24	1.02
1:A:260:GLU:HG2	1:A:297:LYS:HD3	1.48	0.94
1:A:238:GLY:HA2	1:A:256:ILE:HD13	1.54	0.87
1:A:217:GLU:HG3	1:A:218:THR:N	1.89	0.85

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	$226/246 \ (92\%)$	213 (94%)	10 (4%)	3 (1%)	12 6
2	S	16/17 (94%)	16 (100%)	0	0	100 100
All	All	242/263 (92%)	229 (95%)	10 (4%)	3 (1%)	12 7

All (3) Ramachandran outliers are listed below:



Mol	Chain	Res	Type
1	A	246	ASP
1	A	304	PRO
1	A	245	SER

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	A	187/206 (91%)	176 (94%)	11 (6%)	19 15		
2	S	17/16 (106%)	16 (94%)	1 (6%)	19 15		
All	All	204/222 (92%)	192 (94%)	12 (6%)	21 15		

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	337	LYS
1	A	403[A]	TYR
2	S	574	LEU
1	A	403[B]	TYR
1	A	256	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	220	GLN
1	A	243	GLN
1	A	372	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, 1 is monoatomic - leaving 1 for Mogul analysis.

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		nain Res	Ros	Ros	Link		ond leng	,		ond ang	·
		Туре	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	>2 Counts RMSZ # $ Z >2$				
	4	OGA	A	600	3	9,9,9	1.59	1 (11%)	10,11,11	1.33	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
4	OGA	A	600	3	-	0/8/9/9	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(ext{\AA})$
4	A	600	OGA	C2-C1	-4.20	1.49	1.54

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)

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	225/246 (91%)	0.61	13 (5%) 23 22	11, 23, 38, 47	0
2	S	17/17 (100%)	1.41	5 (29%) 0 0	16, 32, 50, 52	0
All	All	242/263 (92%)	0.67	18 (7%) 14 13	11, 23, 39, 52	0

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ	
1	A	403[A]	TYR	5.0	
1	A	407	GLU	4.5	
2	S	568[A]	MET	4.2	
1	A	185	THR	3.9	
2	S	560	GLU	3.3	

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)

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
4	OGA	A	600	10/10	0.92	0.16	15,19,21,23	0
3	MN	A	501	1/1	1.00	0.12	12,12,12,12	0

6.5 Other polymers (i)

There are no such residues in this entry.

