



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 08:22 AM GMT

PDB ID : 3E3Q
Title : Structure of the 3alpham13 high-affinity mutant of the 2C TCR in complex with Ld/QL9
Authors : Colf, L.A.; Garcia, K.C.
Deposited on : 2008-08-07
Resolution : 2.95 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

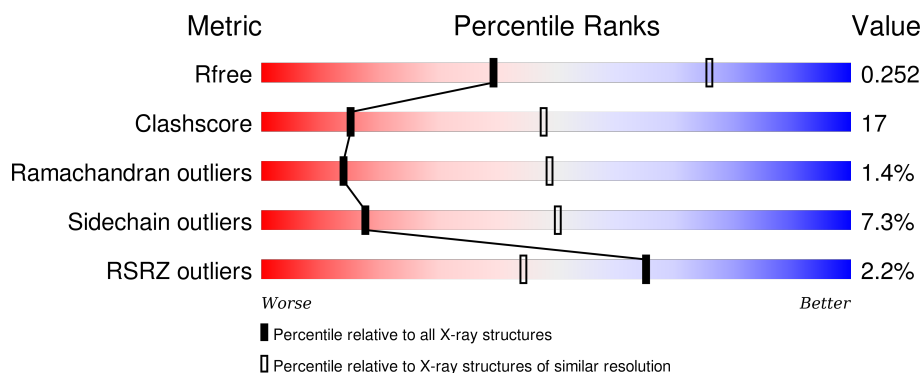
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.95 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	2184 (3.00-2.92)
Clashscore	102246	2552 (3.00-2.92)
Ramachandran outliers	100387	2468 (3.00-2.92)
Sidechain outliers	100360	2471 (3.00-2.92)
RSRZ outliers	91569	2201 (3.00-2.92)

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	175	<div> <div>3%</div> <div>66%</div> <div>27%</div> <div>5%</div> </div>
1	B	175	<div> <div>3%</div> <div>69%</div> <div>26%</div> <div>• •</div> </div>
1	H	175	<div> <div>5%</div> <div>66%</div> <div>29%</div> <div>• •</div> </div>
1	L	175	<div> <div>3%</div> <div>65%</div> <div>30%</div> <div>• •</div> </div>
1	P	175	<div> <div>3%</div> <div>69%</div> <div>27%</div> <div>• •</div> </div>

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Mol	Chain	Length	Quality of chain
1	U	175	
1	Y	175	
1	c	175	
2	G	9	
2	K	9	
2	O	9	
2	Q	9	
2	T	9	
2	X	9	
2	b	9	
2	f	9	
3	C	109	
3	D	109	
3	I	109	
3	M	109	
3	R	109	
3	V	109	
3	Z	109	
3	d	109	
4	E	111	
4	F	111	
4	J	111	
4	N	111	
4	S	111	
4	W	111	

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Mol	Chain	Length	Quality of chain
4	a	111	<div><div></div><div>2%</div><div>94%</div><div>6%</div></div>
4	e	111	<div><div></div><div>%</div><div>94%</div><div>6%</div></div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 25808 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 H-2 class I histocompatibility antigen, L-D alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	175	Total	C	N	O	S	0	0	0
			1449	908	257	277	7			
1	B	175	Total	C	N	O	S	0	0	0
			1449	908	257	277	7			
1	c	175	Total	C	N	O	S	0	0	0
			1449	908	257	277	7			
1	H	175	Total	C	N	O	S	0	0	0
			1449	908	257	277	7			
1	L	175	Total	C	N	O	S	0	0	0
			1449	908	257	277	7			
1	P	175	Total	C	N	O	S	0	0	0
			1449	908	257	277	7			
1	U	175	Total	C	N	O	S	0	0	0
			1449	908	257	277	7			
1	Y	175	Total	C	N	O	S	0	0	0
			1449	908	257	277	7			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	8	TYR	PHE	ENGINEERED	UNP P01897
A	12	THR	VAL	ENGINEERED	UNP P01897
A	15	ARG	PRO	ENGINEERED	UNP P01897
A	23	THR	ILE	ENGINEERED	UNP P01897
A	30	ASP	ASN	ENGINEERED	UNP P01897
A	49	VAL	ALA	ENGINEERED	UNP P01897
A	66	VAL	ILE	ENGINEERED	UNP P01897
A	97	ARG	TRP	ENGINEERED	UNP P01897
A	131	ARG	LYS	ENGINEERED	UNP P01897
B	8	TYR	PHE	ENGINEERED	UNP P01897
B	12	THR	VAL	ENGINEERED	UNP P01897
B	15	ARG	PRO	ENGINEERED	UNP P01897
B	23	THR	ILE	ENGINEERED	UNP P01897

