



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 25, 2024 – 10:17 AM EST

PDB ID : 4HGM
Title : Shark IgNAR Variable Domain
Authors : Olland, A.; Kovalenko, O.V.; King, D.; Svenson, K.
Deposited on : 2012-10-08
Resolution : 2.34 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

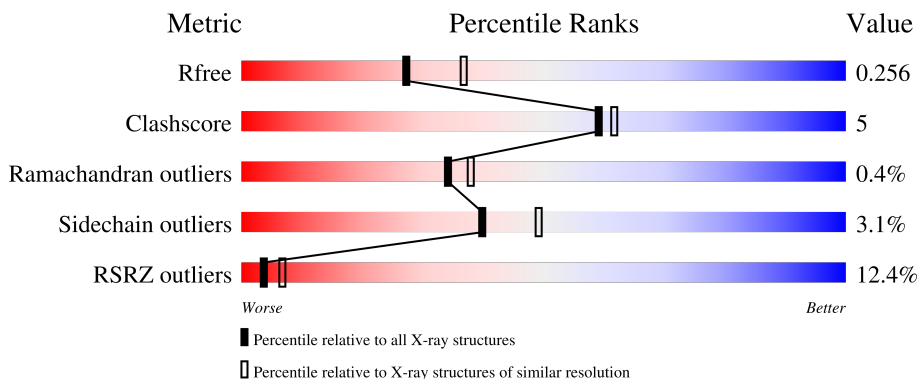
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.34 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}	130704	2096 (2.36-2.32)
Clashscore	141614	2193 (2.36-2.32)
Ramachandran outliers	138981	2159 (2.36-2.32)
Sidechain outliers	138945	2160 (2.36-2.32)
RSRZ outliers	127900	2067 (2.36-2.32)

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 $\leq 5\%$. 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	112	
2	B	585	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4577 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 Shark V-NAR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	103	791	494	130	164	3	0	0	0

- Molecule 2 is a protein called Serum albumin.

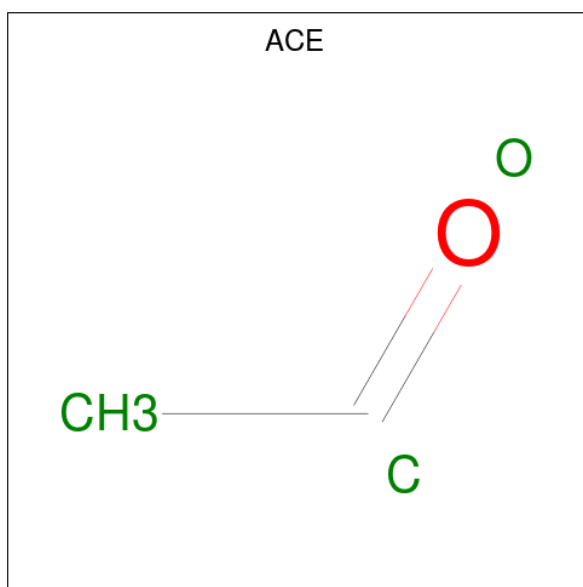
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	478	3707	2342	632	697	36	0	0	0

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	B	1	4	2	2	0	0

- Molecule 4 is ACETYL GROUP (three-letter code: ACE) (formula: C₂H₄O).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C O 3 2 1	0	0


- Molecule 5 is water.

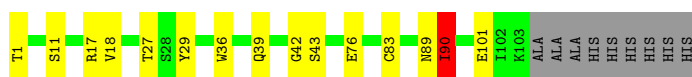
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	22	Total O 22 22	0	0
5	B	50	Total O 50 50	0	0

3 Residue-property plots

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.

