



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 12, 2021 – 04:02 PM EDT

PDB ID : 7N1F  
Title : SARS-CoV-2 YLQ peptide-specific TCR pYLQ7 binds to YLQ-HLA-A2  
Authors : Wu, D.; Mariuzza, R.A.  
Deposited on : 2021-05-27  
Resolution : 2.39 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

<https://www.wwpdb.org/validation/2017/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  
Xtriage (Phenix) : 1.13  
EDS : 2.23.1  
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) : 2.23.1

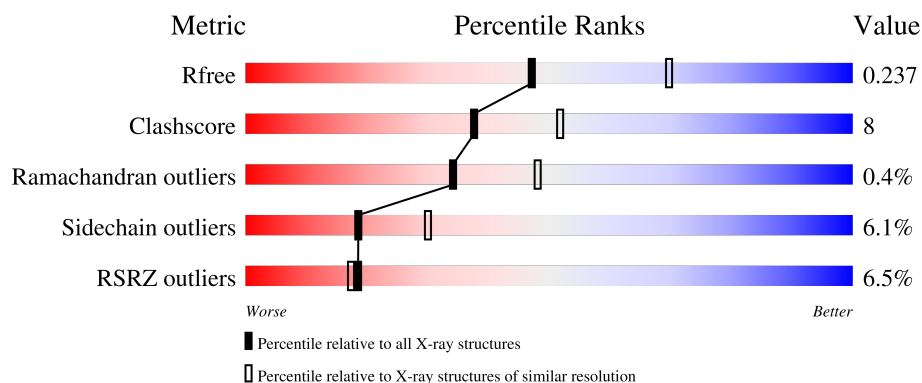
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.39 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	D	204	<div> <div>7%</div> <div> <div></div> <div>73%</div> <div>20%</div> <div>.</div> <div>.</div> </div> </div>
2	E	242	<div> <div>2%</div> <div> <div></div> <div>83%</div> <div>14%</div> <div>.</div> <div>.</div> </div> </div>
3	A	275	<div> <div>12%</div> <div> <div></div> <div>80%</div> <div>17%</div> <div>.</div> <div>.</div> </div> </div>
4	B	100	<div> <div>%</div> <div> <div></div> <div>85%</div> <div>14%</div> <div>.</div> </div> </div>
5	C	9	<div> <div></div> <div> <div></div> <div>78%</div> <div>22%</div> </div> </div>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6654 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 pYLQ7 T cell receptor alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	197	Total	C	N	O	S	0	0	0
			1542	963	259	312	8			

- Molecule 2 is a protein called pYLQ7 T cell receptor beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	240	Total	C	N	O	S	0	0	0
			1934	1213	345	370	6			

- Molecule 3 is a protein called MHC class I antigen, A-2 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	272	Total	C	N	O	S	0	0	0
			2180	1366	393	412	9			

- Molecule 4 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	B	100	Total	C	N	O	S	0	0	0
			829	528	140	157	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	initiating methionine	UNP P61769

- Molecule 5 is a protein called Spike protein S1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	C	9	Total	C	N	O	0	0	0
			82	56	13	13			

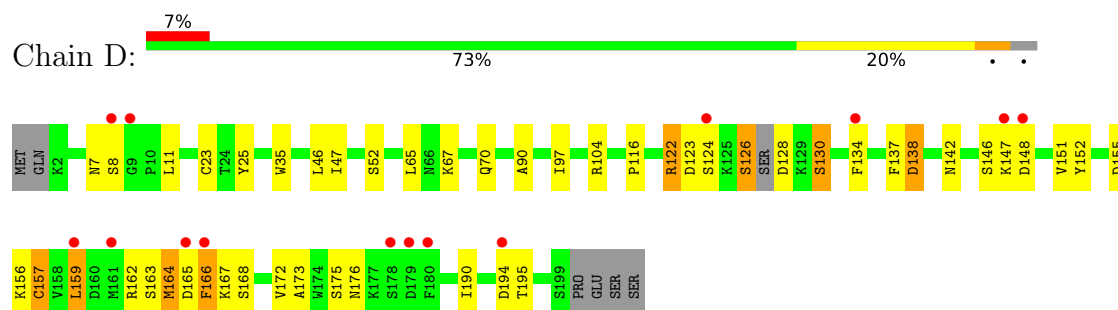
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	D	14	Total 14	O 14	0	0
6	E	26	Total 26	O 26	0	0
6	A	31	Total 31	O 31	0	0
6	B	13	Total 13	O 13	0	0
6	C	3	Total 3	O 3	0	0

