

Full wwPDB X-ray Structure Validation Report (i)

Nov 2, 2023 – 12:50 PM EDT

PDB ID	:	3VNO
Title	:	Cytochrome P450SP alpha (CYP152B1) mutant R241E
Authors	:	Fujishiro, T.; Shoji, O.; Sugimoto, H.; Shiro, Y.; Watanabe, Y.
Deposited on		
Resolution	:	2.17 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:

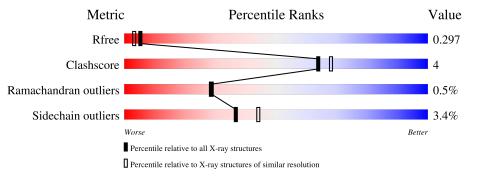
Xtriage (Phenix) EDS buster-report Percentile statistics Refmac CCP4 Ideal geometry (proteins) Ideal geometry (DNA, RNA)	:::::::::::::::::::::::::::::::::::::::	20191225.v01 (using entries in the PDB archive December 25th 2019) 5.8.0158 7.0.044 (Gargrove) Engh & Huber (2001) Parkinson et al. (1996)
Ideal geometry (DNA, RNA) Validation Pipeline (wwPDB-VP)		Parkinson et al. (1996) 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 2.17 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	6864 (2.20-2.16)
Clashscore	141614	7689 (2.20-2.16)
Ramachandran outliers	138981	7564 (2.20-2.16)
Sidechain outliers	138945	7564 (2.20-2.16)

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	407	90%	8%	•			



3VNO

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 3359 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.

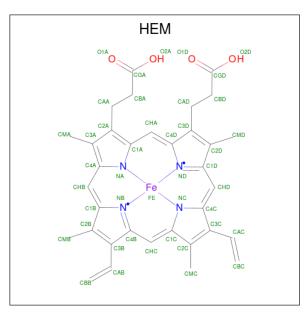
• Molecule 1 is a protein called Fatty acid alpha-hydroxylase.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	А	407	Total 3227	C 2051	N 588	O 575	S 13	0	2	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	241	GLU	ARG	engineered mutation	UNP O24782

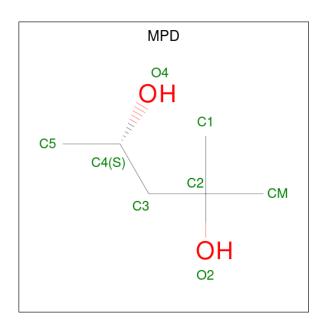
• Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2	Δ	1	Total	С	Fe	Ν	0	0	0
2	2 A	1	43	34	1	4	4	0	U

• Molecule 3 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: $C_6H_{14}O_2$).





Mol	Chain	Residues	Atoms	ZeroOc	c AltConf
3	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 8 & 6 & 2 \end{array}$	0	0

• Molecule 4 is water.

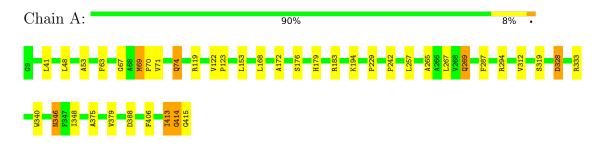
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	81	Total O 81 81	0	0



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: Fatty acid alpha-hydroxylase





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants	94.54Å 94.54Å 113.00Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Descrite
Resolution (Å)	$\begin{array}{rrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrr$	Depositor EDS
% Data completeness	99.6 (19.79-2.17)	Depositor
(in resolution range)	99.6 (19.79-2.17)	EDS
R _{merge}	0.05	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$6.99 (at 2.17 \text{\AA})$	Xtriage
Refinement program	REFMAC	Depositor
D D	0.199 , 0.227	Depositor
R, R_{free}	0.271 , 0.297	DCC
R_{free} test set	1516 reflections (4.85%)	wwPDB-VP
Wilson B-factor $(Å^2)$	41.7	Xtriage
Anisotropy	0.141	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.38, 39.5	EDS
L-test for twinning ²	$< L >=0.51, < L^2>=0.35$	Xtriage
Estimated twinning fraction	0.016 for -h,-k,l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	3359	wwPDB-VP
Average B, all atoms $(Å^2)$	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.55% 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: MPD, HEM

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		
NIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.59	0/3319	0.61	0/4502	

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	А	3227	0	3150	27	0
2	А	43	0	30	1	0
3	А	8	0	14	1	0
4	А	81	0	0	0	0
All	All	3359	0	3194	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 4.

