Full wwPDB X-ray Structure Validation Report (i)

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PDB ID	:	3WCY
Title	:	Murine Ifnar1 in complex with interferon-beta
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Deposited on	:	2013-06-04
Resolution	:	2.90 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:

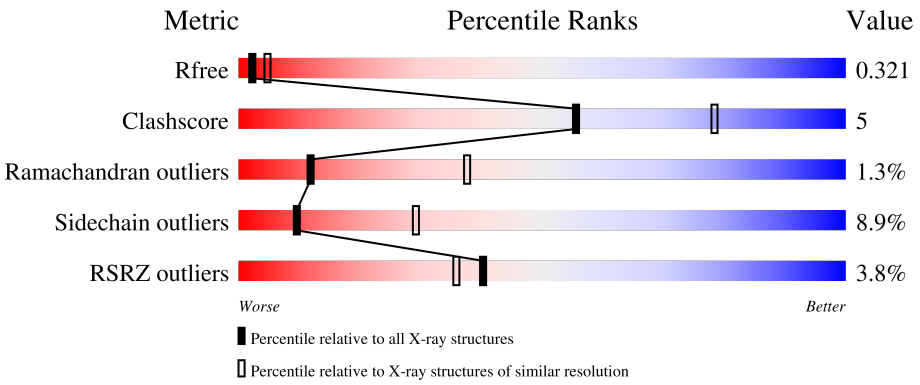
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 2.90 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	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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	403	4% 61% 16% • 21%
2	I	161	% 83% 14% • •

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 3896 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 Interferon alpha/beta receptor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	318	2519	1614	404	488	13	0	0	0

- Molecule 2 is a protein called Interferon beta.

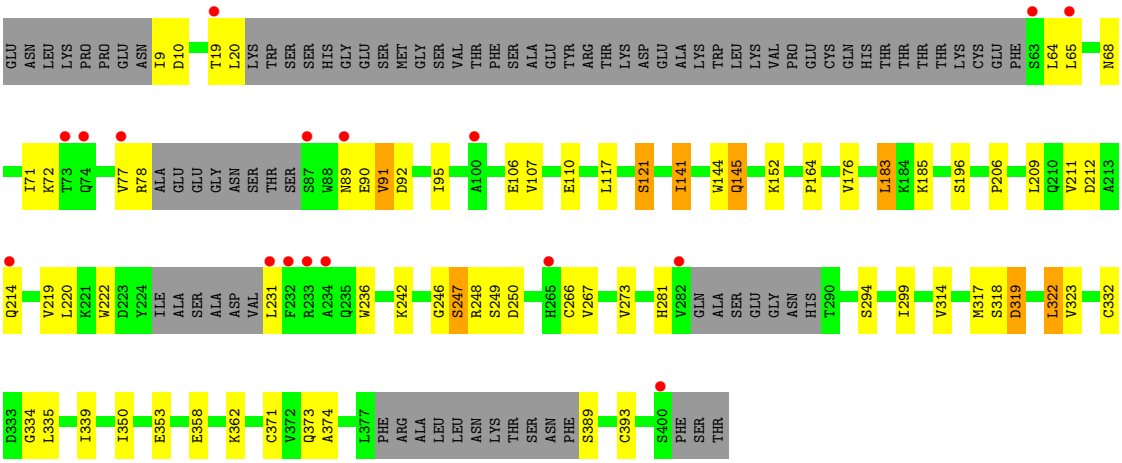
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	I	160	1377	886	241	242	8	0	0	0

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: Interferon alpha/beta receptor 1

Chain A:



- Molecule 2: Interferon beta

Chain I:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α, β, γ	54.59Å 54.59Å 239.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	17.99 – 2.90 17.91 – 2.90	Depositor EDS
% Data completeness (in resolution range)	(Not available) (17.99-2.90) 98.9 (17.91-2.90)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.29 (at 2.92Å)	Xtriage
Refinement program	BUSTER 2.8.0	Depositor
R, R_{free}	0.237 , 0.286 0.256 , 0.321	Depositor DCC
R_{free} test set	777 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å^2)	92.9	Xtriage
Anisotropy	0.475	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 73.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.091 for h,-k,-l	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	3896	wwPDB-VP
Average B, all atoms (Å^2)	113.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.56% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical 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.

5 Model quality (i)

5.1 Standard geometry (i)

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	0.43	0/2584	0.68	2/3527 (0.1%)
2	I	0.42	0/1404	0.64	0/1890
All	All	0.42	0/3988	0.66	2/5417 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	145	GLN	CB-CA-C	8.12	126.63	110.40
1	A	248	ARG	N-CA-CB	-5.01	101.57	110.60