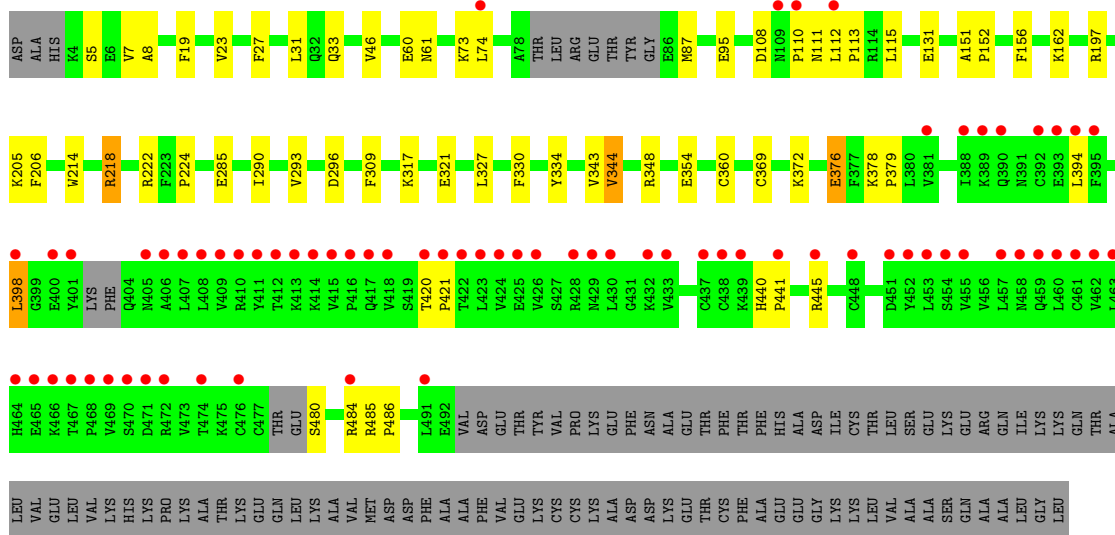
- Molecule 1: Shark V-NAR

Chain A: 



- Molecule 2: Serum albumin

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	131.34Å 131.34Å 74.52Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	37.91 – 2.34 65.67 – 2.34	Depositor EDS
% Data completeness (in resolution range)	95.4 (37.91-2.34) 99.5 (65.67-2.34)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.36 (at 2.34Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.6.1_357)	Depositor
R, R_{free}	0.221 , 0.259 0.218 , 0.256	Depositor DCC
R_{free} test set	1604 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	48.4	Xtrriage
Anisotropy	0.198	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 56.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	0.038 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4577	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.01% 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

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, ACE

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	0.31	0/807	0.50	0/1096
2	B	0.27	0/3779	0.41	0/5111
All	All	0.27	0/4586	0.43	0/6207

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

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	791	0	766	8	0
2	B	3707	0	3546	33	0
3	B	4	0	6	0	0
4	B	3	0	3	0	0
5	A	22	0	0	0	0
5	B	50	0	0	0	0
All	All	4577	0	4321	41	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 5.

All (41) 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)
2:B:485:ARG:HB3	2:B:486:PRO:HD3	1.70	0.73
2:B:317:LYS:HE2	2:B:321:GLU:OE2	2.04	0.57
2:B:378:LYS:HB2	2:B:379:PRO:HD3	1.86	0.56
1:A:89:ASN:O	1:A:90:ILE:HG22	2.06	0.56
2:B:222:ARG:C	2:B:224:PRO:HD3	2.28	0.53
2:B:112:LEU:HB3	2:B:113:PRO:HD2	1.90	0.53
2:B:156:PHE:CE1	2:B:285:GLU:HB3	2.45	0.52
1:A:76:GLU:H	1:A:76:GLU:CD	2.14	0.51
2:B:344:VAL:O	2:B:348:ARG:HG3	2.10	0.51
2:B:224:PRO:HD2	2:B:296:ASP:HB3	1.93	0.51
2:B:327:LEU:HD11	2:B:354:GLU:HG3	1.94	0.49
2:B:376:GLU:O	2:B:379:PRO:HD2	2.12	0.49
2:B:480:SER:O	2:B:484:ARG:HG3	2.13	0.49
2:B:441:PRO:O	2:B:445:ARG:HG3	2.13	0.49
1:A:11:SER:HA	1:A:101:GLU:O	2.12	0.49
2:B:5:SER:HB3	2:B:8:ALA:HB3	1.95	0.48
2:B:420:THR:N	2:B:421:PRO:HD2	2.28	0.48
2:B:372:LYS:HE2	2:B:372:LYS:HA	1.96	0.47
2:B:394:LEU:O	2:B:398:LEU:HB2	2.14	0.47
2:B:218:ARG:O	2:B:218:ARG:HD3	2.14	0.47
2:B:214:TRP:CD1	2:B:343:VAL:HG11	2.49	0.46
1:A:29:TYR:CD1	1:A:89:ASN:HB3	2.51	0.46
2:B:60:GLU:O	2:B:61:ASN:HB2	2.17	0.45
2:B:31:LEU:HD22	2:B:74:LEU:HD22	1.99	0.45
1:A:36:TRP:CZ3	1:A:83:CYS:HB3	2.52	0.45
2:B:156:PHE:HE1	2:B:285:GLU:HB3	1.81	0.45
2:B:290:ILE:O	2:B:293:VAL:HG12	2.18	0.44
1:A:42:GLY:O	1:A:43:SER:HB2	2.18	0.44
2:B:46:VAL:HG23	2:B:73:LYS:HG2	2.00	0.43
2:B:218:ARG:HD3	2:B:218:ARG:C	2.38	0.43
2:B:440:HIS:HB3	2:B:441:PRO:HD2	2.00	0.43
1:A:1:THR:HG23	1:A:27:THR:HB	2.00	0.43
2:B:309:PHE:CZ	2:B:330:PHE:HA	2.54	0.43
1:A:39:GLN:HG2	1:A:43:SER:HA	2.00	0.42
2:B:115:LEU:HD23	2:B:115:LEU:HA	1.93	0.42
2:B:27:PHE:CD1	2:B:74:LEU:HD21	2.55	0.41
2:B:151:ALA:N	2:B:152:PRO:HD2	2.36	0.41
2:B:19:PHE:O	2:B:23:VAL:HG23	2.21	0.41
2:B:360:CYS:HB3	2:B:369:CYS:HB3	1.93	0.40
2:B:205:LYS:HB3	2:B:206:PHE:HD2	1.86	0.40
2:B:131:GLU:OE2	2:B:162:LYS:HE3	2.21	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	Percentiles	
1	A	101/112 (90%)	97 (96%)	3 (3%)	1 (1%)	15	14
2	B	470/585 (80%)	447 (95%)	22 (5%)	1 (0%)	47	55
All	All	571/697 (82%)	544 (95%)	25 (4%)	2 (0%)	34	38

