



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 20, 2016 – 05:15 PM EDT

PDB ID : 5SWS  
Title : Crystal Structure of NP2-B17 TCR-H2Db-NP complex  
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Deposited on : 2016-08-08  
Resolution : 2.86 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.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	:	unknown
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20027939
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)	:	rb-20027939

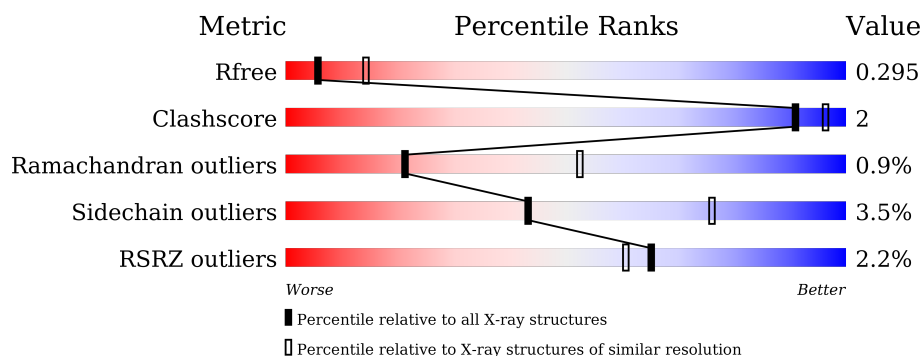
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.86 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	2228 (2.90-2.82)
Clashscore	102246	2499 (2.90-2.82)
Ramachandran outliers	100387	2439 (2.90-2.82)
Sidechain outliers	100360	2442 (2.90-2.82)
RSRZ outliers	91569	2236 (2.90-2.82)

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.

Mol	Chain	Length	Quality of chain
1	A	280	<div> <div>4%</div> <div>88%</div> <div>9%</div> <div>••</div> </div>
2	B	99	<div> <div>91%</div> <div>7%</div> <div>•</div> </div>
3	C	9	<div> <div>89%</div> <div>11%</div> </div>
4	D	207	<div> <div>2%</div> <div>88%</div> <div>7%</div> <div>•</div> </div>
5	E	242	<div> <div>%</div> <div>90%</div> <div>9%</div> <div>•</div> </div>

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 6758 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, D-B alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	273	Total	C	N	O	S	0	0	0
			2240	1417	396	418	9			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	97	Total	C	N	O	S	0	2	0
			818	523	138	149	8			

- Molecule 3 is a protein called influenza NP366 epitope.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	9	Total	C	N	O	S	0	0	0
			69	38	11	18	2			

- Molecule 4 is a protein called NP1-B17 TCR alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	198	Total	C	N	O	S	0	0	0
			1558	975	258	317	8			

- Molecule 5 is a protein called NP1-B17 TCR beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	239	Total	C	N	O	S	0	1	0
			1934	1230	335	360	9			

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	46	Total	O	0	0
			46	46		

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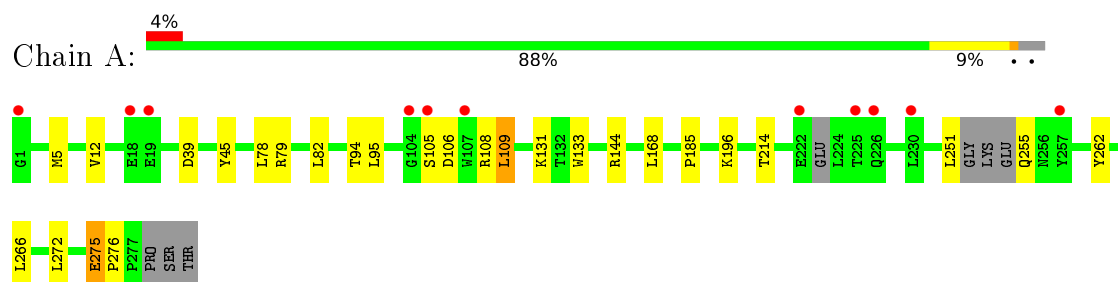
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	15	Total 15	O 15	0	0
6	C	2	Total 2	O 2	0	0
6	D	35	Total 35	O 35	0	0
6	E	41	Total 41	O 41	0	0

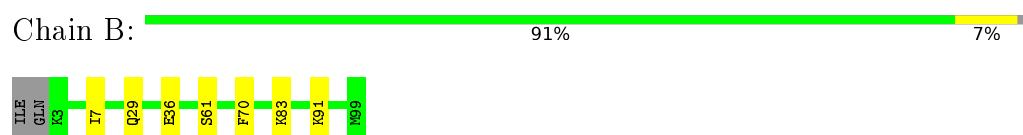
### 3 Residue-property plots [i](#)

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.