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Chain	Residue	Modelled	Actual	Comment	Reference
B	30	ASP	ASN	ENGINEERED	UNP P01897
B	49	VAL	ALA	ENGINEERED	UNP P01897
B	66	VAL	ILE	ENGINEERED	UNP P01897
B	97	ARG	TRP	ENGINEERED	UNP P01897
B	131	ARG	LYS	ENGINEERED	UNP P01897
c	8	TYR	PHE	ENGINEERED	UNP P01897
c	12	THR	VAL	ENGINEERED	UNP P01897
c	15	ARG	PRO	ENGINEERED	UNP P01897
c	23	THR	ILE	ENGINEERED	UNP P01897
c	30	ASP	ASN	ENGINEERED	UNP P01897
c	49	VAL	ALA	ENGINEERED	UNP P01897
c	66	VAL	ILE	ENGINEERED	UNP P01897
c	97	ARG	TRP	ENGINEERED	UNP P01897
c	131	ARG	LYS	ENGINEERED	UNP P01897
H	8	TYR	PHE	ENGINEERED	UNP P01897
H	12	THR	VAL	ENGINEERED	UNP P01897
H	15	ARG	PRO	ENGINEERED	UNP P01897
H	23	THR	ILE	ENGINEERED	UNP P01897
H	30	ASP	ASN	ENGINEERED	UNP P01897
H	49	VAL	ALA	ENGINEERED	UNP P01897
H	66	VAL	ILE	ENGINEERED	UNP P01897
H	97	ARG	TRP	ENGINEERED	UNP P01897
H	131	ARG	LYS	ENGINEERED	UNP P01897
L	8	TYR	PHE	ENGINEERED	UNP P01897
L	12	THR	VAL	ENGINEERED	UNP P01897
L	15	ARG	PRO	ENGINEERED	UNP P01897
L	23	THR	ILE	ENGINEERED	UNP P01897
L	30	ASP	ASN	ENGINEERED	UNP P01897
L	49	VAL	ALA	ENGINEERED	UNP P01897
L	66	VAL	ILE	ENGINEERED	UNP P01897
L	97	ARG	TRP	ENGINEERED	UNP P01897
L	131	ARG	LYS	ENGINEERED	UNP P01897
P	8	TYR	PHE	ENGINEERED	UNP P01897
P	12	THR	VAL	ENGINEERED	UNP P01897
P	15	ARG	PRO	ENGINEERED	UNP P01897
P	23	THR	ILE	ENGINEERED	UNP P01897
P	30	ASP	ASN	ENGINEERED	UNP P01897
P	49	VAL	ALA	ENGINEERED	UNP P01897
P	66	VAL	ILE	ENGINEERED	UNP P01897
P	97	ARG	TRP	ENGINEERED	UNP P01897
P	131	ARG	LYS	ENGINEERED	UNP P01897
U	8	TYR	PHE	ENGINEERED	UNP P01897

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Chain	Residue	Modelled	Actual	Comment	Reference
U	12	THR	VAL	ENGINEERED	UNP P01897
U	15	ARG	PRO	ENGINEERED	UNP P01897
U	23	THR	ILE	ENGINEERED	UNP P01897
U	30	ASP	ASN	ENGINEERED	UNP P01897
U	49	VAL	ALA	ENGINEERED	UNP P01897
U	66	VAL	ILE	ENGINEERED	UNP P01897
U	97	ARG	TRP	ENGINEERED	UNP P01897
U	131	ARG	LYS	ENGINEERED	UNP P01897
Y	8	TYR	PHE	ENGINEERED	UNP P01897
Y	12	THR	VAL	ENGINEERED	UNP P01897
Y	15	ARG	PRO	ENGINEERED	UNP P01897
Y	23	THR	ILE	ENGINEERED	UNP P01897
Y	30	ASP	ASN	ENGINEERED	UNP P01897
Y	49	VAL	ALA	ENGINEERED	UNP P01897
Y	66	VAL	ILE	ENGINEERED	UNP P01897
Y	97	ARG	TRP	ENGINEERED	UNP P01897
Y	131	ARG	LYS	ENGINEERED	UNP P01897

- Molecule 2 is a protein called QL9 peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	Q	9	Total	C	N	O	0	0	0
			76	52	10	14			
2	G	9	Total	C	N	O	0	0	0
			76	52	10	14			
2	f	9	Total	C	N	O	0	0	0
			76	52	10	14			
2	K	9	Total	C	N	O	0	0	0
			76	52	10	14			
2	O	9	Total	C	N	O	0	0	0
			76	52	10	14			
2	T	9	Total	C	N	O	0	0	0
			76	52	10	14			
2	X	9	Total	C	N	O	0	0	0
			76	52	10	14			
2	b	9	Total	C	N	O	0	0	0
			76	52	10	14			

- Molecule 3 is a protein called T-cell receptor alpha chain V region PHDS58.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	109	Total 854	C 550	N 142	O 160	S 2	0	0	0
3	C	109	Total 854	C 550	N 142	O 160	S 2	0	0	0
3	d	109	Total 854	C 550	N 142	O 160	S 2	0	0	0
3	I	109	Total 854	C 550	N 142	O 160	S 2	0	0	0
3	M	109	Total 854	C 550	N 142	O 160	S 2	0	0	0
3	R	109	Total 854	C 550	N 142	O 160	S 2	0	0	0
3	V	109	Total 854	C 550	N 142	O 160	S 2	0	0	0
3	Z	109	Total 854	C 550	N 142	O 160	S 2	0	0	0

