



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2018 – 07:21 pm GMT

PDB ID : 4JRY  
Title : Crystal Structure of SB47 TCR-HLA B\*3505-LPEP complex  
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Deposited on : 2013-03-22  
Resolution : 2.80 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

<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 : trunk30967  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk30967

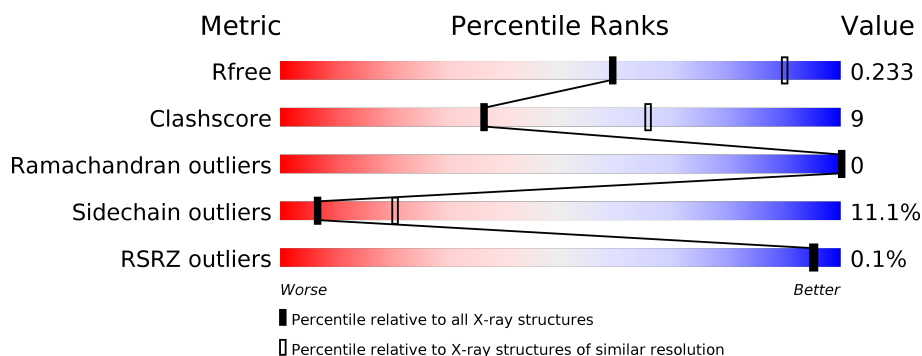
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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))
$R_{free}$	111664	2792 (2.80-2.80)
Clashscore	122126	3209 (2.80-2.80)
Ramachandran outliers	120053	3158 (2.80-2.80)
Sidechain outliers	120020	3160 (2.80-2.80)
RSRZ outliers	108989	2726 (2.80-2.80)

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	276	<div> <div>73%</div> <div>23%</div> <div>.</div> </div>
2	B	100	<div> <div>76%</div> <div>22%</div> <div>.</div> </div>
3	C	13	<div> <div>69%</div> <div>31%</div> </div>
4	D	201	<div> <div>71%</div> <div>25%</div> <div>.</div> </div>
5	E	242	<div> <div>81%</div> <div>19%</div> <div>.</div> </div>

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 6830 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 MHC class I antigen.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	276	Total	C	N	O	S	0	0	0
			2257	1405	414	431	7			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	100	Total	C	N	O	S	0	0	0
			837	533	141	159	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	EXPRESSION TAG	UNP P61769

- Molecule 3 is a protein called Trans-activator protein BZLF1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	13	Total	C	N	O	0	0	0
			101	66	15	20			

- Molecule 4 is a protein called SB47 TCR alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	201	Total	C	N	O	S	0	0	0
			1574	991	261	313	9			

- Molecule 5 is a protein called SB47 TCR beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	242	Total	C	N	O	S	1	0	0
			1934	1216	340	373	5			

- Molecule 6 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total 1	Na 1	0	0

- Molecule 7 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	2	Total 2	Mg 2	0	0

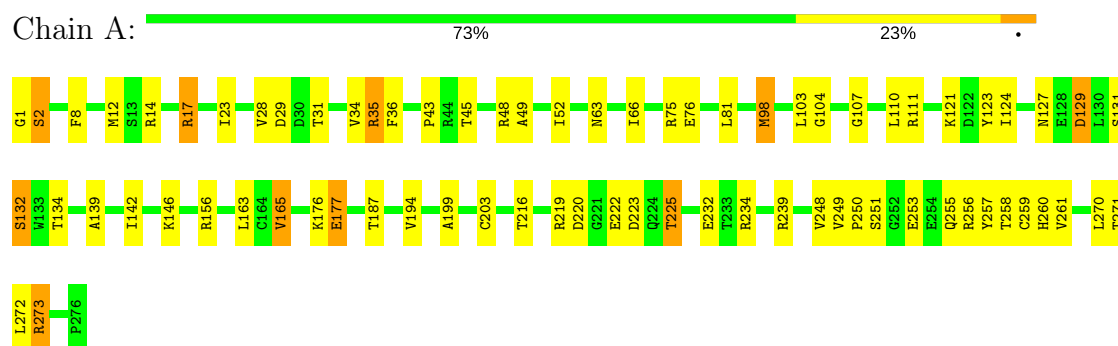
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	20	Total 20	O 20	0	0
8	B	14	Total 14	O 14	0	0
8	C	2	Total 2	O 2	0	0
8	D	32	Total 32	O 32	0	0
8	E	56	Total 56	O 56	0	0