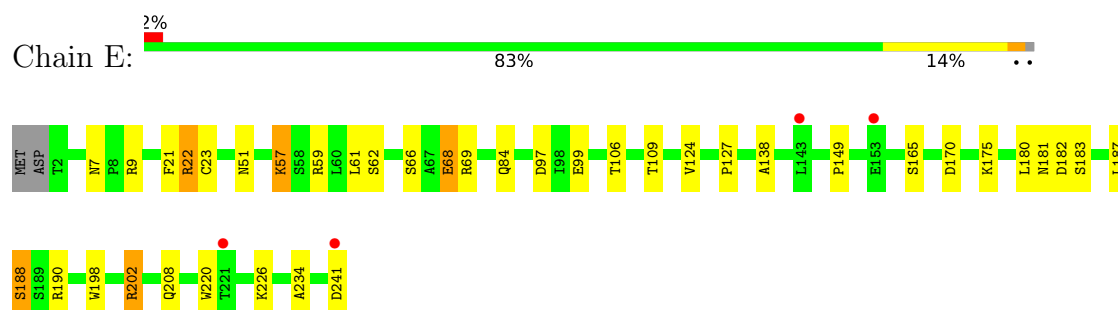
### 3 Residue-property plots [i](#)

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.

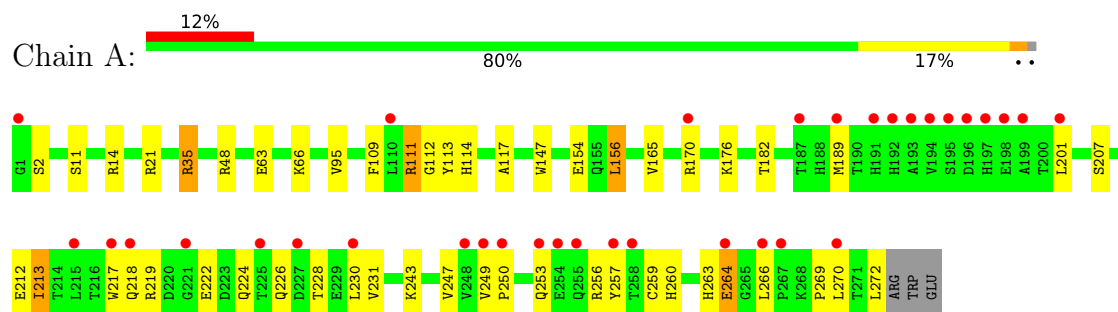
- Molecule 1: pYLQ7 T cell receptor alpha chain



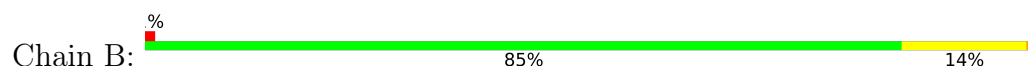
- Molecule 2: pYLQ7 T cell receptor beta chain