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	43	PRO	LEU	ENGINEERED	UNP P01738
D	82	ARG	TRP	ENGINEERED	UNP P01738
D	99	ASP	GLY	ENGINEERED	UNP P01738
D	100	PRO	PHE	ENGINEERED	UNP P01738
D	101	PRO	ALA	ENGINEERED	UNP P01738
D	102	PRO	SER	ENGINEERED	UNP P01738
D	103	LEU	ALA	ENGINEERED	UNP P01738
C	43	PRO	LEU	ENGINEERED	UNP P01738
C	82	ARG	TRP	ENGINEERED	UNP P01738
C	99	ASP	GLY	ENGINEERED	UNP P01738
C	100	PRO	PHE	ENGINEERED	UNP P01738
C	101	PRO	ALA	ENGINEERED	UNP P01738
C	102	PRO	SER	ENGINEERED	UNP P01738
C	103	LEU	ALA	ENGINEERED	UNP P01738
d	43	PRO	LEU	ENGINEERED	UNP P01738
d	82	ARG	TRP	ENGINEERED	UNP P01738
d	99	ASP	GLY	ENGINEERED	UNP P01738
d	100	PRO	PHE	ENGINEERED	UNP P01738
d	101	PRO	ALA	ENGINEERED	UNP P01738
d	102	PRO	SER	ENGINEERED	UNP P01738
d	103	LEU	ALA	ENGINEERED	UNP P01738
I	43	PRO	LEU	ENGINEERED	UNP P01738
I	82	ARG	TRP	ENGINEERED	UNP P01738
I	99	ASP	GLY	ENGINEERED	UNP P01738

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Chain	Residue	Modelled	Actual	Comment	Reference
I	100	PRO	PHE	ENGINEERED	UNP P01738
I	101	PRO	ALA	ENGINEERED	UNP P01738
I	102	PRO	SER	ENGINEERED	UNP P01738
I	103	LEU	ALA	ENGINEERED	UNP P01738
M	43	PRO	LEU	ENGINEERED	UNP P01738
M	82	ARG	TRP	ENGINEERED	UNP P01738
M	99	ASP	GLY	ENGINEERED	UNP P01738
M	100	PRO	PHE	ENGINEERED	UNP P01738
M	101	PRO	ALA	ENGINEERED	UNP P01738
M	102	PRO	SER	ENGINEERED	UNP P01738
M	103	LEU	ALA	ENGINEERED	UNP P01738
R	43	PRO	LEU	ENGINEERED	UNP P01738
R	82	ARG	TRP	ENGINEERED	UNP P01738
R	99	ASP	GLY	ENGINEERED	UNP P01738
R	100	PRO	PHE	ENGINEERED	UNP P01738
R	101	PRO	ALA	ENGINEERED	UNP P01738
R	102	PRO	SER	ENGINEERED	UNP P01738
R	103	LEU	ALA	ENGINEERED	UNP P01738
V	43	PRO	LEU	ENGINEERED	UNP P01738
V	82	ARG	TRP	ENGINEERED	UNP P01738
V	99	ASP	GLY	ENGINEERED	UNP P01738
V	100	PRO	PHE	ENGINEERED	UNP P01738
V	101	PRO	ALA	ENGINEERED	UNP P01738
V	102	PRO	SER	ENGINEERED	UNP P01738
V	103	LEU	ALA	ENGINEERED	UNP P01738
Z	43	PRO	LEU	ENGINEERED	UNP P01738
Z	82	ARG	TRP	ENGINEERED	UNP P01738
Z	99	ASP	GLY	ENGINEERED	UNP P01738
Z	100	PRO	PHE	ENGINEERED	UNP P01738
Z	101	PRO	ALA	ENGINEERED	UNP P01738
Z	102	PRO	SER	ENGINEERED	UNP P01738
Z	103	LEU	ALA	ENGINEERED	UNP P01738

- Molecule 4 is a protein called TCR beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	111	Total	C	N	O	S	0	0	0
			847	523	147	174	3			
4	F	111	Total	C	N	O	S	0	0	0
			847	523	147	174	3			
4	e	111	Total	C	N	O	S	0	0	0
			847	523	147	174	3			

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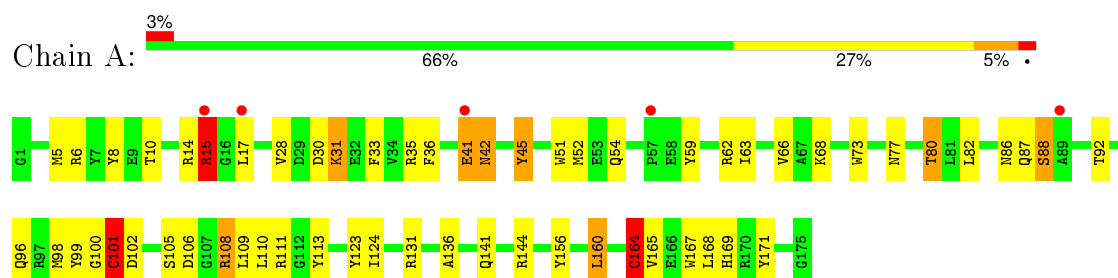
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	J	111	Total 847	C 523	N 147	O 174	S 3	0	0	0
4	N	111	Total 847	C 523	N 147	O 174	S 3	0	0	0
4	S	111	Total 847	C 523	N 147	O 174	S 3	0	0	0
4	W	111	Total 847	C 523	N 147	O 174	S 3	0	0	0
4	a	111	Total 847	C 523	N 147	O 174	S 3	0	0	0

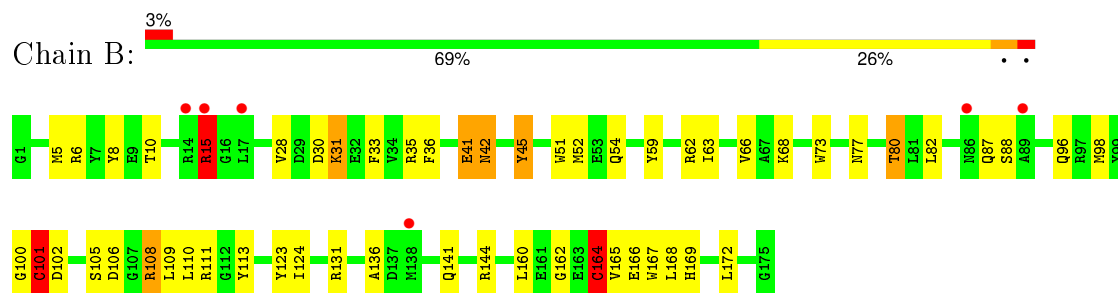
3 Residue-property plots [i](#)

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.