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	A	2519	0	2418	30	0
2	I	1377	0	1395	11	0
All	All	3896	0	3813	39	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 (39) 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:A:91:VAL:HG22	1:A:92:ASP:H	1.22	1.01
1:A:144:TRP:HD1	1:A:145:GLN:O	1.53	0.90
1:A:246:GLY:O	1:A:247:SER:HB2	1.71	0.88
1:A:144:TRP:CD1	1:A:145:GLN:O	2.30	0.83
1:A:246:GLY:O	1:A:247:SER:CB	2.38	0.71
1:A:91:VAL:HG22	1:A:92:ASP:N	2.02	0.68
1:A:206:PRO:HD2	1:A:294:SER:HB2	1.75	0.67
2:I:102:GLN:HA	2:I:105:ARG:HD2	1.82	0.60
1:A:220:LEU:HB3	1:A:266:CYS:HB3	1.84	0.60
1:A:91:VAL:CG2	1:A:92:ASP:H	2.04	0.59
2:I:62:VAL:HG22	2:I:145:ILE:HD12	1.85	0.58
1:A:318:SER:O	1:A:319:ASP:CB	2.51	0.57
1:A:95:ILE:HG21	2:I:115:LEU:HD11	1.88	0.56
1:A:68:ASN:HB3	1:A:71:ILE:HG12	1.88	0.55
1:A:183:LEU:HD12	2:I:109:GLU:HB3	1.89	0.55
1:A:249:SER:HB2	1:A:250:ASP:HA	1.89	0.54
2:I:51:THR:HG21	2:I:158:ASN:HB2	1.89	0.54
1:A:77:VAL:H	1:A:89:ASN:HB3	1.72	0.54
1:A:374:ALA:H	1:A:389:SER:HB3	1.73	0.53
2:I:7:GLN:HE22	2:I:160:GLN:HB2	1.75	0.51
1:A:334:GLY:O	1:A:335:LEU:HD12	2.12	0.49
1:A:91:VAL:HG13	1:A:92:ASP:N	2.28	0.48
1:A:318:SER:O	1:A:319:ASP:HB3	2.13	0.48
1:A:236:TRP:CG	1:A:273:VAL:HG12	2.51	0.46
1:A:141:ILE:HG23	1:A:176:VAL:HG22	1.98	0.45
1:A:314:VAL:HG12	1:A:323:VAL:HG22	1.99	0.45
2:I:20:LEU:HD13	2:I:83:LEU:HA	1.99	0.45
1:A:211:VAL:HG22	1:A:220:LEU:HD12	1.99	0.44
1:A:106:GLU:HB3	1:A:121:SER:HB3	2.00	0.44
1:A:211:VAL:HB	1:A:299:ILE:HG21	2.00	0.43
1:A:110:GLU:HB3	1:A:117:LEU:HB2	1.99	0.43
1:A:334:GLY:C	1:A:335:LEU:HD12	2.39	0.43
2:I:4:LYS:HE3	2:I:160:GLN:HA	2.01	0.42
2:I:154:ARG:HG3	2:I:157:ARG:HH21	1.85	0.42
2:I:21:LEU:HA	2:I:24:LEU:HD13	2.01	0.42
1:A:219:VAL:HG22	1:A:267:VAL:HG22	2.00	0.42
2:I:55:ILE:HD12	2:I:152:ILE:HG23	2.02	0.42
1:A:209:LEU:HD13	1:A:222:TRP:HB3	2.03	0.41
1:A:322:LEU:HD21	1:A:358:GLU:HG2	2.03	0.41

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	306/403 (76%)	275 (90%)	26 (8%)	5 (2%)	9 32
2	I	158/161 (98%)	152 (96%)	5 (3%)	1 (1%)	25 58
All	All	464/564 (82%)	427 (92%)	31 (7%)	6 (1%)	12 37

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	247	SER
1	A	319	ASP
1	A	90	GLU
2	I	26	GLY
1	A	91	VAL
1	A	164	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	289/371 (78%)	259 (90%)	30 (10%)	7 21
2	I	151/153 (99%)	142 (94%)	9 (6%)	19 49
All	All	440/524 (84%)	401 (91%)	39 (9%)	9 29

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	ILE
1	A	10	ASP
1	A	19	THR
1	A	20	LEU
1	A	64	LEU
1	A	65	LEU
1	A	72	LYS
1	A	78	ARG
1	A	107	VAL
1	A	121	SER
1	A	141	ILE
1	A	152	LYS
1	A	183	LEU
1	A	185	LYS
1	A	196	SER
1	A	212	ASP
1	A	214	GLN
1	A	231	LEU
1	A	242	LYS
1	A	281	HIS
1	A	317	MET
1	A	322	LEU
1	A	332	CYS
1	A	339	ILE
1	A	350	ILE
1	A	353	GLU
1	A	362	LYS
1	A	371	CYS
1	A	373	GLN
1	A	393	CYS
2	I	35	ASP
2	I	48	LYS
2	I	71	SER
2	I	77	GLU
2	I	79	ILE
2	I	105	ARG
2	I	125	GLN
2	I	158	ASN
2	I	160	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	I	7	GLN
2	I	68	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)

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	318/403 (78%)	0.35	17 (5%)	26	22	71, 116, 157, 179	0
2	I	160/161 (99%)	0.14	1 (0%)	89	89	64, 103, 138, 157	0
All	All	478/564 (84%)	0.28	18 (3%)	40	36	64, 111, 151, 179	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	233	ARG	6.4
1	A	234	ALA	5.6
2	I	1	ILE	4.7
1	A	282	VAL	4.2
1	A	63	SER	4.2
1	A	65	LEU	4.1
1	A	400	SER	4.0
1	A	73	THR	3.9
1	A	265	HIS	3.8
1	A	231	LEU	3.7
1	A	89	ASN	3.2
1	A	232	PHE	3.2
1	A	74	GLN	3.1
1	A	19	THR	2.9
1	A	100	ALA	2.3
1	A	77	VAL	2.1
1	A	214	GLN	2.1
1	A	87	SER	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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.