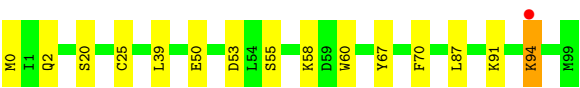


- Molecule 3: MHC class I antigen, A-2 alpha chain

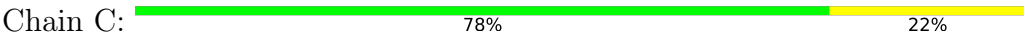


- Molecule 4: Beta-2-microglobulin





● Molecule 5: Spike protein S1



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	225.33Å 49.07Å 91.45Å 90.00° 91.81° 90.00°	Depositor
Resolution (Å)	48.63 – 2.39 48.63 – 2.39	Depositor EDS
% Data completeness (in resolution range)	99.0 (48.63-2.39) 99.0 (48.63-2.39)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.07 (at 2.39Å)	Xtriage
Refinement program	PHENIX 1.16_3549	Depositor
R, $R_{free}$	0.197 , 0.236 0.200 , 0.237	Depositor DCC
$R_{free}$ test set	1987 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	48.3	Xtriage
Anisotropy	0.885	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 40.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.017 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	6654	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.21% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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	D	0.50	0/1574	0.68	2/2130 (0.1%)
2	E	0.45	0/1986	0.56	0/2700
3	A	0.48	0/2243	0.60	0/3049
4	B	0.42	0/852	0.62	0/1153
5	C	0.48	0/84	0.65	0/112
All	All	0.47	0/6739	0.61	2/9144 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	7	ASN	CB-CA-C	5.39	121.19	110.40
1	D	164	MET	C-N-CA	5.08	134.40	121.70

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	D	1542	0	1455	34	6
2	E	1934	0	1835	29	2
3	A	2180	0	2022	36	6
4	B	829	0	788	6	2
5	C	82	0	88	2	0
6	A	31	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	13	0	0	1	0
6	C	3	0	0	0	0
6	D	14	0	0	1	0
6	E	26	0	0	3	0
All	All	6654	0	6188	98	8

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 8.

The worst 5 of 98 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)
3:A:182:THR:OG1	3:A:264:GLU:OE2	1.63	1.12
1:D:164:MET:O	6:D:301:HOH:O	1.89	0.90
2:E:208:GLN:OE1	6:E:301:HOH:O	1.89	0.89
1:D:151:VAL:HG12	1:D:175:SER:HB2	1.53	0.88
3:A:182:THR:CB	3:A:264:GLU:OE2	2.35	0.75

The worst 5 of 8 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:D:194:ASP:OD1	3:A:170:ARG:NH1[2_555]	1.20	1.00
1:D:194:ASP:OD1	3:A:170:ARG:CZ[2_555]	1.41	0.79
1:D:194:ASP:OD1	3:A:170:ARG:NH2[2_555]	1.50	0.70
1:D:194:ASP:CG	3:A:170:ARG:NH2[2_555]	1.55	0.65
2:E:68:GLU:OE1	4:B:94:LYS:NZ[4_545]	1.55	0.65

## 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	D	193/204 (95%)	182 (94%)	9 (5%)	2 (1%)	15	23
2	E	238/242 (98%)	228 (96%)	10 (4%)	0	100	100
3	A	270/275 (98%)	263 (97%)	6 (2%)	1 (0%)	34	48
4	B	98/100 (98%)	95 (97%)	3 (3%)	0	100	100
5	C	7/9 (78%)	7 (100%)	0	0	100	100
All	All	806/830 (97%)	775 (96%)	28 (4%)	3 (0%)	34	48

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	156	LYS
1	D	157	CYS
3	A	269	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	D	175/184 (95%)	160 (91%)	15 (9%)	10	16
2	E	211/214 (99%)	201 (95%)	10 (5%)	26	42
3	A	221/231 (96%)	209 (95%)	12 (5%)	22	36
4	B	93/95 (98%)	87 (94%)	6 (6%)	17	27
5	C	9/9 (100%)	9 (100%)	0	100	100
All	All	709/733 (97%)	666 (94%)	43 (6%)	18	30

5 of 43 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	113	TYR
3	A	226	GLN
3	A	156	LEU
3	A	207	SER
4	B	0	MET

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

Mol	Chain	Res	Type
2	E	181	ASN
3	A	224	GLN
3	A	262	GLN

### 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](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	D	197/204 (96%)	0.45	14 (7%) 16 14	38, 59, 97, 109	0
2	E	240/242 (99%)	0.21	4 (1%) 70 68	37, 59, 86, 95	0
3	A	272/275 (98%)	0.76	34 (12%) 3 3	37, 58, 128, 138	0
4	B	100/100 (100%)	0.30	1 (1%) 82 80	41, 53, 75, 87	0
5	C	9/9 (100%)	0.16	0 100 100	39, 42, 48, 50	0
All	All	818/830 (98%)	0.46	53 (6%) 18 17	37, 58, 106, 138	0

The worst 5 of 53 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	A	193	ALA	7.1
3	A	199	ALA	6.8
3	A	266	LEU	6.7
3	A	257	TYR	6.6
3	A	194	VAL	6.0

### 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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.