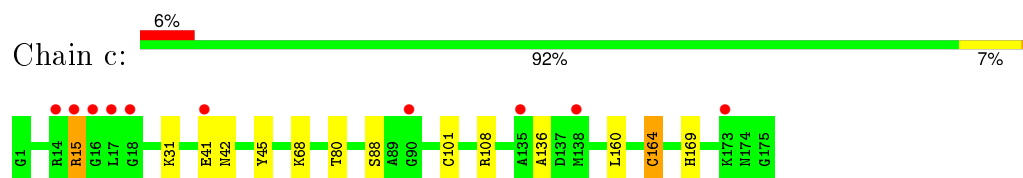
- Molecule 1: H-2 class I histocompatibility antigen, L-D alpha chain



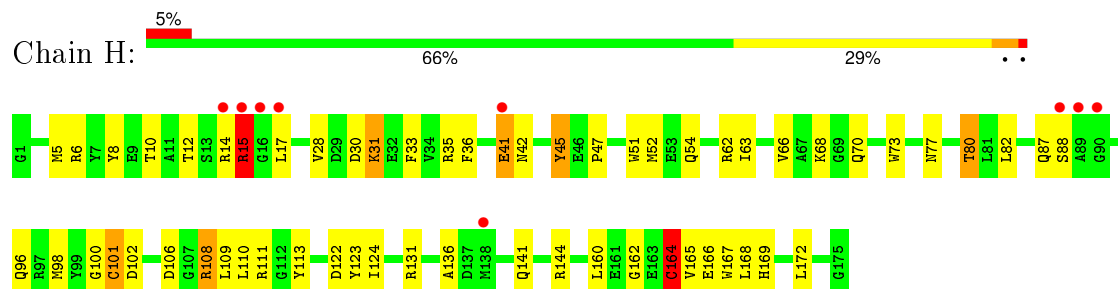
- Molecule 1: H-2 class I histocompatibility antigen, L-D alpha chain



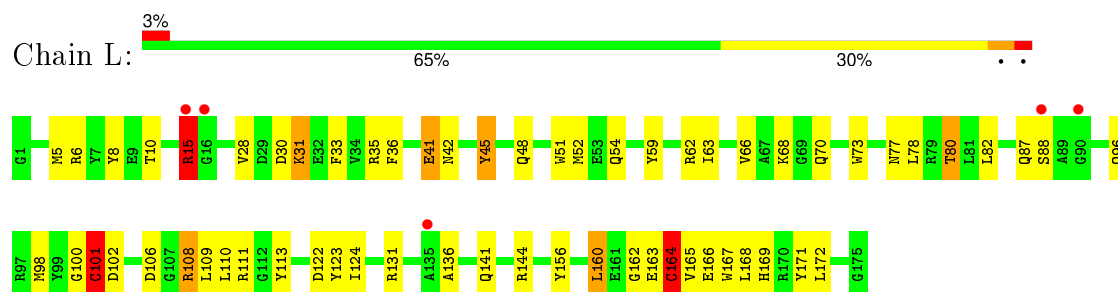
- Molecule 1: H-2 class I histocompatibility antigen, L-D alpha chain



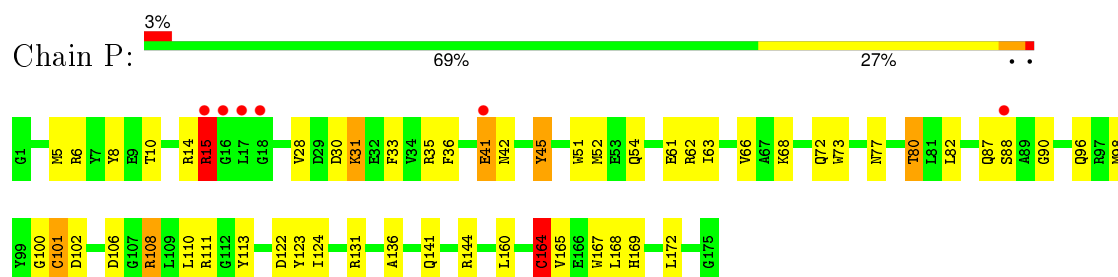
- Molecule 1: H-2 class I histocompatibility antigen, L-D alpha chain



