



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 11:08 PM GMT

PDB ID : 1WIP  
Title : STRUCTURE OF T-CELL SURFACE GLYCOPROTEIN CD4, MONO-CLINIC CRYSTAL FORM  
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Deposited on : 1996-12-18  
Resolution : 4.00 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](mailto: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.

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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) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

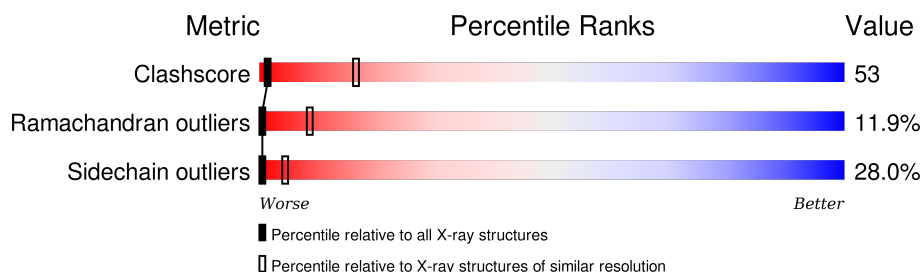
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 4.00 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))
Clashscore	102246	1052 (4.40-3.60)
Ramachandran outliers	100387	1005 (4.40-3.60)
Sidechain outliers	100360	1013 (4.42-3.58)

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  $\geq 3$ , 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	363	
1	B	363	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 5624 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 T-CELL SURFACE GLYCOPROTEIN CD4.

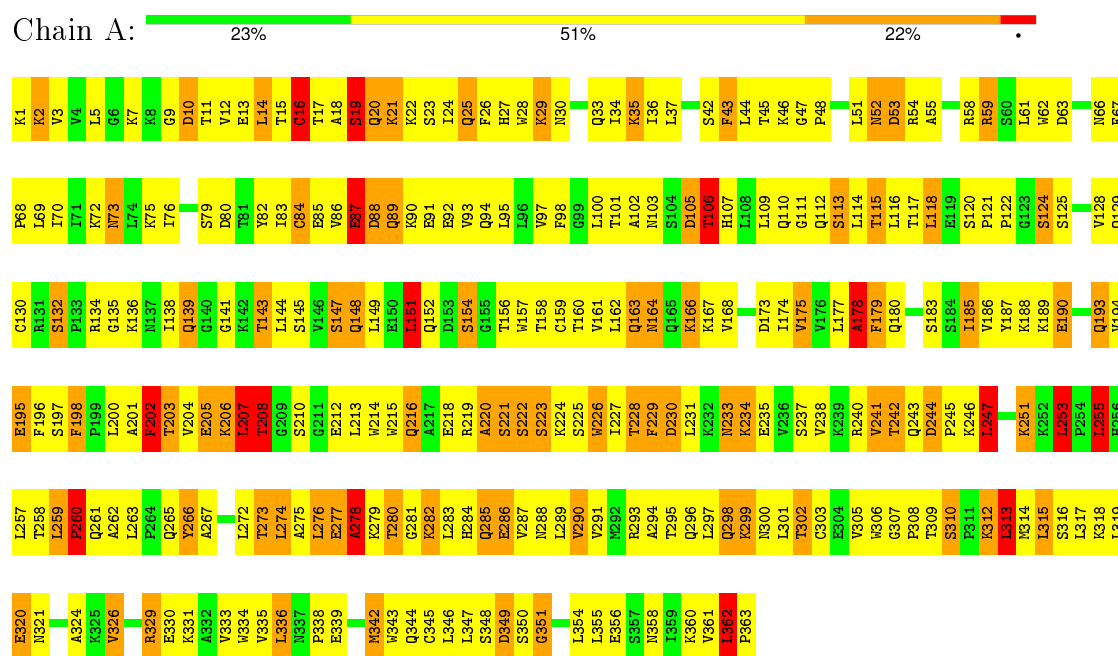
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	363	Total	C	N	O	S	0	0	0
			2812	1784	479	539	10			
1	B	363	Total	C	N	O	S	0	0	0
			2812	1784	479	539	10			

### 3 Residue-property plots

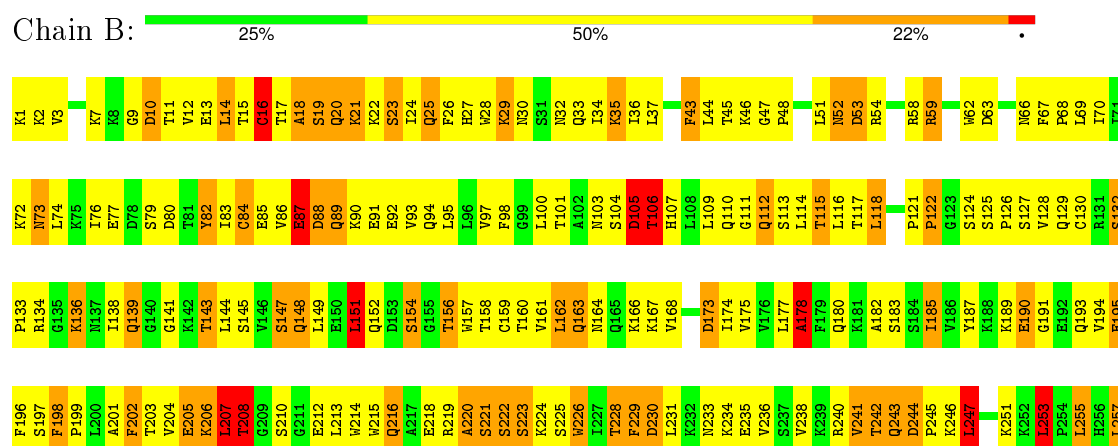
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

