wwPDB X-ray Structure Validation Summary Report (i)

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PDB ID	:	6FIB
Title	:	Structure of human 4-1BB ligand
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Deposited on	:	2018-01-17
Resolution	:	2.70 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

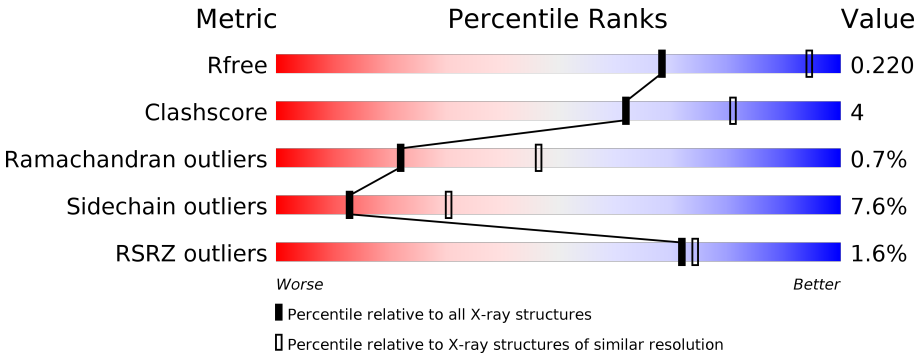
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 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	188	3% 63% 13% • 22%
2	B	311	39% 6% 55%
3	C	292	% 42% 7% • 50%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3347 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 Tumor necrosis factor ligand superfamily member 9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	146	Total	C	N	O	S	0	0	0
			1100	706	195	198	1			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	249	GLY	-	expression tag	UNP P41273
A	250	GLY	-	expression tag	UNP P41273
A	251	GLY	-	expression tag	UNP P41273
A	252	GLY	-	expression tag	UNP P41273
A	253	SER	-	expression tag	UNP P41273
A	254	GLY	-	expression tag	UNP P41273
A	255	GLY	-	expression tag	UNP P41273
A	256	GLY	-	expression tag	UNP P41273
A	257	GLY	-	expression tag	UNP P41273
A	258	SER	-	expression tag	UNP P41273

- Molecule 2 is a protein called Tumor necrosis factor ligand superfamily member 9,4-1BBL -CH/CL fusion.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	140	Total	C	N	O	S	0	0	0
			1063	683	189	190	1			

- Molecule 3 is a protein called Tumor necrosis factor ligand superfamily member 9,Uncharacterized protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	146	Total	C	N	O	S	0	0	0
			1102	706	198	197	1			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	70	ARG	-	expression tag	UNP P41273
C	249	GLY	-	linker	UNP P41273
C	250	GLY	-	linker	UNP P41273
C	251	GLY	-	linker	UNP P41273
C	252	GLY	-	linker	UNP P41273
C	253	SER	-	linker	UNP P41273
C	254	GLY	-	linker	UNP P41273
C	255	GLY	-	linker	UNP P41273
C	256	GLY	-	linker	UNP P41273
C	257	GLY	-	linker	UNP P41273
C	288	GLU	LYS	conflict	UNP A8K008
C	354	GLU	LYS	conflict	UNP A8K008

- Molecule 4 is water.

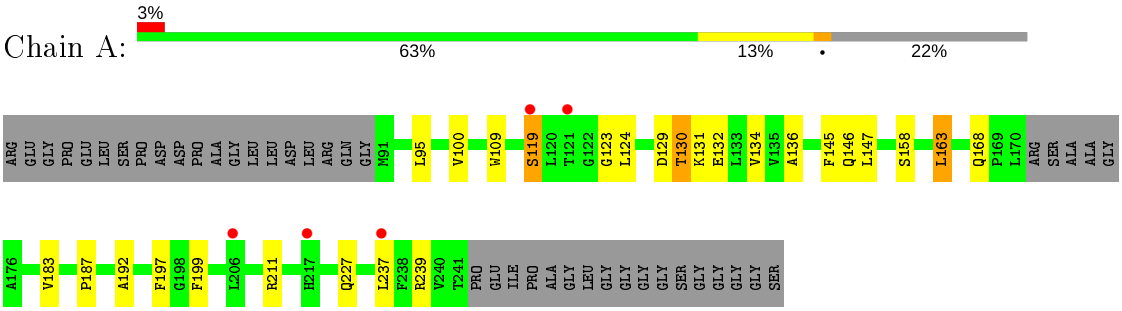
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	22	Total O 22 22	0	0
4	B	29	Total O 29 29	0	0
4	C	31	Total O 31 31	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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.

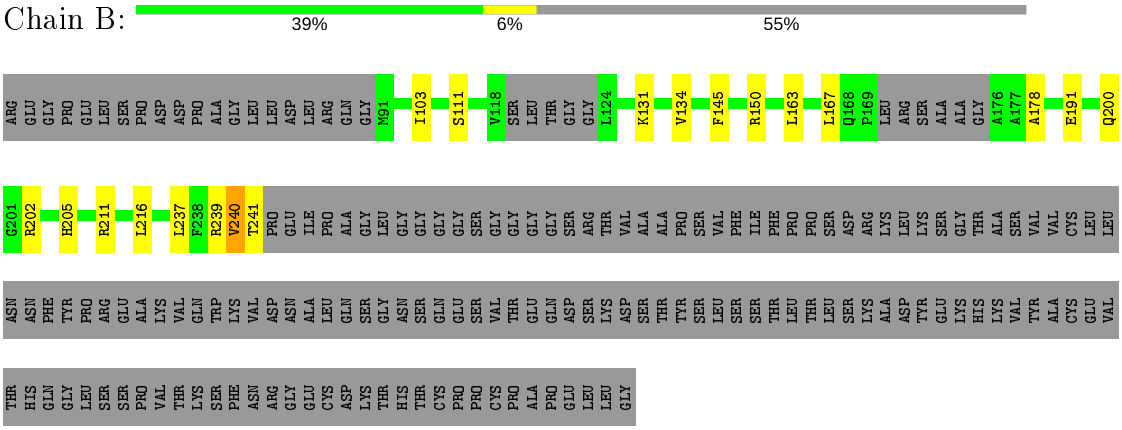
- Molecule 1: Tumor necrosis factor ligand superfamily member 9