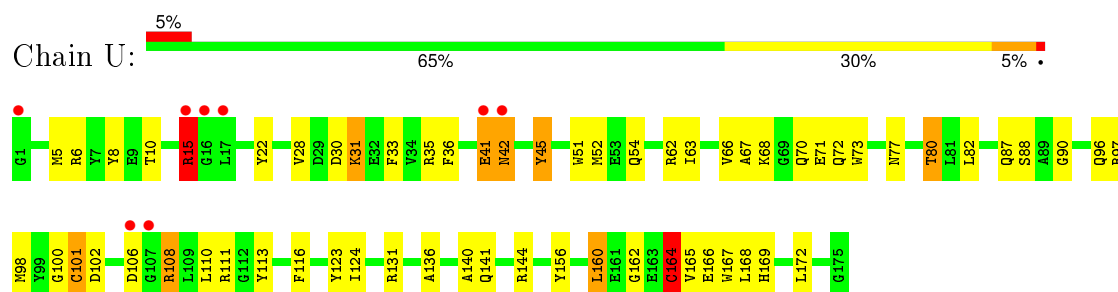
- Molecule 1: H-2 class I histocompatibility antigen, L-D alpha chain



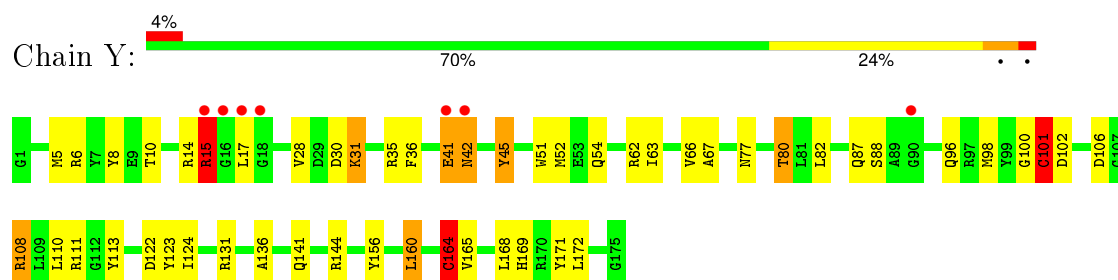
- Molecule 1: H-2 class I histocompatibility antigen, L-D alpha chain



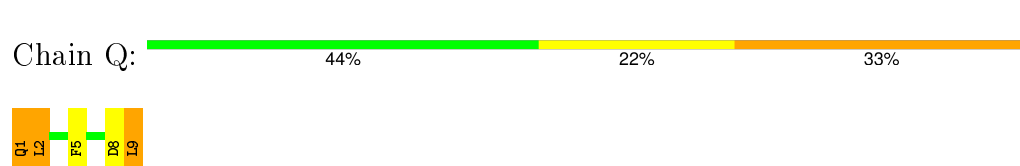
- Molecule 1: H-2 class I histocompatibility antigen, L-D alpha chain



- Molecule 1: H-2 class I histocompatibility antigen, L-D alpha chain



- Molecule 2: QL9 peptide



- Molecule 2: QL9 peptide



- Molecule 2: QL9 peptide



- Molecule 2: QL9 peptide



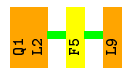
- Molecule 2: QL9 peptide



- Molecule 2: QL9 peptide



- Molecule 2: QL9 peptide

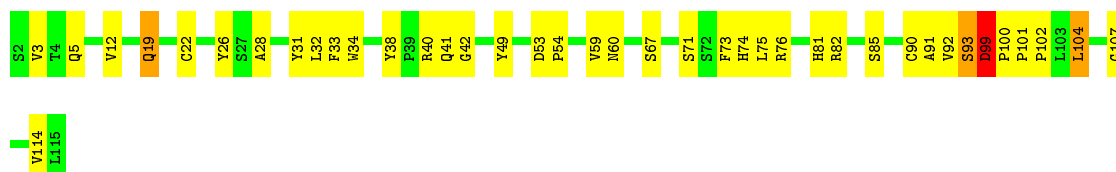


- Molecule 2: QL9 peptide



- Molecule 3: T-cell receptor alpha chain V region PHDS58





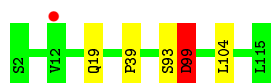
- Molecule 3: T-cell receptor alpha chain V region PHDS58

Chain C: 70% 27% ..



- Molecule 3: T-cell receptor alpha chain V region PHDS58

Chain d: 95% ..



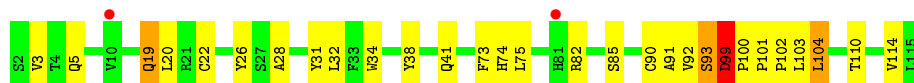
- Molecule 3: T-cell receptor alpha chain V region PHDS58

Chain I: 69% 28% ..



- Molecule 3: T-cell receptor alpha chain V region PHDS58

Chain M: 2% 73% 23% ..



- Molecule 3: T-cell receptor alpha chain V region PHDS58

Chain R: 3% 67% 30% ..



- Molecule 3: T-cell receptor alpha chain V region PHDS58

Chain V: 2% 66% 30% ..



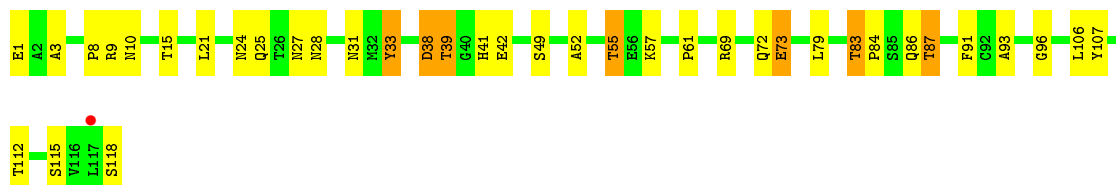
- Molecule 3: T-cell receptor alpha chain V region PHDS58

Chain Z:  72% 24% . .