#### • Molecule 1: T-CELL SURFACE GLYCOPROTEIN CD4



#### • Molecule 1: T-CELL SURFACE GLYCOPROTEIN CD4



T258	A324
L259	K325
P260	V326
Q261	
A262	R329
L263	E330
	K331
Y266	A332
	V333
M271	M334
L272	V335
T273	L336
L274	M337
A275	P338
L276	E339
E277	
A278	M342
	M343
K279	Q344
T280	C345
G281	L346
K282	L347
L283	S348
H284	D349
Q285	S350
F286	G351
V287	
N288	L354
	L355
L289	
V290	M358
V291	I359
M292	K360
R293	V361
A294	L362
T295	P363
Q296	
L297	
L298	
Q299	
M300	
L301	
T302	
C303	
E304	
V305	
M306	
E307	
P308	
T309	
S310	
P311	
K312	
L313	
M314	
L315	
S316	
L317	
K318	
L319	
E320	
M321	

## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	100.50 Å   123.40 Å   100.60 Å 90.00°   103.40°   90.00°	Depositor
Resolution (Å)	8.00 – 4.00	Depositor
% Data completeness (in resolution range)	76.0 (8.00-4.00)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, $R_{free}$	0.452 , 0.427	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5624	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	20.0	wwPDB-VP

## 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	0.73	2/2861 (0.1%)	1.11	14/3871 (0.4%)
1	B	0.68	1/2861 (0.0%)	1.02	10/3871 (0.3%)
All	All	0.71	3/5722 (0.1%)	1.07	24/7742 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
All	All	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	178	ALA	C-N	10.32	1.57	1.34
1	A	202	PHE	C-O	-5.16	1.13	1.23
1	A	290	VAL	CB-CG1	5.07	1.63	1.52

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	178	ALA	O-C-N	-23.02	85.88	122.70
1	B	178	ALA	O-C-N	-9.52	107.47	122.70
1	B	208	THR	N-CA-C	8.38	133.62	111.00
1	A	208	THR	N-CA-C	7.53	131.33	111.00
1	A	277	GLU	O-C-N	7.00	133.91	122.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	178	ALA	Mainchain
1	B	178	ALA	Mainchain

## 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	2812	0	2873	296	19
1	B	2812	0	2873	316	19
All	All	5624	0	5746	602	19

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 53.

The worst 5 of 602 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:B:112:GLN:OE1	1:B:281:GLY:CA	1.68	1.41
1:A:109:LEU:HD23	1:A:283:LEU:CD2	1.67	1.22
1:B:112:GLN:OE1	1:B:281:GLY:HA3	1.44	1.14
1:B:276:LEU:HD23	1:B:276:LEU:N	1.63	1.11
1:A:276:LEU:CD2	1:A:276:LEU:H	1.63	1.09

The worst 5 of 19 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:9:GLY:O	1:B:73:ASN:OD1[2_867]	0.59	1.61
1:A:73:ASN:ND2	1:B:73:ASN:CA[2_867]	0.99	1.21
1:A:73:ASN:OD1	1:B:9:GLY:O[2_867]	1.06	1.14
1:A:73:ASN:OD1	1:B:9:GLY:C[2_867]	1.27	0.93
1:A:9:GLY:C	1:B:73:ASN:OD1[2_867]	1.58	0.62



## 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	361/363 (99%)	259 (72%)	58 (16%)	44 (12%)	0	8
1	B	361/363 (99%)	260 (72%)	59 (16%)	42 (12%)	0	9
All	All	722/726 (99%)	519 (72%)	117 (16%)	86 (12%)	0	8

5 of 86 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	21	LYS
1	A	52	ASN
1	A	73	ASN
1	A	87	GLU
1	A	88	ASP

### 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	318/324 (98%)	227 (71%)	91 (29%)	0	4
1	B	318/324 (98%)	231 (73%)	87 (27%)	0	5
All	All	636/648 (98%)	458 (72%)	178 (28%)	0	4

5 of 178 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	313	LEU

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Mol	Chain	Res	Type
1	B	25	GLN
1	B	305	VAL
1	A	316	SER
1	A	362	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	344	GLN
1	B	20	GLN
1	B	344	GLN
1	A	358	ASN
1	B	66	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 carbohydrates 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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.