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



Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
1:A:67:GLY:HA3	1:A:294:ARG:CZ	2.03	0.89
1:A:340:TRP:HE1	1:A:346:ASN:HD21	1.29	0.81
1:A:67:GLY:HA3	1:A:294:ARG:NH2	1.96	0.80
1:A:119:ARG:O	1:A:122:VAL:HG22	2.01	0.61
1:A:122:VAL:HG23	1:A:123:PRO:HD3	1.83	0.61
1:A:168:LEU:O	1:A:172:ALA:HB2	2.04	0.58
1:A:122:VAL:CG2	1:A:123:PRO:HD3	2.35	0.57
1:A:242:PRO:HB2	2:A:501:HEM:C1C	2.45	0.52
1:A:257:LEU:HD21	1:A:267:LEU:HD12	1.92	0.52
1:A:179:HIS:CD2	1:A:183:ARG:HE	2.28	0.51
1:A:265:ALA:O	1:A:269:GLN:HG2	2.10	0.50
1:A:63:PHE:HE1	1:A:312:VAL:HG21	1.77	0.50
1:A:122:VAL:HG11	1:A:413:ILE:HD13	1.94	0.49
1:A:328:ASP:CG	1:A:333:ARG:HH12	2.15	0.49
1:A:413:ILE:HG13	1:A:414:GLY:H	1.79	0.48
1:A:340:TRP:HE1	1:A:346:ASN:ND2	2.05	0.48
1:A:119:ARG:NH2	1:A:415:GLY:HA2	2.30	0.47
1:A:346:ASN:HD22	1:A:346:ASN:C	2.17	0.47
1:A:71:VAL:HA	1:A:74:GLN:HG3	1.97	0.46
1:A:375:ALA:O	1:A:379:VAL:HG22	2.18	0.43
1:A:70:PRO:HG2	3:A:502:MPD:H11	2.01	0.43
1:A:48:LEU:HB3	1:A:53:ALA:HB1	2.01	0.42
1:A:119:ARG:HH22	1:A:415:GLY:HA2	1.85	0.42
1:A:69:MET:HE3	1:A:69:MET:HB2	2.00	0.41
1:A:319:SER:CB	1:A:348:ILE:HD11	2.51	0.41
1:A:194:LYS:HE3	1:A:229:PRO:HB2	2.02	0.40
1:A:71:VAL:HA	1:A:74:GLN:CG	2.51	0.40

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	Percentile
1	А	407/407~(100%)	390~(96%)	15~(4%)	2~(0%)	29 28

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	406	PHE
1	А	414	GLY

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 Rotameric		Outliers	Percentiles	
1	А	324/322~(101%)	313~(97%)	11 (3%)	37 44	

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	41	LEU
1	А	69	MET
1	А	74	GLN
1	А	153	LEU
1	А	176	SER
1	А	269	GLN
1	А	287	PHE
1	А	328	ASP
1	А	346	ASN
1	А	388	ASP
1	А	413	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	29	GLN
1	А	160	ASN
1	А	179	HIS

Continued on next page...



Continued from previous page...

Mol	Chain	Res	Type
1	А	269	GLN
1	А	346	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)

2 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	Dec	Link	Bo	ond leng	\mathbf{ths}	В	ond ang	les
	Type	Unam	Res	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
3	MPD	А	502	-	7,7,7	0.27	0	$9,\!10,\!10$	0.28	0
2	HEM	А	501	4,1	41,50,50	1.94	7 (17%)	45,82,82	1.84	9 (20%)

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	MPD	А	502	-	-	2/5/5/5	-
2	HEM	А	501	4,1	-	2/12/54/54	-



Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	А	501	HEM	C3D-C2D	7.48	1.52	1.36
2	А	501	HEM	C3C-C2C	-4.19	1.34	1.40
2	А	501	HEM	C3C-CAC	3.85	1.55	1.47
2	А	501	HEM	CAB-C3B	3.03	1.55	1.47
2	А	501	HEM	FE-NB	2.38	2.08	1.96
2	А	501	HEM	CAA-C2A	2.29	1.55	1.52
2	А	501	HEM	FE-ND	2.27	2.08	1.96

All (7) bond length outliers are listed below:

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms		$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
2	А	501	HEM	C4D-ND-C1D	5.87	111.14	105.07
2	А	501	HEM	C4C-CHD-C1D	4.25	128.17	122.56
2	А	501	HEM	C4B-CHC-C1C	3.84	127.63	122.56
2	А	501	HEM	C1B-NB-C4B	2.96	108.14	105.07
2	А	501	HEM	CMA-C3A-C4A	-2.88	124.04	128.46
2	А	501	HEM	C3B-C2B-C1B	2.61	108.42	106.49
2	А	501	HEM	CBD-CAD-C3D	-2.19	106.55	112.63
2	А	501	HEM	CBA-CAA-C2A	2.18	116.34	112.62
2	А	501	HEM	C4A-C3A-C2A	2.03	108.41	107.00

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	А	502	MPD	C2-C3-C4-C5
3	А	502	MPD	C2-C3-C4-O4
2	А	501	HEM	CAA-CBA-CGA-O2A
2	А	501	HEM	CAA-CBA-CGA-O1A

There are no ring outliers.

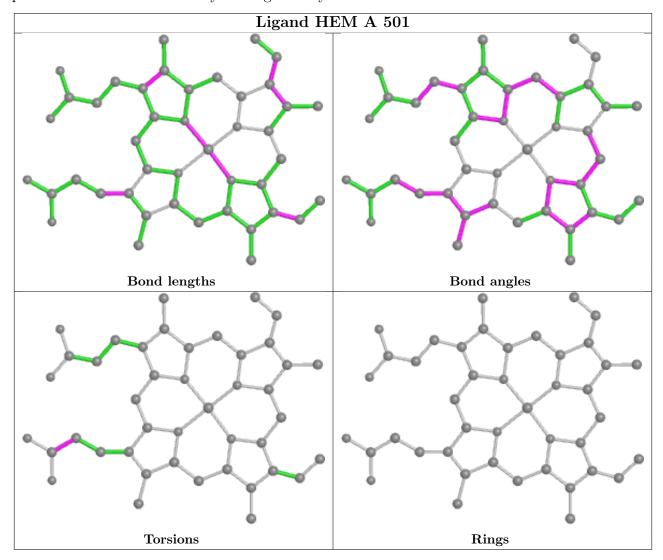
2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	А	502	MPD	1	0
2	А	501	HEM	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 all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will



also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and similar rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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)

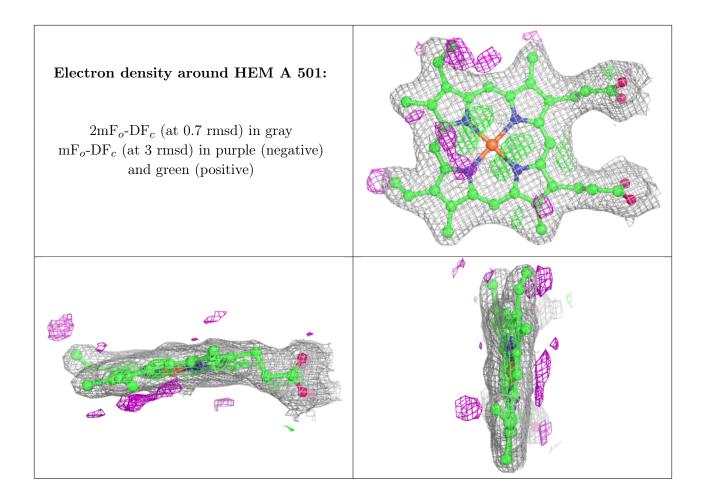
Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands (i)

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

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





6.5 Other polymers (i)

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