• Molecule 4: TCR beta chain

Chain E:  66% 28% 6%



• Molecule 4: TCR beta chain

Chain F:  69% 23% 7%



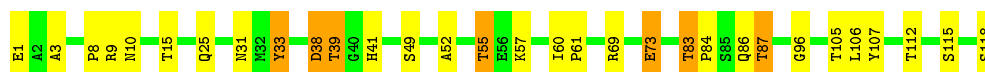
• Molecule 4: TCR beta chain

Chain e:  94% 6%



• Molecule 4: TCR beta chain

Chain J:  72% 22% 6%



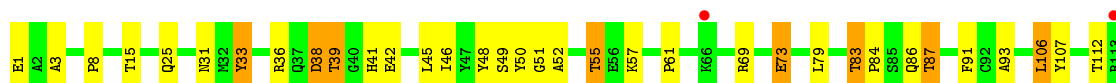
• Molecule 4: TCR beta chain

Chain N:  70% 24% 5%



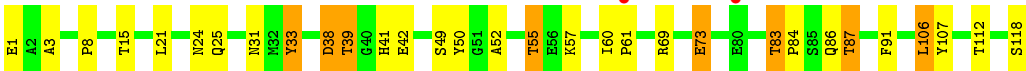
• Molecule 4: TCR beta chain

Chain S:  68% 24% 7%

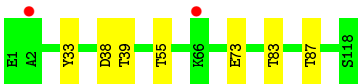




● Molecule 4: TCR beta chain



● Molecule 4: TCR beta chain



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	158.47Å 160.46Å 357.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.52 – 2.95 41.51 – 2.93	Depositor EDS
% Data completeness (in resolution range)	97.4 (41.52-2.95) 96.8 (41.51-2.93)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.21 (at 2.95Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.250 , 0.275 0.251 , 0.252	Depositor DCC
R_{free} test set	4663 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	49.2	Xtriage
Anisotropy	0.262	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 35.5	EDS
Estimated twinning fraction	0.054 for -k,-h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	5 of 94226 reflections (0.005%)	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	25808	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 45.77 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.2603e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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 ⓘ

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	0.48	0/1489	0.67	2/2015 (0.1%)
1	B	0.44	0/1489	0.65	2/2015 (0.1%)
1	H	0.44	0/1489	0.64	1/2015 (0.0%)
1	L	0.45	0/1489	0.65	2/2015 (0.1%)
1	P	0.43	0/1489	0.64	1/2015 (0.0%)
1	U	0.43	0/1489	0.65	1/2015 (0.0%)
1	Y	0.44	0/1489	0.65	2/2015 (0.1%)
1	c	0.42	0/1489	0.63	1/2015 (0.0%)
2	G	0.58	0/79	0.74	0/106
2	K	0.54	0/79	0.68	0/106
2	O	0.58	0/79	0.74	0/106
2	Q	0.58	0/79	0.77	0/106
2	T	0.50	0/79	0.73	0/106
2	X	0.50	0/79	0.71	0/106
2	b	0.55	0/79	0.70	0/106
2	f	0.53	0/79	0.68	0/106
3	C	0.47	0/879	0.73	1/1196 (0.1%)
3	D	0.47	0/879	0.73	1/1196 (0.1%)
3	I	0.48	0/879	0.73	1/1196 (0.1%)
3	M	0.47	0/879	0.73	0/1196
3	R	0.46	0/879	0.73	1/1196 (0.1%)
3	V	0.44	0/879	0.70	0/1196
3	Z	0.46	0/879	0.72	1/1196 (0.1%)
3	d	0.44	0/879	0.71	1/1196 (0.1%)
4	E	0.50	0/865	0.72	0/1172
4	F	0.47	0/865	0.69	0/1172
4	J	0.46	0/865	0.69	0/1172
4	N	0.45	0/865	0.69	0/1172
4	S	0.46	0/865	0.68	0/1172
4	W	0.44	0/865	0.68	0/1172
4	a	0.46	0/865	0.67	0/1172
4	e	0.43	0/865	0.66	0/1172
All	All	0.45	0/26496	0.68	18/35912 (0.1%)

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
3	D	0	1

There are no bond length outliers.

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	P	164	CYS	CA-CB-SG	-7.21	101.02	114.00
1	Y	164	CYS	CA-CB-SG	-7.14	101.15	114.00
1	U	164	CYS	CA-CB-SG	-7.02	101.37	114.00
1	L	164	CYS	CA-CB-SG	-6.94	101.50	114.00
1	H	164	CYS	CA-CB-SG	-6.62	102.08	114.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	D	49	TYR	Sidechain

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	1449	0	1337	66	3
1	B	1449	0	1337	59	0
1	H	1449	0	1337	62	0
1	L	1449	0	1337	62	0
1	P	1449	0	1337	55	0
1	U	1449	0	1337	60	0
1	Y	1449	0	1337	48	0
1	c	1449	0	1337	0	0
2	G	76	0	73	17	0
2	K	76	0	73	19	0
2	O	76	0	73	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	Q	76	0	73	19	0
2	T	76	0	73	13	0
2	X	76	0	73	17	0
2	b	76	0	73	0	0
2	f	76	0	73	0	0
3	C	854	0	832	37	0
3	D	854	0	832	51	0
3	I	854	0	832	30	0
3	M	854	0	832	23	0
3	R	854	0	832	34	0
3	V	854	0	832	37	0
3	Z	854	0	832	26	0
3	d	854	0	832	0	0
4	E	847	0	799	31	3
4	F	847	0	799	26	0
4	J	847	0	799	24	0
4	N	847	0	799	26	0
4	S	847	0	799	26	0
4	W	847	0	799	25	0
4	a	847	0	799	0	0
4	e	847	0	799	0	0
All	All	25808	0	24328	772	3

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 17.

