

# Full wwPDB X-ray Structure Validation Report (i)

#### Oct 4, 2023 – 07:35 AM EDT

PDB ID : 6P50

Title : Crystal Structure of a Complex of human IL-7Ralpha with an anti-IL-7Ralpha

Fab 4A10

Authors: Walsh, S.T.R.; Kashi, L.; Kohnhorst, C.L.

Deposited on : 2019-05-29

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.orgA 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:

Mol Probity : 4.02b-467

Mogul: 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS : 2.35.1

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$ 

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

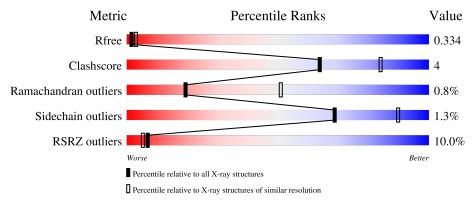
Validation Pipeline (wwPDB-VP) : 2.35.1

## 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	Similar resolution		
Metric	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$		
$R_{free}$	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	С	223	31%	9%	60%		_		
2	Н	225	8%	89%		9%	-		
3	L	213	10%	86%		13%			



# 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 3990 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-7 receptor subunit alpha.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	С	90	Total 679	C 440	N 110	O 123	S 6	0	0	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference	
С	-3	GLY	-	expression tag	UNP P16871	
С	-2	SER	-	expression tag	UNP P16871	
С	-1	HIS	-	expression tag	UNP P16871	
С	0	MET	-	expression tag	UNP P16871	
С	46	THR	ILE	conflict	UNP P16871	

• Molecule 2 is a protein called anti-IL-7R 4A10 Fab heavy chain.

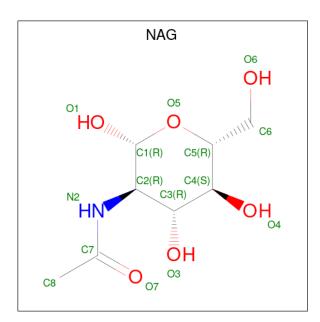
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	Н	221	Total 1668	C 1059	N 269	O 331	S	0	0	0

• Molecule 3 is a protein called anti-IL-7R 4A10 Fab light chain.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
3	L	211	Total 1629	C 1019	N 278	O 326	S 6	0	0	0

• Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).





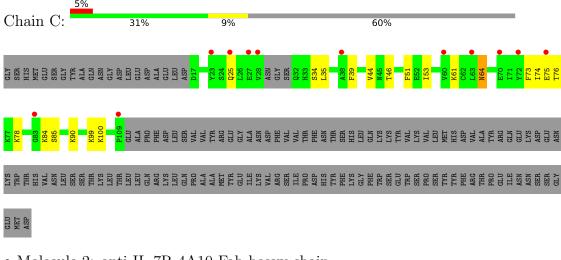
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	С	1	Total	С	N	Ō	0	0
			14	8	Ţ	5		



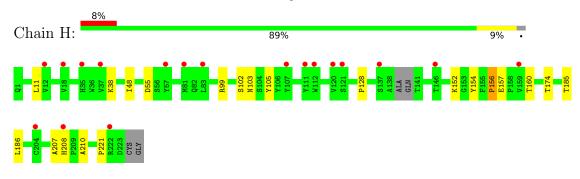
# 3 Residue-property plots (i)

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.

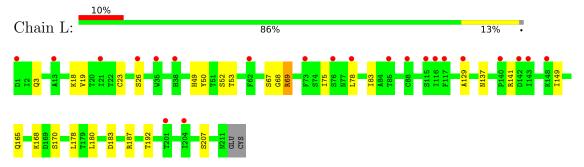
• Molecule 1: Interleukin-7 receptor subunit alpha



