



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 14, 2018 – 01:56 pm GMT

PDB ID : 1VHK
Title : Crystal structure of an hypothetical protein
Authors : Structural GenomiX
Deposited on : 2003-12-01
Resolution : 2.60 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : trunk31020
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk31020

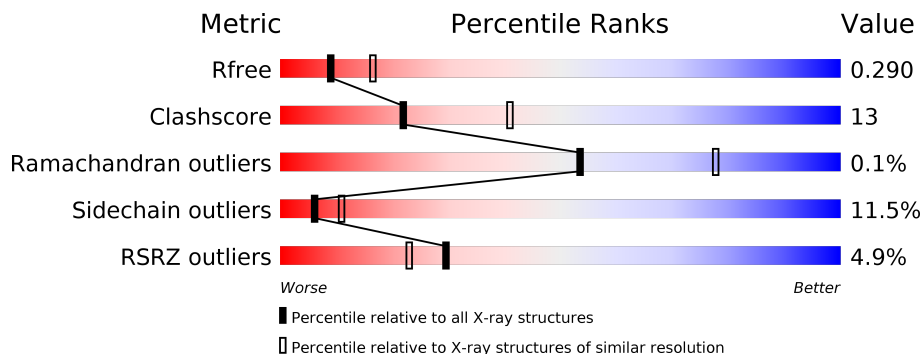
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	111664	2767 (2.60-2.60)
Clashscore	122126	3110 (2.60-2.60)
Ramachandran outliers	120053	3062 (2.60-2.60)
Sidechain outliers	120020	3062 (2.60-2.60)
RSRZ outliers	108989	2706 (2.60-2.60)

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. 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 $\leq 5\%$. 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	268	<div> <div>4%</div> <div> <div></div> <div>57%</div> <div>25%</div> <div>5%</div> <div>12%</div> </div> </div>
1	B	268	<div> <div>6%</div> <div> <div></div> <div>50%</div> <div>19%</div> <div>•</div> <div>27%</div> </div> </div>
1	C	268	<div> <div>%</div> <div> <div></div> <div>53%</div> <div>32%</div> <div>6%</div> <div>9%</div> </div> </div>
1	D	268	<div> <div>4%</div> <div> <div></div> <div>49%</div> <div>16%</div> <div>•</div> <div>34%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6788 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 Hypothetical protein yqeU.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	235	Total	C	N	O	S	Se	0	0	0
			1847	1168	314	355	6	4			
1	B	196	Total	C	N	O	S	Se	0	0	0
			1534	975	262	289	6	2			
1	C	244	Total	C	N	O	S	Se	0	1	0
			1923	1216	331	366	6	4			
1	D	178	Total	C	N	O	S	Se	0	0	0
			1397	886	241	264	4	2			

There are 68 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MSE	-	cloning artifact	UNP P54461
A	0	SER	-	cloning artifact	UNP P54461
A	1	LEU	-	cloning artifact	UNP P54461
A	33	MSE	MET	modified residue	UNP P54461
A	35	MSE	MET	modified residue	UNP P54461
A	152	MSE	MET	modified residue	UNP P54461
A	164	MSE	MET	modified residue	UNP P54461
A	257	GLU	-	cloning artifact	UNP P54461
A	258	GLY	-	cloning artifact	UNP P54461
A	259	GLY	-	cloning artifact	UNP P54461
A	260	SER	-	cloning artifact	UNP P54461
A	261	HIS	-	cloning artifact	UNP P54461
A	262	HIS	-	cloning artifact	UNP P54461
A	263	HIS	-	cloning artifact	UNP P54461
A	264	HIS	-	cloning artifact	UNP P54461
A	265	HIS	-	cloning artifact	UNP P54461
A	266	HIS	-	cloning artifact	UNP P54461
B	-1	MSE	-	cloning artifact	UNP P54461
B	0	SER	-	cloning artifact	UNP P54461
B	1	LEU	-	cloning artifact	UNP P54461
B	33	MSE	MET	modified residue	UNP P54461