The worst 5 of 772 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:D:82:ARG:NH2	3:V:60:ASN:HD21	1.37	1.21
3:D:60:ASN:HD21	3:C:82:ARG:NH2	109.53	1.07
3:V:99:ASP:HB3	3:V:100:PRO:HD2	1.45	0.99
3:Z:99:ASP:HB3	3:Z:100:PRO:HD2	1.45	0.98
3:I:99:ASP:HB3	3:I:100:PRO:HD2	1.45	0.97

All (3) 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:88:SER:OG	4:E:73:GLU:OE2[6_545]	1.93	0.27

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88:SER:OG	4:E:73:GLU:OE1[6_545]	2.12	0.08
1:A:86:ASN:O	4:E:28:ASN:OD1[6_545]	2.14	0.06

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	173/175 (99%)	158 (91%)	12 (7%)	3 (2%)	11	43
1	B	173/175 (99%)	155 (90%)	15 (9%)	3 (2%)	11	43
1	H	173/175 (99%)	155 (90%)	15 (9%)	3 (2%)	11	43
1	L	173/175 (99%)	157 (91%)	13 (8%)	3 (2%)	11	43
1	P	173/175 (99%)	156 (90%)	14 (8%)	3 (2%)	11	43
1	U	173/175 (99%)	158 (91%)	12 (7%)	3 (2%)	11	43
1	Y	173/175 (99%)	157 (91%)	13 (8%)	3 (2%)	11	43
1	c	173/175 (99%)	156 (90%)	14 (8%)	3 (2%)	11	43
2	G	7/9 (78%)	7 (100%)	0	0	100	100
2	K	7/9 (78%)	7 (100%)	0	0	100	100
2	O	7/9 (78%)	7 (100%)	0	0	100	100
2	Q	7/9 (78%)	7 (100%)	0	0	100	100
2	T	7/9 (78%)	7 (100%)	0	0	100	100
2	X	7/9 (78%)	7 (100%)	0	0	100	100
2	b	7/9 (78%)	7 (100%)	0	0	100	100
2	f	7/9 (78%)	7 (100%)	0	0	100	100
3	C	107/109 (98%)	98 (92%)	7 (6%)	2 (2%)	10	40
3	D	107/109 (98%)	101 (94%)	5 (5%)	1 (1%)	21	61
3	I	107/109 (98%)	100 (94%)	6 (6%)	1 (1%)	21	61

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	M	107/109 (98%)	100 (94%)	6 (6%)	1 (1%)	21	61
3	R	107/109 (98%)	100 (94%)	5 (5%)	2 (2%)	10	40
3	V	107/109 (98%)	100 (94%)	5 (5%)	2 (2%)	10	40
3	Z	107/109 (98%)	101 (94%)	4 (4%)	2 (2%)	10	40
3	d	107/109 (98%)	100 (94%)	5 (5%)	2 (2%)	10	40
4	E	109/111 (98%)	105 (96%)	3 (3%)	1 (1%)	21	61
4	F	109/111 (98%)	105 (96%)	3 (3%)	1 (1%)	21	61
4	J	109/111 (98%)	106 (97%)	2 (2%)	1 (1%)	21	61
4	N	109/111 (98%)	105 (96%)	3 (3%)	1 (1%)	21	61
4	S	109/111 (98%)	106 (97%)	2 (2%)	1 (1%)	21	61
4	W	109/111 (98%)	106 (97%)	2 (2%)	1 (1%)	21	61
4	a	109/111 (98%)	106 (97%)	2 (2%)	1 (1%)	21	61
4	e	109/111 (98%)	106 (97%)	2 (2%)	1 (1%)	21	61
All	All	3168/3232 (98%)	2953 (93%)	170 (5%)	45 (1%)	14	49

5 of 45 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	D	99	ASP
3	C	99	ASP
3	d	99	ASP
3	I	99	ASP
3	M	99	ASP

