



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 05:14 AM GMT

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 validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

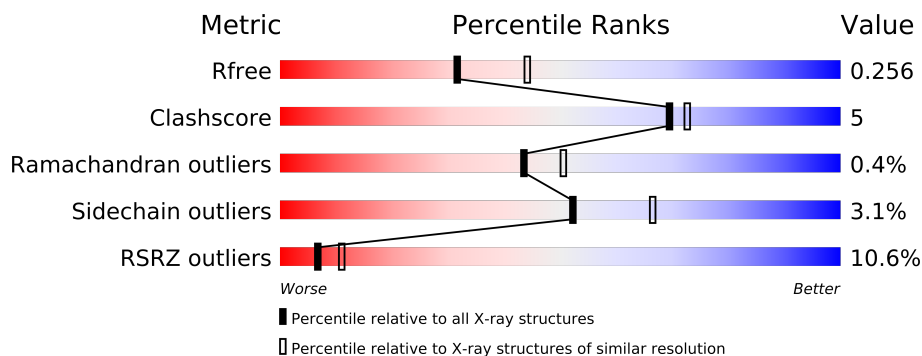
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance



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}	66092	4049 (2.38-2.30)
Clashscore	79885	1094 (2.36-2.32)
Ramachandran outliers	78287	1080 (2.36-2.32)
Sidechain outliers	78261	1081 (2.36-2.32)
RSRZ outliers	66119	4050 (2.38-2.30)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	112	
2	B	585	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
4	ACE	B	602	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4577 atoms, of which 0 are hydrogen and 0 are deuterium.

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
1	A	103	Total	C	N	O	S	0	0	0
			791	494	130	164	3			

- Molecule 2 is a protein called Serum albumin.

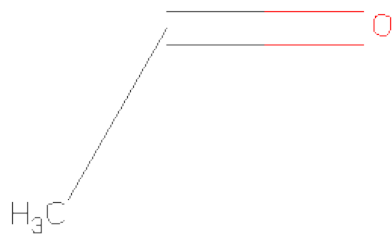
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	478	Total	C	N	O	S	0	0	0
			3707	2342	632	697	36			

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



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

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



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

- Molecule 5 is water.

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

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)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.1.357)	Depositor
R, R_{free}	0.221 , 0.259 0.219 , 0.256	Depositor DCC
R_{free} test set	1604 reflections (5.10%)	DCC
Wilson B-factor (Å ²)	48.4	Xtriage
Anisotropy	0.198	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 54.7	EDS
Estimated twinning fraction	0.038 for -h,-k,l	Xtriage
L-test for twinning	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 31462 reflections	Xtriage
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

Xtriage'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.

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 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

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

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 5.

All (41) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(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:376:GLU:O	2:B:379:PRO:HD2	2.12	0.49
2:B:327:LEU:HD11	2:B:354:GLU:HG3	1.94	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:HD3	2:B:218:ARG:O	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:C	2:B:218:ARG:HD3	2.38	0.43
2:B:440:HIS:HB3	2:B:441:PRO:HD2	2.00	0.43
2:B:309:PHE:CZ	2:B:330:PHE:HA	2.54	0.43
1:A:1:THR:HG23	1:A:27:THR:HB	2.00	0.43
1:A:39:GLN:HG2	1:A:43:SER:HA	2.00	0.42
2:B:115:LEU:HA	2:B:115:LEU:HD23	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

5.3.1 Protein backbone ⓘ

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%)	22	23
2	B	470/585 (80%)	447 (95%)	22 (5%)	1 (0%)	56	67
All	All	571/697 (82%)	544 (95%)	25 (4%)	2 (0%)	43	50

All (2) Ramachandran outliers are listed below:

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

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	90/97 (93%)	87 (97%)	3 (3%)	50	64
2	B	392/511 (77%)	380 (97%)	12 (3%)	52	66
All	All	482/608 (79%)	467 (97%)	15 (3%)	52	66

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

Mol	Chain	Res	Type
1	A	17	ARG
1	A	18	VAL
1	A	90	ILE
2	B	7	VAL

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Mol	Chain	Res	Type
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

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

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

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	0.46	0	2,2,2	0.49	0
4	ACE	B	602	-	2,2,2	0.40	0	1,1,1	0.15	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	0/0/0/0
4	ACE	B	602	-	-	0/0/0/0	0/0/0/0

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.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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%)	0.23	0 100 100	32, 47, 65, 80	0
2	B	478/585 (81%)	0.88	62 (12%) 4 7	33, 58, 155, 173	0
All	All	581/697 (83%)	0.76	62 (10%) 7 11	32, 55, 152, 173	0

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	415	VAL	10.0
2	B	470	SER	8.9
2	B	468	PRO	7.9
2	B	423	LEU	7.8
2	B	472	ARG	7.7
2	B	411	TYR	7.3
2	B	460	LEU	7.2
2	B	465	GLU	7.2
2	B	474	THR	6.9
2	B	109	ASN	6.8
2	B	466	LYS	6.7
2	B	418	VAL	6.4
2	B	410	ARG	6.0
2	B	455	VAL	5.8
2	B	416	PRO	5.8
2	B	469	VAL	5.8
2	B	491	LEU	5.8
2	B	405	ASN	5.6
2	B	457	LEU	5.3
2	B	401	TYR	5.2
2	B	467	THR	5.2
2	B	406	ALA	5.0
2	B	421	PRO	5.0
2	B	464	HIS	4.8

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Mol	Chain	Res	Type	RSRZ
2	B	432	LYS	4.8
2	B	453	LEU	4.6
2	B	462	VAL	4.6
2	B	424	VAL	4.6
2	B	458	ASN	4.6
2	B	430	LEU	4.5
2	B	414	LYS	4.5
2	B	400	GLU	4.5
2	B	437	CYS	4.4
2	B	417	GLN	4.4
2	B	463	LEU	4.3
2	B	395	PHE	4.3
2	B	407	LEU	4.0
2	B	420	THR	4.0
2	B	429	ASN	4.0
2	B	471	ASP	3.8
2	B	390	GLN	3.7
2	B	398	LEU	3.7
2	B	459	GLN	3.5
2	B	394	LEU	3.5
2	B	425	GLU	3.5
2	B	428	ARG	3.5
2	B	413	LYS	3.4
2	B	408	LEU	3.2
2	B	389	LYS	3.1
2	B	426	VAL	3.1
2	B	452	TYR	3.1
2	B	412	THR	3.0
2	B	439	LYS	2.8
2	B	409	VAL	2.8
2	B	204	GLN	2.7
2	B	445	ARG	2.6
2	B	433	VAL	2.6
2	B	381	VAL	2.5
2	B	388	ILE	2.5
2	B	492	GLU	2.4
2	B	404	GLN	2.1
2	B	74	LEU	2.1

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	ACE	B	602	3/3	0.21	2.18	46,46,48,52	0
3	EDO	B	601	4/4	0.16	0.51	55,56,59,64	0

6.5 Other polymers

There are no such residues in this entry.