• Molecule 2: anti-IL-7R 4A10 Fab heavy chain



• Molecule 3: anti-IL-7R 4A10 Fab light chain





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	145.11Å 40.17Å 105.10Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 105.48° 90.00°	Depositor
Resolution (Å)	38.61 - 2.90	Depositor
Resolution (A)	38.61 - 2.90	EDS
% Data completeness	96.0 (38.61-2.90)	Depositor
(in resolution range)	96.4 (38.61-2.90)	EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.33 (at 2.90Å)	Xtriage
Refinement program	PHENIX 1.16rc1_3535	Depositor
P. P.	0.285 , 0.330	Depositor
$R, R_{free}$	0.286 , $0.334$	DCC
$R_{free}$ test set	644 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	62.5	Xtriage
Anisotropy	0.506	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.32, 55.8	EDS
L-test for twinning <sup>2</sup>	$ < L >=0.43, < L^2>=0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	3990	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.00% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 5 Model quality (i)

### 5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG

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		
MIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	С	0.24	0/689	0.45	0/931	
2	Н	0.25	0/1714	0.44	0/2345	
3	L	0.24	0/1667	0.45	0/2265	
All	All	0.24	0/4070	0.44	0/5541	

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	С	679	0	664	10	0
2	Н	1668	0	1603	12	0
3	L	1629	0	1564	13	0
4	С	14	0	13	0	0
All	All	3990	0	3844	33	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.

All (33) 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:H:11:LEU:HD22	2:H:156:PRO:HG3	1.70	0.71
2:H:99:ARG:NH2	2:H:102:SER:O	2.32	0.62
3:L:18:LYS:HA	3:L:75:ILE:O	2.01	0.60
3:L:49:HIS:O	3:L:53:THR:OG1	2.19	0.59
3:L:165:GLN:NE2	3:L:170:SER:OG	2.36	0.58
1:C:73:PHE:HE1	1:C:75:GLU:HB2	1.69	0.57
2:H:38:LYS:HB2	2:H:48:ILE:HD11	1.86	0.57
1:C:76:THR:HG22	1:C:78:LYS:H	1.71	0.56
1:C:51:PHE:O	1:C:64:ASN:ND2	2.41	0.53
2:H:152:LYS:HG2	2:H:185:THR:HG23	1.91	0.53
3:L:67:SER:O	3:L:69:ARG:N	2.42	0.52
1:C:99:LYS:HD3	1:C:100:LYS:H	1.74	0.51
3:L:149:ILE:HD11	3:L:178:LEU:HD21	1.94	0.49
3:L:19:VAL:HG13	3:L:78:LEU:HD11	1.94	0.48
3:L:183:ASP:O	3:L:187:ARG:HG3	2.14	0.48
1:C:35:LEU:HB3	1:C:74:ILE:HG23	1.96	0.48
3:L:83:ILE:HG21	3:L:165:GLN:HB3	1.96	0.47
2:H:128:PRO:HA	2:H:154:TYR:HB3	1.97	0.47
3:L:50:TYR:O	3:L:52:SER:N	2.44	0.47
2:H:208:HIS:CE1	2:H:210:ALA:HB3	2.50	0.47
1:C:44:VAL:HG12	1:C:46:THR:H	1.80	0.46
2:H:174:THR:HG23	2:H:186:LEU:HD21	1.97	0.45
1:C:25:GLN:HB2	1:C:34:SER:OG	2.16	0.45
3:L:192:THR:HG23	3:L:207:SER:HB2	1.99	0.44
1:C:53:ILE:HD11	1:C:85:SER:HB3	2.00	0.43
2:H:55:ASP:OD1	2:H:55:ASP:N	2.52	0.43
1:C:90:LYS:HE3	2:H:103:ASN:ND2	2.34	0.43
2:H:156:PRO:HB2	2:H:157:GLU:H	1.72	0.41
2:H:160:THR:OG1	2:H:207:ALA:HB3	2.20	0.41
3:L:129:ALA:O	3:L:180:LEU:N	2.54	0.41
1:C:84:LYS:O	2:H:105:TYR:OH	2.33	0.41
3:L:168:LYS:C	3:L:170:SER:H	2.24	0.40
3:L:3:GLN:HB3	3:L:26:SER:HB3	2.03	0.40

