



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 11:55 AM GMT

PDB ID : 3QB1
Title : Interleukin-2 mutant D10
Authors : Levin, A.M.; Bates, D.L.; Ring, A.M.; Lin, J.T.; Su, L.; Krieg, C.; Bowman, G.R.; Novick, P.; Pande, V.S.; Khort, H.E.; Boyman, O.; Fathman, C.G.; Garcia, K.C.
Deposited on : 2011-01-12
Resolution : 3.10 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
<http://wwpdb.org/validation/2016/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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

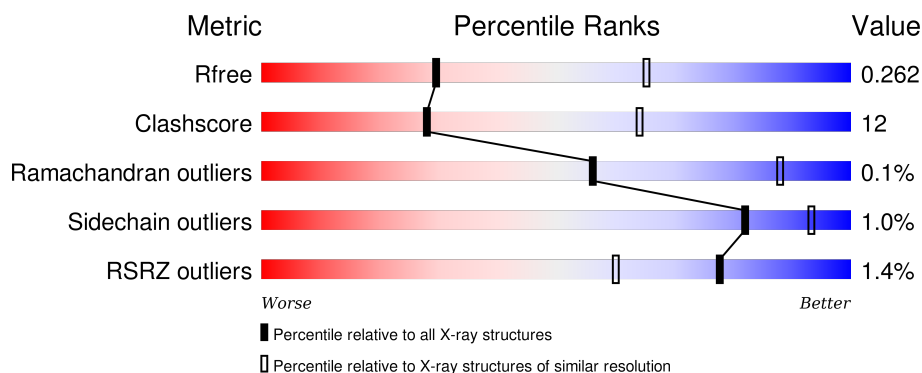
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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}	91344	1114 (3.14-3.06)
Clashscore	102246	1222 (3.14-3.06)
Ramachandran outliers	100387	1174 (3.14-3.06)
Sidechain outliers	100360	1174 (3.14-3.06)
RSRZ outliers	91569	1119 (3.14-3.06)

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	136	
1	B	136	
1	C	136	
1	D	136	
1	E	136	

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Mol	Chain	Length	Quality of chain
1	F	136	<div><div><div></div><div></div><div></div></div><div><div>4%</div><div>65%</div><div>26%</div><div>9%</div></div></div>
1	G	136	<div><div><div></div><div></div><div></div></div><div><div>%</div><div>64%</div><div>18%</div><div>18%</div></div></div>
1	H	136	<div><div><div></div><div></div><div></div></div><div><div></div><div>60%</div><div>26%</div><div>13%</div></div></div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 7786 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 Interleukin-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	124	Total	C	N	O	S	0	0	0
			1022	662	167	186	7			
1	B	124	Total	C	N	O	S	0	0	0
			1022	662	167	186	7			
1	C	119	Total	C	N	O	S	0	0	0
			976	632	158	179	7			
1	D	110	Total	C	N	O	S	0	0	0
			902	586	143	167	6			
1	E	117	Total	C	N	O	S	0	0	0
			961	621	156	177	7			
1	F	124	Total	C	N	O	S	0	0	0
			1022	662	167	186	7			
1	G	111	Total	C	N	O	S	0	0	0
			910	590	145	169	6			
1	H	118	Total	C	N	O	S	0	0	0
			971	629	158	177	7			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	ALA	-	EXPRESSION TAG	UNP P60568
A	-1	ASP	-	EXPRESSION TAG	UNP P60568
A	0	PRO	-	EXPRESSION TAG	UNP P60568
A	74	HIS	GLN	ENGINEERED MUTATION	UNP P60568
A	80	PHE	LEU	ENGINEERED MUTATION	UNP P60568
A	81	ASP	ARG	ENGINEERED MUTATION	UNP P60568
A	85	VAL	LEU	ENGINEERED MUTATION	UNP P60568
A	86	VAL	ILE	ENGINEERED MUTATION	UNP P60568
A	92	PHE	ILE	ENGINEERED MUTATION	UNP P60568
B	-2	ALA	-	EXPRESSION TAG	UNP P60568
B	-1	ASP	-	EXPRESSION TAG	UNP P60568
B	0	PRO	-	EXPRESSION TAG	UNP P60568
B	74	HIS	GLN	ENGINEERED MUTATION	UNP P60568