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	90	ILE
2	B	110	PRO

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	90/97 (93%)	87 (97%)	3 (3%)	38	46
2	B	392/511 (77%)	380 (97%)	12 (3%)	40	49
All	All	482/608 (79%)	467 (97%)	15 (3%)	40	49

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	ARG

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Mol	Chain	Res	Type
1	A	18	VAL
1	A	90	ILE
2	B	7	VAL
2	B	33	GLN
2	B	87	MET
2	B	95	GLU
2	B	108	ASP
2	B	111	ASN
2	B	197	ARG
2	B	218	ARG
2	B	334	TYR
2	B	344	VAL
2	B	376	GLU
2	B	398	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	B	601	-	3,3,3	0.36	0	2,2,2	0.44	0
4	ACE	B	602	-	1,2,2	0.85	0	1,1,1	0.19	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	EDO	B	601	-	-	0/1/1/1	-

There are no bond length outliers.

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

6.1 Protein, DNA and RNA chains

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	103/112 (91%)	0.16	0 100 100	32, 47, 65, 80	0
2	B	478/585 (81%)	0.83	72 (15%) 2 3	33, 58, 155, 173	0
All	All	581/697 (83%)	0.71	72 (12%) 4 7	32, 55, 152, 173	0

All (72) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	460	LEU	9.9
2	B	415	VAL	9.2
2	B	109	ASN	9.0
2	B	468	PRO	8.3
2	B	457	LEU	8.3
2	B	411	TYR	8.3
2	B	474	THR	8.0
2	B	465	GLU	7.5
2	B	410	ARG	7.2
2	B	405	ASN	7.0
2	B	418	VAL	7.0
2	B	401	TYR	6.9
2	B	463	LEU	6.4
2	B	462	VAL	6.2
2	B	423	LEU	5.9
2	B	464	HIS	5.9
2	B	470	SER	5.8
2	B	472	ARG	5.7
2	B	400	GLU	5.7
2	B	432	LYS	5.6
2	B	414	LYS	5.4
2	B	424	VAL	5.4
2	B	467	THR	5.2
2	B	421	PRO	5.1

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Mol	Chain	Res	Type	RSRZ
2	B	455	VAL	4.9
2	B	458	ASN	4.9
2	B	416	PRO	4.8
2	B	466	LYS	4.6
2	B	395	PHE	4.5
2	B	406	ALA	4.4
2	B	445	ARG	4.3
2	B	413	LYS	4.1
2	B	408	LEU	4.1
2	B	412	THR	3.7
2	B	491	LEU	3.7
2	B	389	LYS	3.7
2	B	453	LEU	3.6
2	B	429	ASN	3.6
2	B	430	LEU	3.5
2	B	407	LEU	3.5
2	B	425	GLU	3.5
2	B	394	LEU	3.4
2	B	459	GLN	3.4
2	B	417	GLN	3.2
2	B	420	THR	3.2
2	B	393	GLU	3.1
2	B	392	CYS	3.1
2	B	451	ASP	3.0
2	B	422	THR	3.0
2	B	438	CYS	2.8
2	B	437	CYS	2.8
2	B	110	PRO	2.8
2	B	452	TYR	2.8
2	B	398	LEU	2.8
2	B	461	CYS	2.7
2	B	469	VAL	2.6
2	B	471	ASP	2.6
2	B	476	CYS	2.6
2	B	433	VAL	2.5
2	B	390	GLN	2.5
2	B	439	LYS	2.4
2	B	448	CYS	2.4
2	B	409	VAL	2.4
2	B	454	SER	2.3
2	B	484	ARG	2.2
2	B	441	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
2	B	112	LEU	2.1
2	B	381	VAL	2.1
2	B	426	VAL	2.1
2	B	74	LEU	2.0
2	B	428	ARG	2.0
2	B	388	ILE	2.0

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 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, 95th 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	B-factors(Å ²)	Q<0.9
3	EDO	B	601	4/4	0.83	0.17	55,56,59,64	0
4	ACE	B	602	3/3	0.89	0.23	46,46,48,52	0

6.5 Other polymers [i](#)

There are no such residues in this entry.