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	Favoured Allowed		Percentiles		
1	C	86/223 (39%)	75 (87%)	11 (13%)	0	100	100	
2	Н	$217/225 \ (96\%)$	202 (93%)	13 (6%)	2 (1%)	17	48	
3	L	209/213 (98%)	191 (91%)	16 (8%)	2 (1%)	15	45	
All	All	512/661 (78%)	468 (91%)	40 (8%)	4 (1%)	19	51	

#### All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	L	68	GLY
2	Н	221	PRO
3	L	137	ASN
2	Н	156	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	C	74/204~(36%)	71 (96%)	3 (4%)	30	64
2	Н	188/195 (96%)	188 (100%)	0	100	100
3	L	183/189 (97%)	180 (98%)	3 (2%)	62	86
All	All	445/588 (76%)	439 (99%)	6 (1%)	69	90

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	С	39	PHE
1	С	61	LYS
1	С	64	ASN
3	L	23	CYS
3	L	69	ARG

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Mol	Chain	Res	Type
3	L	141	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	С	64	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)

1 ligand is 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	Bo	ond leng	$ ag{ths}$	В	ond ang	les
IVIOI	туре	Chain	rtes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	NAG	С	301	1	14,14,15	0.26	0	17,19,21	0.46	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
4	NAG	С	301	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	С	301	NAG	O5-C5-C6-O6
4	С	301	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

### 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,  $95^{th}$  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	С	90/223~(40%)	1.11	12 (13%) 3 2	66, 82, 104, 127	0
2	Н	221/225 (98%)	0.75	18 (8%) 12 9	38, 66, 94, 121	0
3	L	211/213 (99%)	0.81	22 (10%) 6 5	35, 68, 92, 107	0
All	All	522/661 (78%)	0.84	52 (9%) 7 5	35, 70, 98, 127	0

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	С	109	PRO	5.6
1	С	70	GLU	5.0
3	L	13	ALA	4.1
3	L	129	ALA	4.1
1	С	28	VAL	3.8
3	L	85	THR	3.4
1	С	23	TYR	3.3
1	С	75	GLU	3.3
3	L	35	TRP	3.3
3	L	142	ASP	3.2
1	С	38	ALA	3.1
2	Н	18	VAL	3.1
1	С	27	GLU	3.1
2	Н	37	VAL	3.0
3	L	117	PHE	3.0
1	С	25	GLN	3.0
1	С	83	GLY	2.9
3	L	78	LEU	2.9
3	L	201	THR	2.8
3	L	116	ILE	2.8
2	Н	120	VAL	2.8
3	L	204	ILE	2.7
1	С	60	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
1	С	63	LEU	2.7
3	L	115	SER	2.6
1	С	72	TYR	2.6
3	L	1	ASP	2.6
2	Н	208	HIS	2.5
3	L	88	CYS	2.4
3	L	21	ILE	2.4
3	L	143	ILE	2.4
2	Н	222	ARG	2.3
3	L	62	PHE	2.3
3	L	76	SER	2.3
2	Н	35	HIS	2.3
2	Н	112	TRP	2.3
2	Н	111	TYR	2.3
3	L	73	PHE	2.2
2	Н	137	SER	2.2
2	Н	159	VAL	2.2
2	Н	121	SER	2.2
2	Н	204	CYS	2.1
2	Н	81	MET	2.1
3	L	148	LYS	2.1
3	L	140	PRO	2.1
2	Н	57	TYR	2.1
2	Н	146	THR	2.1
3	L	38	HIS	2.0
2	Н	12	VAL	2.0
3	L	26	SER	2.0
2	Н	107	TYR	2.0
2	Н	83	LEU	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)

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. The B-factors column lists the minimum, median,  $95^{th}$  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	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
4	NAG	С	301	14/15	0.74	0.25	76,81,86,88	0

### 6.5 Other polymers (i)

There are no such residues in this entry.