Chain A:



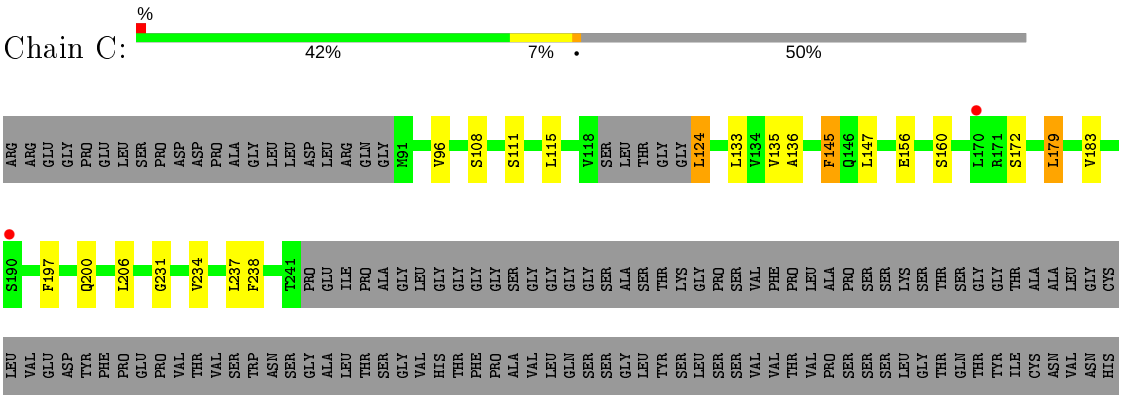
- Molecule 2: Tumor necrosis factor ligand superfamily member 9,4-1BBL -CH/CL fusion

Chain B:



- Molecule 3: Tumor necrosis factor ligand superfamily member 9,Uncharacterized protein

Chain C:



LYS
PRO
SER
ASN
THR
LYS
VAL
ASP
GLU
LYS
VAL
GLU
PRO
LYS
SER
CYS

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 62	Depositor
Cell constants a, b, c, α, β, γ	119.59Å 119.59Å 104.35Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	103.57 – 2.70 103.57 – 2.70	Depositor EDS
% Data completeness (in resolution range)	61.9 (103.57-2.70) 61.9 (103.57-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$< I/\sigma(I) >$ [1]	1.39 (at 2.69Å)	Xtriage
Refinement program	BUSTER 2.11.7	Depositor
R, R_{free}	0.166 , 0.221 0.174 , 0.220	Depositor DCC
R_{free} test set	696 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å^2)	84.7	Xtriage
Anisotropy	0.008	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 72.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.037 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	3347	wwPDB-VP
Average B, all atoms (Å^2)	86.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.78% 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

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	0.52	0/1122	0.81	0/1524
2	B	0.52	0/1084	0.76	0/1471
3	C	0.53	0/1124	0.80	0/1526
All	All	0.52	0/3330	0.79	0/4521

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	1100	0	1114	12	0
2	B	1063	0	1073	10	0
3	C	1102	0	1116	14	0
4	A	22	0	0	0	0
4	B	29	0	0	0	0
4	C	31	0	0	0	0
All	All	3347	0	3303	29	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.

The worst 5 of 29 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:167:LEU:HD11	2:B:178:ALA:HB2	1.73	0.70
1:A:197:PHE:CZ	3:C:200:GLN:HG3	2.31	0.66
3:C:96:VAL:HG11	3:C:231:GLY:HA2	1.83	0.60
2:B:205:HIS:HB2	3:C:115:LEU:HD23	1.85	0.59
3:C:133:LEU:HD21	3:C:237:LEU:HD21	1.85	0.58

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	142/188 (76%)	131 (92%)	9 (6%)	2 (1%)	11 28
2	B	134/311 (43%)	125 (93%)	9 (7%)	0	100 100
3	C	142/292 (49%)	137 (96%)	4 (3%)	1 (1%)	22 46
All	All	418/791 (53%)	393 (94%)	22 (5%)	3 (1%)	22 46

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	192	ALA
3	C	172	SER
1	A	119	SER

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	112/137 (82%)	101 (90%)	11 (10%)	8 18
2	B	108/247 (44%)	101 (94%)	7 (6%)	17 38
3	C	111/227 (49%)	104 (94%)	7 (6%)	18 40
All	All	331/611 (54%)	306 (92%)	25 (8%)	13 30

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	111	SER
2	B	145	PHE
3	C	160	SER
2	B	131	LYS
2	B	150	ARG

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

Mol	Chain	Res	Type
3	C	168	GLN
3	C	215	HIS

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

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, 95^{th} 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	146/188 (77%)	0.47	5 (3%) 45 45	56, 84, 135, 164	0
2	B	140/311 (45%)	0.18	0 100 100	57, 84, 134, 146	0
3	C	146/292 (50%)	0.31	2 (1%) 75 77	55, 78, 127, 159	0
All	All	432/791 (54%)	0.32	7 (1%) 72 74	55, 82, 134, 164	0

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	170	LEU	3.7
1	A	121	THR	2.8
1	A	119	SER	2.7
1	A	206	LEU	2.6
1	A	237	LEU	2.4

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

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.