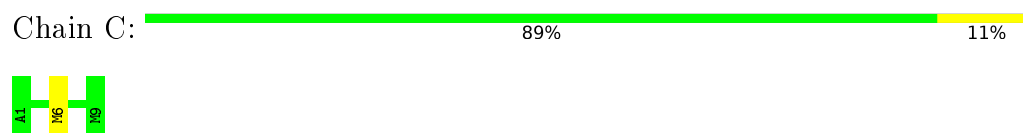
- Molecule 1: H-2 class I histocompatibility antigen, D-B alpha chain



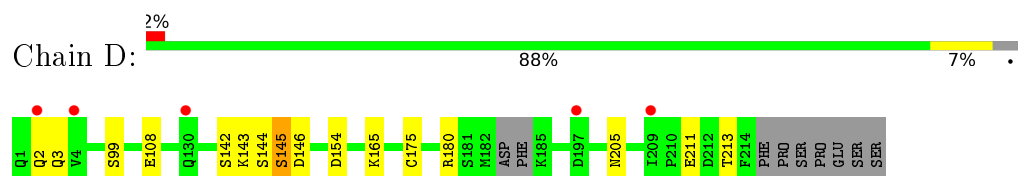
- Molecule 2: Beta-2-microglobulin



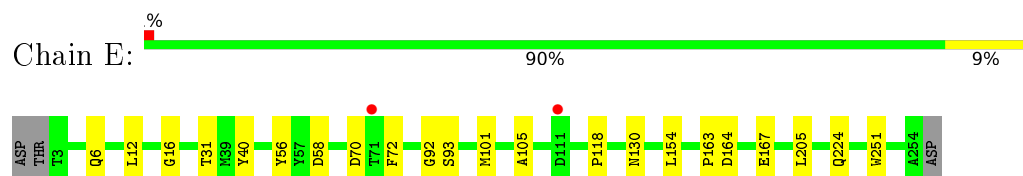
- Molecule 3: influenza NP366 epitope



- Molecule 4: NP1-B17 TCR alpha chain



- Molecule 5: NP1-B17 TCR beta chain



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	48.02Å 126.94Å 80.48Å 90.00° 105.66° 90.00°	Depositor
Resolution (Å)	30.48 – 2.86 46.23 – 2.86	Depositor EDS
% Data completeness (in resolution range)	99.1 (30.48-2.86) 98.9 (46.23-2.86)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	0.12	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.25 (at 2.86Å)	Xtriage
Refinement program	BUSTER-TNT	Depositor
R, $R_{free}$	0.231 , 0.274 0.251 , 0.295	Depositor DCC
$R_{free}$ test set	1102 reflections (5.46%)	DCC
Wilson B-factor (Å <sup>2</sup> )	44.4	Xtriage
Anisotropy	0.538	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 44.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.041 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.88	EDS
Total number of atoms	6758	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.69% 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	A	0.35	0/2306	0.54	0/3132
2	B	0.36	0/844	0.53	0/1142
3	C	0.31	0/68	0.50	0/88
4	D	0.39	0/1593	0.60	0/2158
5	E	0.35	0/1988	0.53	0/2703
All	All	0.36	0/6799	0.55	0/9223

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	A	2240	0	2115	11	0
2	B	818	0	795	4	0
3	C	69	0	61	0	0
4	D	1558	0	1469	6	0
5	E	1934	0	1863	7	0
6	A	46	0	0	0	0
6	B	15	0	0	0	0
6	C	2	0	0	0	0
6	D	35	0	0	0	0
6	E	41	0	0	0	0
All	All	6758	0	6303	28	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 2.