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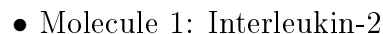
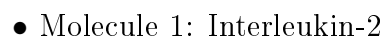
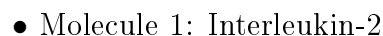
Chain	Residue	Modelled	Actual	Comment	Reference
B	80	PHE	LEU	ENGINEERED MUTATION	UNP P60568
B	81	ASP	ARG	ENGINEERED MUTATION	UNP P60568
B	85	VAL	LEU	ENGINEERED MUTATION	UNP P60568
B	86	VAL	ILE	ENGINEERED MUTATION	UNP P60568
B	92	PHE	ILE	ENGINEERED MUTATION	UNP P60568
C	-2	ALA	-	EXPRESSION TAG	UNP P60568
C	-1	ASP	-	EXPRESSION TAG	UNP P60568
C	0	PRO	-	EXPRESSION TAG	UNP P60568
C	74	HIS	GLN	ENGINEERED MUTATION	UNP P60568
C	80	PHE	LEU	ENGINEERED MUTATION	UNP P60568
C	81	ASP	ARG	ENGINEERED MUTATION	UNP P60568
C	85	VAL	LEU	ENGINEERED MUTATION	UNP P60568
C	86	VAL	ILE	ENGINEERED MUTATION	UNP P60568
C	92	PHE	ILE	ENGINEERED MUTATION	UNP P60568
D	-2	ALA	-	EXPRESSION TAG	UNP P60568
D	-1	ASP	-	EXPRESSION TAG	UNP P60568
D	0	PRO	-	EXPRESSION TAG	UNP P60568
D	74	HIS	GLN	ENGINEERED MUTATION	UNP P60568
D	80	PHE	LEU	ENGINEERED MUTATION	UNP P60568
D	81	ASP	ARG	ENGINEERED MUTATION	UNP P60568
D	85	VAL	LEU	ENGINEERED MUTATION	UNP P60568
D	86	VAL	ILE	ENGINEERED MUTATION	UNP P60568
D	92	PHE	ILE	ENGINEERED MUTATION	UNP P60568
E	-2	ALA	-	EXPRESSION TAG	UNP P60568
E	-1	ASP	-	EXPRESSION TAG	UNP P60568
E	0	PRO	-	EXPRESSION TAG	UNP P60568
E	74	HIS	GLN	ENGINEERED MUTATION	UNP P60568
E	80	PHE	LEU	ENGINEERED MUTATION	UNP P60568
E	81	ASP	ARG	ENGINEERED MUTATION	UNP P60568
E	85	VAL	LEU	ENGINEERED MUTATION	UNP P60568
E	86	VAL	ILE	ENGINEERED MUTATION	UNP P60568
E	92	PHE	ILE	ENGINEERED MUTATION	UNP P60568
F	-2	ALA	-	EXPRESSION TAG	UNP P60568
F	-1	ASP	-	EXPRESSION TAG	UNP P60568
F	0	PRO	-	EXPRESSION TAG	UNP P60568
F	74	HIS	GLN	ENGINEERED MUTATION	UNP P60568
F	80	PHE	LEU	ENGINEERED MUTATION	UNP P60568
F	81	ASP	ARG	ENGINEERED MUTATION	UNP P60568
F	85	VAL	LEU	ENGINEERED MUTATION	UNP P60568
F	86	VAL	ILE	ENGINEERED MUTATION	UNP P60568
F	92	PHE	ILE	ENGINEERED MUTATION	UNP P60568
G	-2	ALA	-	EXPRESSION TAG	UNP P60568