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	144/144 (100%)	132 (92%)	12 (8%)	14	43
1	B	144/144 (100%)	132 (92%)	12 (8%)	14	43
1	H	144/144 (100%)	133 (92%)	11 (8%)	16	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	L	144/144 (100%)	133 (92%)	11 (8%)	16	48
1	P	144/144 (100%)	132 (92%)	12 (8%)	14	43
1	U	144/144 (100%)	132 (92%)	12 (8%)	14	43
1	Y	144/144 (100%)	133 (92%)	11 (8%)	16	48
1	c	144/144 (100%)	132 (92%)	12 (8%)	14	43
2	G	9/9 (100%)	6 (67%)	3 (33%)	0	1
2	K	9/9 (100%)	6 (67%)	3 (33%)	0	1
2	O	9/9 (100%)	7 (78%)	2 (22%)	1	4
2	Q	9/9 (100%)	6 (67%)	3 (33%)	0	1
2	T	9/9 (100%)	6 (67%)	3 (33%)	0	1
2	X	9/9 (100%)	6 (67%)	3 (33%)	0	1
2	b	9/9 (100%)	6 (67%)	3 (33%)	0	1
2	f	9/9 (100%)	6 (67%)	3 (33%)	0	1
3	C	95/95 (100%)	91 (96%)	4 (4%)	36	74
3	D	95/95 (100%)	91 (96%)	4 (4%)	36	74
3	I	95/95 (100%)	91 (96%)	4 (4%)	36	74
3	M	95/95 (100%)	91 (96%)	4 (4%)	36	74
3	R	95/95 (100%)	92 (97%)	3 (3%)	46	80
3	V	95/95 (100%)	91 (96%)	4 (4%)	36	74
3	Z	95/95 (100%)	91 (96%)	4 (4%)	36	74
3	d	95/95 (100%)	91 (96%)	4 (4%)	36	74
4	E	91/91 (100%)	84 (92%)	7 (8%)	16	47
4	F	91/91 (100%)	84 (92%)	7 (8%)	16	47
4	J	91/91 (100%)	85 (93%)	6 (7%)	21	55
4	N	91/91 (100%)	86 (94%)	5 (6%)	27	64
4	S	91/91 (100%)	84 (92%)	7 (8%)	16	47
4	W	91/91 (100%)	84 (92%)	7 (8%)	16	47
4	a	91/91 (100%)	85 (93%)	6 (7%)	21	55
4	e	91/91 (100%)	85 (93%)	6 (7%)	21	55
All	All	2712/2712 (100%)	2514 (93%)	198 (7%)	17	50

5 of 198 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	K	2	LEU
1	L	164	CYS
1	Y	160	LEU
3	I	93	SER
4	J	87	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 102 such sidechains are listed below:

Mol	Chain	Res	Type
3	I	5	GLN
1	L	87	GLN
1	Y	127	ASN
3	I	19	GLN
4	J	30	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 ⓘ

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	175/175 (100%)	0.01	5 (2%) 55 35	24, 40, 68, 92	0
1	B	175/175 (100%)	0.17	6 (3%) 49 30	33, 49, 74, 92	0
1	H	175/175 (100%)	0.21	9 (5%) 32 18	31, 50, 76, 97	0
1	L	175/175 (100%)	0.11	5 (2%) 55 35	32, 46, 69, 89	0
1	P	175/175 (100%)	0.19	6 (3%) 49 30	30, 49, 70, 92	0
1	U	175/175 (100%)	0.21	8 (4%) 36 21	28, 49, 74, 93	0
1	Y	175/175 (100%)	0.12	7 (4%) 42 25	30, 46, 69, 89	0
1	c	175/175 (100%)	0.26	10 (5%) 27 15	38, 53, 76, 94	0
2	G	9/9 (100%)	-0.09	0 100 100	37, 42, 44, 51	0
2	K	9/9 (100%)	-0.16	0 100 100	39, 41, 48, 54	0
2	O	9/9 (100%)	-0.05	0 100 100	36, 38, 46, 48	0
2	Q	9/9 (100%)	-0.01	0 100 100	35, 37, 42, 49	0
2	T	9/9 (100%)	0.46	0 100 100	35, 43, 46, 55	0
2	X	9/9 (100%)	0.08	0 100 100	39, 43, 47, 52	0
2	b	9/9 (100%)	-0.02	0 100 100	32, 36, 43, 45	0
2	f	9/9 (100%)	0.33	0 100 100	45, 47, 53, 56	0
3	C	109/109 (100%)	-0.00	0 100 100	30, 44, 59, 69	0
3	D	109/109 (100%)	-0.06	0 100 100	25, 39, 56, 65	0
3	I	109/109 (100%)	0.00	0 100 100	32, 44, 58, 68	0
3	M	109/109 (100%)	0.02	2 (1%) 71 51	32, 46, 62, 75	0
3	R	109/109 (100%)	0.03	3 (2%) 56 36	31, 44, 58, 71	0
3	V	109/109 (100%)	0.10	2 (1%) 71 51	34, 46, 60, 74	0
3	Z	109/109 (100%)	-0.01	0 100 100	32, 41, 55, 66	0
3	d	109/109 (100%)	0.16	1 (0%) 85 70	35, 49, 61, 72	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
4	E	111/111 (100%)	-0.13	1 (0%) 85 70	26, 38, 58, 74	0
4	F	111/111 (100%)	-0.00	0 100 100	29, 45, 63, 77	0
4	J	111/111 (100%)	-0.09	0 100 100	32, 45, 65, 80	0
4	N	111/111 (100%)	-0.14	0 100 100	30, 42, 58, 80	0
4	S	111/111 (100%)	0.11	2 (1%) 71 51	33, 45, 62, 75	0
4	W	111/111 (100%)	0.23	2 (1%) 71 51	32, 48, 63, 78	0
4	a	111/111 (100%)	0.09	2 (1%) 71 51	31, 44, 59, 72	0
4	e	111/111 (100%)	-0.01	1 (0%) 85 70	35, 49, 64, 79	0
All	All	3232/3232 (100%)	0.08	72 (2%) 65 44	24, 46, 68, 97	0

The worst 5 of 72 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	Y	16	GLY	6.0
1	H	89	ALA	4.6
1	A	17	LEU	4.2
1	c	16	GLY	3.9
1	Y	17	LEU	3.9

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

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.