All (28) 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)
5:E:40:TYR:HB2	5:E:105:ALA:HB3	1.85	0.59
1:A:79:ARG:HA	1:A:82:LEU:HD12	1.91	0.52
4:D:145:SER:HB3	4:D:146:ASP:HA	1.91	0.52
2:B:29:GLN:HA	2:B:61:SER:HB2	1.93	0.51
2:B:36:GLU:HB2	2:B:83[B]:LYS:HB2	1.92	0.50
2:B:36:GLU:HB2	2:B:83[A]:LYS:HB3	1.94	0.49
4:D:144:SER:H	4:D:145:SER:HA	1.77	0.48
4:D:144:SER:N	4:D:145:SER:HA	2.28	0.47
5:E:167:GLU:HB2	5:E:224:GLN:HB3	1.97	0.47
4:D:145:SER:HB3	4:D:146:ASP:CA	2.45	0.47
5:E:154:LEU:HD13	5:E:205:LEU:HD23	1.97	0.46
1:A:275:GLU:CB	1:A:276:PRO:HA	2.44	0.46
1:A:214:THR:HB	1:A:262:TYR:HB2	1.97	0.46
1:A:275:GLU:HB2	1:A:276:PRO:HA	1.97	0.46
1:A:5:MET:HB2	1:A:168:LEU:HD13	1.98	0.45
4:D:2:GLN:H	4:D:3:GLN:HA	1.82	0.45
1:A:105:SER:HA	1:A:106:ASP:HA	1.69	0.45
2:B:7:ILE:HD12	2:B:91:LYS:HD2	1.98	0.45
1:A:133:TRP:HB2	1:A:144:ARG:HG3	1.98	0.44
5:E:12:LEU:HD13	5:E:163:PRO:HG3	2.01	0.42
1:A:108:ARG:O	1:A:109:LEU:HB3	2.20	0.41
4:D:145:SER:CB	4:D:146:ASP:HA	2.50	0.41
1:A:78:LEU:HD13	1:A:95:LEU:HB2	2.02	0.41
5:E:92:GLY:HA2	5:E:93:SER:HA	1.87	0.41
5:E:6:GLN:HB2	5:E:118:PRO:HD2	2.02	0.41
1:A:185:PRO:HD2	1:A:266:LEU:HD23	2.03	0.41
1:A:12:VAL:HG22	1:A:94:THR:HG23	2.03	0.40
5:E:16:GLY:HA2	5:E:93:SER:HB2	2.02	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	267/280 (95%)	247 (92%)	18 (7%)	2 (1%)	26	59
2	B	97/99 (98%)	94 (97%)	3 (3%)	0	100	100
3	C	7/9 (78%)	6 (86%)	0	1 (14%)	0	0
4	D	194/207 (94%)	174 (90%)	17 (9%)	3 (2%)	13	38
5	E	238/242 (98%)	226 (95%)	11 (5%)	1 (0%)	39	71
All	All	803/837 (96%)	747 (93%)	49 (6%)	7 (1%)	21	52

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	275	GLU
4	D	165	LYS
1	A	109	LEU
3	C	6	MET
4	D	99	SER
4	D	211	GLU
5	E	58	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	232/238 (98%)	225 (97%)	7 (3%)	48	80
2	B	93/93 (100%)	92 (99%)	1 (1%)	80	94
3	C	8/8 (100%)	8 (100%)	0	100	100
4	D	178/187 (95%)	169 (95%)	9 (5%)	29	62
5	E	210/212 (99%)	202 (96%)	8 (4%)	40	74
All	All	721/738 (98%)	696 (96%)	25 (4%)	43	76

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	ASP
1	A	45	TYR
1	A	131	LYS
1	A	196	LYS
1	A	251	LEU
1	A	255	GLN
1	A	272	LEU
2	B	70	PHE
4	D	108	GLU
4	D	142	SER
4	D	143	LYS
4	D	145	SER
4	D	154	ASP
4	D	175	CYS
4	D	180	ARG
4	D	205	ASN
4	D	213	THR
5	E	31	THR
5	E	56	TYR
5	E	70	ASP
5	E	72	PHE
5	E	101	MET
5	E	130	ASN
5	E	164	ASP
5	E	251	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	87	GLN
4	D	44	GLN

### 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 [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, 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	A	273/280 (97%)	0.21	11 (4%) 42 34	25, 47, 73, 108	8 (2%)
2	B	97/99 (97%)	-0.08	0 100 100	25, 41, 59, 64	0
3	C	9/9 (100%)	-0.21	0 100 100	26, 31, 36, 39	0
4	D	198/207 (95%)	0.30	5 (2%) 61 56	36, 54, 71, 98	2 (1%)
5	E	239/242 (98%)	0.09	2 (0%) 87 86	20, 43, 67, 75	0
All	All	816/837 (97%)	0.16	18 (2%) 65 61	20, 46, 71, 108	10 (1%)

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	225	THR	6.3
1	A	104	GLY	4.9
1	A	105	SER	4.0
4	D	2	GLN	3.7
1	A	19	GLU	3.6
1	A	1	GLY	3.5
4	D	130	GLN	3.4
1	A	226	GLN	3.4
1	A	230	LEU	2.9
4	D	197	ASP	2.7
1	A	18	GLU	2.6
4	D	209	ILE	2.3
1	A	257	TYR	2.3
5	E	71	THR	2.2
5	E	111	ASP	2.1
1	A	107	TRP	2.1
1	A	222	GLU	2.0
4	D	4	VAL	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 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.