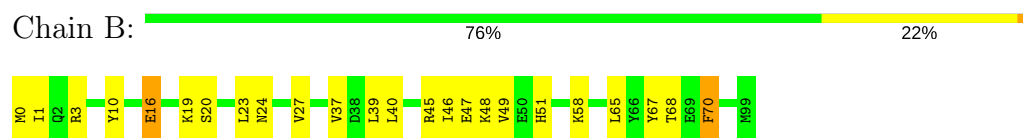
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

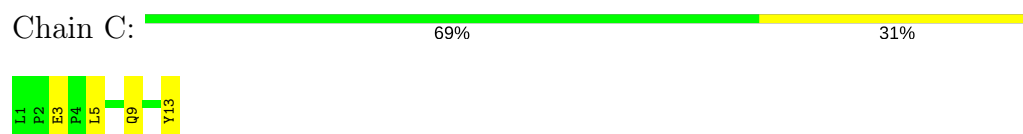
- Molecule 1: MHC class I antigen



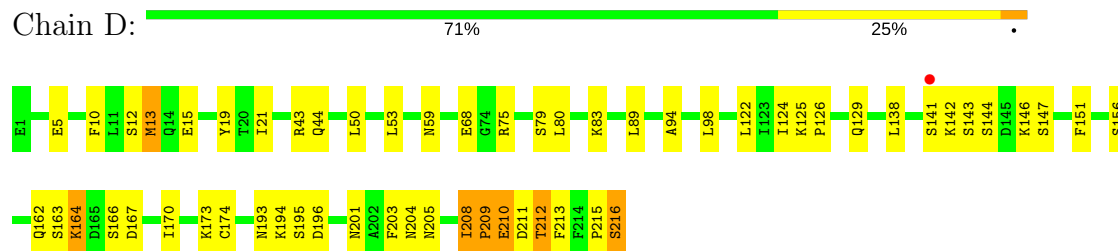
- Molecule 2: Beta-2-microglobulin



- Molecule 3: Trans-activator protein BZLF1



- Molecule 4: SB47 TCR alpha chain

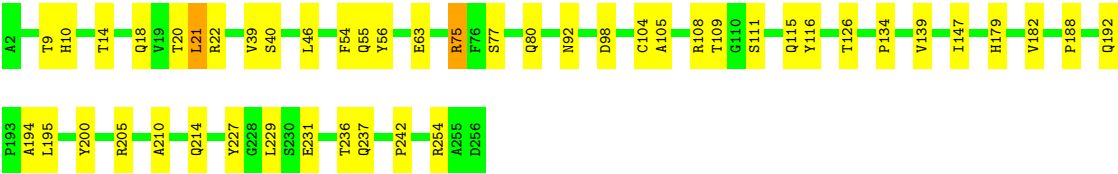


- Molecule 5: SB47 TCR beta chain

Chain E: 

81%

19%



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	237.60 Å   237.60 Å   61.20 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	100.00 – 2.80 168.01 – 2.80	Depositor EDS
% Data completeness (in resolution range)	(Not available) (100.00-2.80) 99.9 (168.01-2.80)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.11 (at 2.82 Å)	Xtriage
Refinement program	BUSTER-TNT, BUSTER	Depositor
R, $R_{free}$	0.200 , 0.233 0.202 , 0.233	Depositor DCC
$R_{free}$ test set	2147 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	48.8	Xtriage
Anisotropy	0.161	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 54.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.022 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	6830	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.74% 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

### 5.1 Standard geometry

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

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	0.60	0/2320	0.76	1/3153 (0.0%)
2	B	0.53	0/860	0.72	0/1162
3	C	0.48	0/104	0.69	0/142
4	D	0.67	0/1607	0.78	1/2178 (0.0%)
5	E	0.63	0/1989	0.76	0/2710
All	All	0.62	0/6880	0.76	2/9345 (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	A	129	ASP	N-CA-C	-6.23	94.18	111.00
4	D	138	LEU	CA-CB-CG	5.06	126.94	115.30

There are no chirality outliers.

There are no planarity outliers.

### 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	2257	0	2123	40	0
2	B	837	0	803	12	0
3	C	101	0	102	2	0
4	D	1574	0	1522	37	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	E	1934	0	1817	23	0
6	B	1	0	0	0	0
7	B	2	0	0	0	0
8	A	20	0	0	0	0
8	B	14	0	0	0	0
8	C	2	0	0	0	0
8	D	32	0	0	1	0
8	E	56	0	0	0	0
All	All	6830	0	6367	109	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 9.