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Chain	Residue	Modelled	Actual	Comment	Reference
B	35	MSE	MET	modified residue	UNP P54461
B	152	MSE	MET	modified residue	UNP P54461
B	164	MSE	MET	modified residue	UNP P54461
B	257	GLU	-	cloning artifact	UNP P54461
B	258	GLY	-	cloning artifact	UNP P54461
B	259	GLY	-	cloning artifact	UNP P54461
B	260	SER	-	cloning artifact	UNP P54461
B	261	HIS	-	cloning artifact	UNP P54461
B	262	HIS	-	cloning artifact	UNP P54461
B	263	HIS	-	cloning artifact	UNP P54461
B	264	HIS	-	cloning artifact	UNP P54461
B	265	HIS	-	cloning artifact	UNP P54461
B	266	HIS	-	cloning artifact	UNP P54461
C	-1	MSE	-	cloning artifact	UNP P54461
C	0	SER	-	cloning artifact	UNP P54461
C	1	LEU	-	cloning artifact	UNP P54461
C	33	MSE	MET	modified residue	UNP P54461
C	35	MSE	MET	modified residue	UNP P54461
C	152	MSE	MET	modified residue	UNP P54461
C	164	MSE	MET	modified residue	UNP P54461
C	257	GLU	-	cloning artifact	UNP P54461
C	258	GLY	-	cloning artifact	UNP P54461
C	259	GLY	-	cloning artifact	UNP P54461
C	260	SER	-	cloning artifact	UNP P54461
C	261	HIS	-	cloning artifact	UNP P54461
C	262	HIS	-	cloning artifact	UNP P54461
C	263	HIS	-	cloning artifact	UNP P54461
C	264	HIS	-	cloning artifact	UNP P54461
C	265	HIS	-	cloning artifact	UNP P54461
C	266	HIS	-	cloning artifact	UNP P54461
D	-1	MSE	-	cloning artifact	UNP P54461
D	0	SER	-	cloning artifact	UNP P54461
D	1	LEU	-	cloning artifact	UNP P54461
D	33	MSE	MET	modified residue	UNP P54461
D	35	MSE	MET	modified residue	UNP P54461
D	152	MSE	MET	modified residue	UNP P54461
D	164	MSE	MET	modified residue	UNP P54461
D	257	GLU	-	cloning artifact	UNP P54461
D	258	GLY	-	cloning artifact	UNP P54461
D	259	GLY	-	cloning artifact	UNP P54461
D	260	SER	-	cloning artifact	UNP P54461
D	261	HIS	-	cloning artifact	UNP P54461

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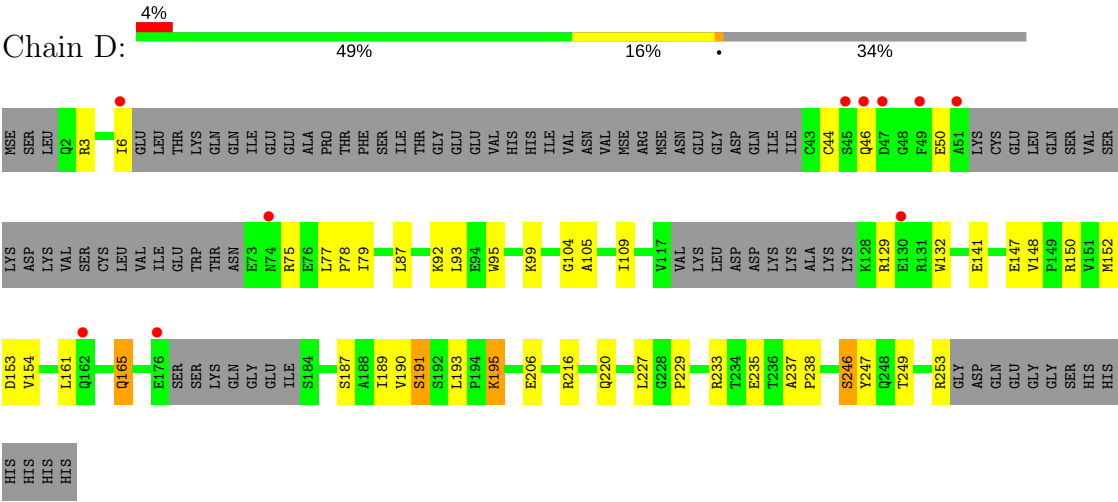
Chain	Residue	Modelled	Actual	Comment	Reference
D	262	HIS	-	cloning artifact	UNP P54461
D	263	HIS	-	cloning artifact	UNP P54461
D	264	HIS	-	cloning artifact	UNP P54461
D	265	HIS	-	cloning artifact	UNP P54461
D	266	HIS	-	cloning artifact	UNP P54461

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	21	Total O 21 21	0	0
2	B	24	Total O 24 24	0	0
2	C	32	Total O 32 32	0	0
2	D	10	Total O 10 10	0	0