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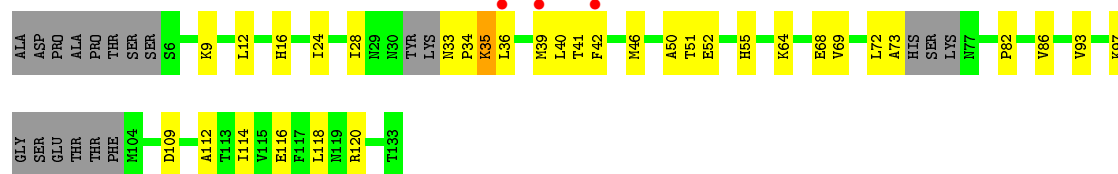
Chain	Residue	Modelled	Actual	Comment	Reference
G	-1	ASP	-	EXPRESSION TAG	UNP P60568
G	0	PRO	-	EXPRESSION TAG	UNP P60568
G	74	HIS	GLN	ENGINEERED MUTATION	UNP P60568
G	80	PHE	LEU	ENGINEERED MUTATION	UNP P60568
G	81	ASP	ARG	ENGINEERED MUTATION	UNP P60568
G	85	VAL	LEU	ENGINEERED MUTATION	UNP P60568
G	86	VAL	ILE	ENGINEERED MUTATION	UNP P60568
G	92	PHE	ILE	ENGINEERED MUTATION	UNP P60568
H	-2	ALA	-	EXPRESSION TAG	UNP P60568
H	-1	ASP	-	EXPRESSION TAG	UNP P60568
H	0	PRO	-	EXPRESSION TAG	UNP P60568
H	74	HIS	GLN	ENGINEERED MUTATION	UNP P60568
H	80	PHE	LEU	ENGINEERED MUTATION	UNP P60568
H	81	ASP	ARG	ENGINEERED MUTATION	UNP P60568
H	85	VAL	LEU	ENGINEERED MUTATION	UNP P60568
H	86	VAL	ILE	ENGINEERED MUTATION	UNP P60568
H	92	PHE	ILE	ENGINEERED MUTATION	UNP P60568

- Molecule 1: Interleukin-2



- Molecule 1: Interleukin-2

Chain E: 



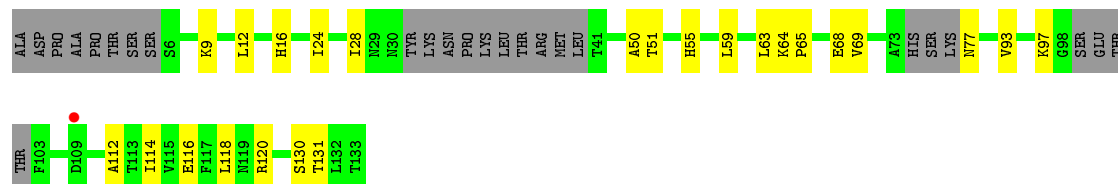
- Molecule 1: Interleukin-2

Chain F: 



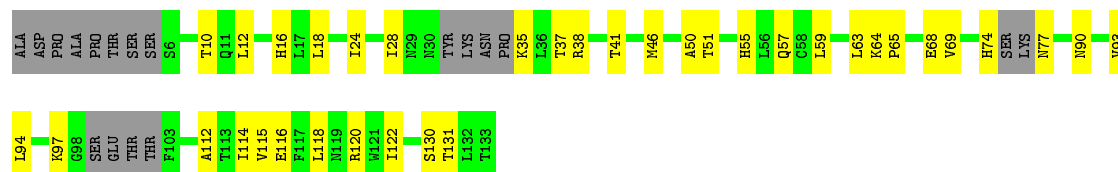
- Molecule 1: Interleukin-2

Chain G: 



- Molecule 1: Interleukin-2

Chain H: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	55.87Å 75.02Å 76.81Å 101.46° 102.29° 104.31°	Depositor
Resolution (Å)	42.40 – 3.10 42.40 – 3.09	Depositor EDS
% Data completeness (in resolution range)	97.4 (42.40-3.10) 89.4 (42.40-3.09)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.33 (at 3.06Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_621)	Depositor
R, R_{free}	0.221 , 0.263 0.222 , 0.262	Depositor DCC
R_{free} test set	1044 reflections (5.42%)	DCC
Wilson B-factor (Å ²)	82.1	Xtriage
Anisotropy	0.317	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 44.2	EDS
Estimated twinning fraction	0.008 for -h,-l,-k	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 20373 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7786	wwPDB-VP
Average B, all atoms (Å ²)	84.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.92% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	0.46	0/1041	0.54	0/1404
1	B	0.44	0/1041	0.54	0/1404
1	C	0.45	0/991	0.52	0/1335
1	D	0.43	0/916	0.53	0/1234
1	E	0.44	0/975	0.52	0/1314
1	F	0.41	0/1041	0.55	0/1404
1	G	0.41	0/924	0.53	0/1245
1	H	0.44	0/986	0.53	0/1327
All	All	0.44	0/7915	0.53	0/10667

