



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 1Y6K
Title : Crystal structure of human IL-10 complexed with the soluble IL-10R1 chain
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Deposited on : 2004-12-06
Resolution : 2.52 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

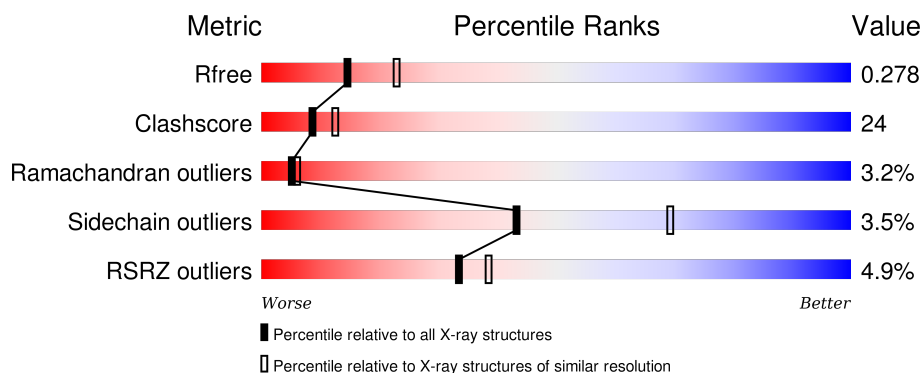
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 2.52 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	4241 (2.54-2.50)
Clashscore	102246	4968 (2.54-2.50)
Ramachandran outliers	100387	4873 (2.54-2.50)
Sidechain outliers	100360	4875 (2.54-2.50)
RSRZ outliers	91569	4253 (2.54-2.50)

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	L	160	
2	R	214	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2888 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-10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	145	Total	C	N	O	S	0	0	0
			1194	760	205	218	11			

- Molecule 2 is a protein called Interleukin-10 receptor alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	R	205	Total	C	N	O	S	0	0	0
			1647	1049	283	309	6			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	29	GLN	ASN	ENGINEERED	UNP Q13651
R	53	GLN	ASN	ENGINEERED	UNP Q13651
R	89	GLN	ASN	ENGINEERED	UNP Q13651
R	133	GLN	ASN	ENGINEERED	UNP Q13651
R	156	GLN	ASN	ENGINEERED	UNP Q13651
R	168	GLN	ASN	ENGINEERED	UNP Q13651

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	L	9	Total	O	0	0
			9	9		
3	R	38	Total	O	0	0
			38	38		

4 Data and refinement statistics

Property	Value	Source
Space group	P 32 1 2	Depositor
Cell constants a, b, c, α , β , γ	46.44Å 46.44Å 309.25Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.52 34.36 – 2.52	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.52) 84.6 (34.36-2.52)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.61 (at 2.51Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.229 , 0.279 0.227 , 0.278	Depositor DCC
R_{free} test set	661 reflections (5.82%)	DCC
Wilson B-factor (Å ²)	49.5	Xtriage
Anisotropy	0.308	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 48.4	EDS
Estimated twinning fraction	0.094 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 11365 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	2888	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.11% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	L	0.35	0/1216	0.57	0/1630
2	R	0.43	0/1693	0.69	0/2301
All	All	0.40	0/2909	0.64	0/3931

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	L	1194	0	1190	49	0
2	R	1647	0	1592	85	0
3	L	9	0	0	0	0
3	R	38	0	0	4	0
All	All	2888	0	2782	133	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 24.

The worst 5 of 133 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:R:191:ARG:HD2	3:R:236:HOH:O	1.60	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:143:PHE:HB3	2:R:189:ALA:HB3	1.54	0.90
2:R:172:LEU:HD23	2:R:172:LEU:H	1.39	0.87
2:R:177:VAL:HG22	2:R:178:GLY:H	1.37	0.86
2:R:68:ASP:OD2	2:R:75:TYR:OH	1.94	0.83

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	L	143/160 (89%)	124 (87%)	13 (9%)	6 (4%)	3	3
2	R	203/214 (95%)	183 (90%)	15 (7%)	5 (2%)	7	10
All	All	346/374 (92%)	307 (89%)	28 (8%)	11 (3%)	5	6

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	109	HIS
1	L	110	ARG
2	R	115	ASN
2	R	174	SER
1	L	17	GLY

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	L	132/145 (91%)	127 (96%)	5 (4%)	40	65
2	R	185/194 (95%)	179 (97%)	6 (3%)	46	73
All	All	317/339 (94%)	306 (96%)	11 (4%)	43	69

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	59	TYR
2	R	16	GLU
2	R	133	GLN
1	L	55	ASP
2	R	126	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	L	132	GLN
2	R	53	GLN
2	R	156	GLN
1	L	129	ASN
2	R	110	ASN

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 [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	L	145/160 (90%)	0.38	8 (5%)	29 33	39, 61, 96, 113	0
2	R	205/214 (95%)	0.13	9 (4%)	38 43	25, 43, 77, 92	0
All	All	350/374 (93%)	0.24	17 (4%)	33 38	25, 50, 87, 113	0

The worst 5 of 17 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	14	HIS	5.5
2	R	175	GLY	4.6
2	R	206	THR	4.1
1	L	110	ARG	4.1
2	R	174	SER	4.1

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 [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.