● Molecule 1: Hypothetical protein yqeU



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	62.71Å 145.05Å 66.01Å 90.00° 109.40° 90.00°	Depositor
Resolution (Å)	38.19 – 2.60 38.19 – 2.60	Depositor EDS
% Data completeness (in resolution range)	(Not available) (38.19-2.60) 99.6 (38.19-2.60)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.62 (at 2.61Å)	Xtriage
Refinement program	REFMAC 4.0	Depositor
R, R_{free}	0.270 , 0.327 0.238 , 0.290	Depositor DCC
R_{free} test set	1684 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	43.6	Xtriage
Anisotropy	0.133	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 63.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	6788	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.28% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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.

5 Model quality

5.1 Standard geometry

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	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.59	0/1874	1.03	3/2524 (0.1%)
1	B	0.67	0/1557	1.08	5/2099 (0.2%)
1	C	0.63	0/1956	1.07	6/2631 (0.2%)
1	D	0.59	0/1418	0.98	1/1907 (0.1%)
All	All	0.62	0/6805	1.04	15/9161 (0.2%)

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	1
1	C	0	1
All	All	0	2

There are no bond length outliers.

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	75	ARG	NE-CZ-NH1	-7.38	116.61	120.30
1	B	75	ARG	NE-CZ-NH1	6.96	123.78	120.30
1	C	230	ARG	NE-CZ-NH2	6.92	123.76	120.30
1	A	242	LEU	CA-CB-CG	6.27	129.71	115.30
1	C	47	ASP	CB-CG-OD2	6.09	123.78	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	81	VAL	Mainchain
1	C	201	ILE	Mainchain

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	1847	0	1837	55	0
1	B	1534	0	1521	41	0
1	C	1923	0	1932	53	0
1	D	1397	0	1383	28	0
2	A	21	0	0	2	0
2	B	24	0	0	1	0
2	C	32	0	0	1	0
2	D	10	0	0	1	0
All	All	6788	0	6673	170	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 13.

The worst 5 of 170 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:75:ARG:HG2	1:D:229:PRO:HB2	1.39	1.01
1:A:57:SER:HB3	1:A:64:SER:HB2	1.46	0.94
1:C:9:THR:HG22	1:C:12:GLN:H	1.40	0.84
1:B:210:THR:HG22	1:B:213:GLU:H	1.42	0.83
1:B:6:ILE:HD11	1:B:43:CYS:HB3	1.61	0.83

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	229/268 (85%)	217 (95%)	12 (5%)	0	100	100
1	B	186/268 (69%)	178 (96%)	8 (4%)	0	100	100
1	C	241/268 (90%)	228 (95%)	12 (5%)	1 (0%)	36	60
1	D	168/268 (63%)	160 (95%)	8 (5%)	0	100	100
All	All	824/1072 (77%)	783 (95%)	40 (5%)	1 (0%)	53	78

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	61	ASP

5.3.2 Protein sidechains ⓘ

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	202/227 (89%)	177 (88%)	25 (12%)	5	9
1	B	164/227 (72%)	149 (91%)	15 (9%)	10	20
1	C	210/227 (92%)	177 (84%)	33 (16%)	3	4
1	D	148/227 (65%)	138 (93%)	10 (7%)	17	35
All	All	724/908 (80%)	641 (88%)	83 (12%)	6	11

5 of 83 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	198	SER
1	C	52	LYS
1	D	154	VAL
1	B	210	THR
1	C	15	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	112	GLN
1	B	162	GLN
1	C	106	HIS
1	B	46	GLN
1	C	56	GLN

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](#)

There are no ligands in this entry.

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, 95th 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	A	231/268 (86%)	0.17	12 (5%) 27 20	17, 40, 76, 92	0
1	B	194/268 (72%)	0.26	17 (8%) 10 6	17, 34, 71, 92	0
1	C	240/268 (89%)	0.10	2 (0%) 86 84	21, 41, 61, 70	0
1	D	176/268 (65%)	0.28	10 (5%) 24 17	22, 45, 80, 91	0
All	All	841/1072 (78%)	0.19	41 (4%) 29 23	17, 40, 73, 92	0

The worst 5 of 41 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	41	ILE	5.2
1	B	66	LEU	5.1
1	B	65	CYS	4.6
1	D	47	ASP	4.2
1	B	43	CYS	3.8

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.