All (109) 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)
4:D:146:LYS:N	4:D:147:SER:HA	1.51	1.18
4:D:146:LYS:H	4:D:147:SER:CA	1.59	1.16
1:A:273:ARG:HG3	1:A:273:ARG:HH11	1.17	1.06
5:E:9:THR:HG23	5:E:10:HIS:HD2	1.23	0.97
4:D:13:MET:HG3	4:D:124:ILE:HG13	1.52	0.91
5:E:9:THR:HG23	5:E:10:HIS:CD2	2.07	0.90
4:D:146:LYS:N	4:D:147:SER:CA	2.20	0.86
4:D:146:LYS:H	4:D:147:SER:HA	0.74	0.85
4:D:204:ASN:O	4:D:205:ASN:HB3	1.80	0.82
4:D:209:PRO:O	4:D:210:GLU:CG	2.30	0.80
4:D:209:PRO:O	4:D:210:GLU:CB	2.29	0.77
1:A:273:ARG:HG3	1:A:273:ARG:NH1	1.90	0.76
1:A:17:ARG:HH11	1:A:17:ARG:HG2	1.54	0.72
4:D:209:PRO:O	4:D:210:GLU:HG3	1.90	0.69
4:D:208:ILE:HG13	4:D:212:THR:HG21	1.75	0.69
4:D:204:ASN:O	4:D:205:ASN:CB	2.41	0.68
1:A:129:ASP:OD1	1:A:129:ASP:C	2.32	0.67
5:E:214:GLN:HA	5:E:254:ARG:O	1.95	0.66
1:A:17:ARG:CG	1:A:17:ARG:HH11	2.09	0.66
4:D:205:ASN:O	4:D:205:ASN:ND2	2.30	0.65
1:A:255:GLN:HA	1:A:255:GLN:OE1	1.97	0.65
1:A:273:ARG:HH11	1:A:273:ARG:CG	2.02	0.64
5:E:9:THR:CG2	5:E:10:HIS:HD2	2.04	0.63
4:D:59:ASN:HD21	4:D:83:LYS:HE2	1.65	0.61
4:D:209:PRO:O	4:D:210:GLU:HB2	1.99	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:103:LEU:HD11	1:A:107:GLY:HA2	1.83	0.60
4:D:210:GLU:H	4:D:212:THR:HG23	1.66	0.60
4:D:94:ALA:HB1	4:D:124:ILE:HG12	1.84	0.60
1:A:28:VAL:O	1:A:29:ASP:HB2	2.04	0.58
4:D:15:GLU:HG2	4:D:126:PRO:HA	1.85	0.58
5:E:179:HIS:O	5:E:182:VAL:HG22	2.05	0.56
1:A:121:LYS:HE3	2:B:1:ILE:HD11	1.87	0.56
1:A:260:HIS:CE1	1:A:271:THR:HG23	2.41	0.56
4:D:213:PHE:CE2	4:D:215:PRO:HG3	2.41	0.55
4:D:209:PRO:HB2	4:D:212:THR:HG22	1.88	0.55
4:D:215:PRO:O	4:D:216:SER:HB2	2.07	0.55
5:E:63:GLU:HA	5:E:80:GLN:HB3	1.89	0.54
1:A:250:PRO:HB2	1:A:253:GLU:HG3	1.91	0.53
4:D:146:LYS:N	4:D:147:SER:CB	2.72	0.53
2:B:1:ILE:HD12	2:B:1:ILE:H	1.72	0.53
1:A:223:ASP:HB3	1:A:225:THR:HG22	1.90	0.53
5:E:192:GLN:C	5:E:194:ALA:H	2.13	0.52
5:E:18:GLN:HG3	5:E:92:ASN:HB3	1.92	0.52
1:A:203:CYS:CB	1:A:259:CYS:SG	2.98	0.51
5:E:20:THR:C	5:E:21:LEU:HD23	2.31	0.51
5:E:229:LEU:HD12	5:E:242:PRO:HD2	1.92	0.51
4:D:209:PRO:C	4:D:210:GLU:CG	2.77	0.50
5:E:10:HIS:CG	5:E:227:TYR:HB3	2.46	0.50
4:D:196:ASP:C	4:D:196:ASP:OD1	2.48	0.50
2:B:24:ASN:HB3	2:B:65:LEU:HD11	1.94	0.50
1:A:129:ASP:OD2	1:A:132:SER:OG	2.30	0.50
1:A:103:LEU:HD13	1:A:165:VAL:HG22	1.94	0.50
1:A:129:ASP:OD1	1:A:129:ASP:O	2.30	0.49
4:D:210:GLU:H	4:D:212:THR:CG2	2.24	0.49