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 [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	1022	0	1042	33	0
1	B	1022	0	1042	17	0
1	C	976	0	993	29	0
1	D	902	0	910	17	0
1	E	961	0	981	30	0
1	F	1022	0	1042	32	0
1	G	910	0	916	14	0
1	H	971	0	987	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	7786	0	7913	183	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 12.

The worst 5 of 183 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:33:ASN:HB3	1:C:34:PRO:HD2	1.36	1.03
1:C:39:MET:HG3	1:C:72:LEU:HB3	1.43	0.97
1:E:33:ASN:HB3	1:E:34:PRO:HD2	1.49	0.93
1:C:43:LYS:O	1:F:38:ARG:HD3	1.75	0.86
1:C:33:ASN:HB3	1:C:34:PRO:CD	2.06	0.85

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	120/136 (88%)	114 (95%)	6 (5%)	0	100	100
1	B	120/136 (88%)	116 (97%)	4 (3%)	0	100	100
1	C	111/136 (82%)	106 (96%)	4 (4%)	1 (1%)	21	61
1	D	102/136 (75%)	99 (97%)	3 (3%)	0	100	100
1	E	109/136 (80%)	105 (96%)	4 (4%)	0	100	100
1	F	120/136 (88%)	116 (97%)	4 (3%)	0	100	100
1	G	103/136 (76%)	101 (98%)	2 (2%)	0	100	100
1	H	110/136 (81%)	107 (97%)	3 (3%)	0	100	100
All	All	895/1088 (82%)	864 (96%)	30 (3%)	1 (0%)	56	88

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	34	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	118/128 (92%)	118 (100%)	0	100	100
1	B	118/128 (92%)	115 (98%)	3 (2%)	55	84
1	C	113/128 (88%)	112 (99%)	1 (1%)	84	94
1	D	104/128 (81%)	104 (100%)	0	100	100
1	E	112/128 (88%)	111 (99%)	1 (1%)	84	94
1	F	118/128 (92%)	118 (100%)	0	100	100
1	G	105/128 (82%)	103 (98%)	2 (2%)	65	87
1	H	112/128 (88%)	110 (98%)	2 (2%)	66	88
All	All	900/1024 (88%)	891 (99%)	9 (1%)	82	93

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	35	LYS
1	H	130	SER
1	G	130	SER
1	B	131	THR
1	G	77	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	GLN
1	C	33	ASN
1	H	57	GLN

5.3.3 RNA ⓘ

There are no RNA molecules 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 ⓘ

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 [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	124/136 (91%)	-0.24	0 100 100	52, 83, 114, 149	0
1	B	124/136 (91%)	-0.20	1 (0%) 87 75	54, 83, 118, 151	0
1	C	119/136 (87%)	-0.19	0 100 100	55, 81, 114, 145	0
1	D	110/136 (80%)	-0.16	2 (1%) 71 50	55, 80, 115, 149	0
1	E	117/136 (86%)	-0.07	3 (2%) 59 35	53, 83, 120, 147	0
1	F	124/136 (91%)	-0.16	6 (4%) 34 15	56, 85, 133, 175	0
1	G	111/136 (81%)	-0.13	1 (0%) 85 72	55, 79, 119, 147	0
1	H	118/136 (86%)	-0.29	0 100 100	56, 84, 129, 175	0
All	All	947/1088 (87%)	-0.18	13 (1%) 78 60	52, 82, 128, 175	0

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	36	LEU	3.8
1	G	109	ASP	3.5
1	F	75	SER	3.0
1	D	103	PHE	2.9
1	E	42	PHE	2.7

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

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.