1:A:129:ASP:OD1	1:A:131:SER:N	2.40	0.49
5:E:105:ALA:HA	5:E:116:TYR:O	2.12	0.49
1:A:127:ASN:O	1:A:129:ASP:O	2.29	0.49
4:D:196:ASP:OD1	4:D:196:ASP:O	2.30	0.49
1:A:81:LEU:HD11	3:C:13:TYR:HB3	1.94	0.49
5:E:39:VAL:HG13	5:E:104:CYS:SG	2.53	0.49
4:D:43:ARG:HB2	4:D:53:LEU:HD11	1.95	0.48
1:A:187:THR:HB	1:A:272:LEU:HD11	1.94	0.48
2:B:16:GLU:HB3	2:B:19:LYS:HG3	1.95	0.48
4:D:163:SER:HB2	4:D:170:ILE:CD1	2.43	0.48
1:A:139:ALA:HA	1:A:142:ILE:HD12	1.95	0.47
4:D:13:MET:HB2	4:D:19:TYR:CE2	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35:ARG:HG2	1:A:48:ARG:HD3	1.97	0.47
5:E:108:ARG:HG2	5:E:111:SER:HB2	1.97	0.47
4:D:43:ARG:HD3	8:D:330:HOH:O	2.13	0.47
5:E:134:PRO:HD3	5:E:242:PRO:HB3	1.97	0.47
4:D:151:PHE:HB2	4:D:203:PHE:CE1	2.50	0.47
5:E:192:GLN:C	5:E:194:ALA:N	2.68	0.46
1:A:261:VAL:HB	1:A:270:LEU:HB2	1.97	0.46
4:D:164:LYS:HE3	4:D:205:ASN:OD1	2.16	0.46
5:E:75:ARG:HH22	5:E:98:ASP:CG	2.20	0.46
1:A:220:ASP:OD1	1:A:256:ARG:HD2	2.16	0.45
4:D:75:ARG:HD2	4:D:98:LEU:HD11	1.99	0.45
5:E:147:ILE:HG23	5:E:210:ALA:HB1	1.98	0.45
5:E:188:PRO:HB2	5:E:200:TYR:HB3	1.98	0.44
5:E:14:THR:HA	5:E:126:THR:O	2.18	0.44
1:A:123:TYR:HD2	1:A:124:ILE:HG22	1.83	0.44
4:D:167:ASP:HB3	4:D:194:LYS:HE3	1.99	0.43
1:A:66:ILE:HA	3:C:5:LEU:HD21	2.01	0.43
1:A:36:PHE:CE2	1:A:43:PRO:HB2	2.53	0.43
1:A:199:ALA:O	1:A:249:VAL:HG22	2.19	0.43
1:A:104:GLY:CA	1:A:110:LEU:HB2	2.49	0.43
1:A:31:THR:HG23	1:A:239:ARG:HD3	2.00	0.42
4:D:21:ILE:HD11	4:D:89:LEU:HD23	2.01	0.42
1:A:1:GLY:HA3	1:A:2:SER:HA	1.74	0.42
1:A:219:ARG:HD3	1:A:257:TYR:OH	2.19	0.42
1:A:8:PHE:CE2	1:A:98:MET:HG3	2.54	0.42
4:D:125:LYS:HB3	4:D:156:SER:HB3	2.02	0.42
5:E:56:TYR:HB3	5:E:80:GLN:HB2	2.01	0.42
1:A:49:ALA:O	1:A:52:ILE:HG22	2.20	0.41
1:A:234:ARG:HG3	2:B:10:TYR:CE2	2.55	0.41
4:D:13:MET:CB	4:D:19:TYR:CE2	3.03	0.41
5:E:105:ALA:HB1	5:E:115:GLN:HG2	2.02	0.41
2:B:23:LEU:HB2	2:B:70:PHE:CD2	2.55	0.41
2:B:51:HIS:HA	2:B:65:LEU:O	2.21	0.41
2:B:49:VAL:HG22	2:B:68:THR:HB	2.03	0.41
1:A:45:THR:HG21	1:A:63:ASN:HB3	2.02	0.41
2:B:23:LEU:O	2:B:67:TYR:HA	2.21	0.41
2:B:39:LEU:HB3	2:B:46:ILE:HD12	2.02	0.41
5:E:192:GLN:O	5:E:194:ALA:N	2.53	0.41
1:A:177:GLU:OE1	1:A:177:GLU:HA	2.20	0.41
1:A:258:THR:HG22	1:A:260:HIS:NE2	2.36	0.41
4:D:44:GLN:HB2	4:D:50:LEU:HD23	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:234:ARG:HG3	2:B:10:TYR:CZ	2.57	0.40
2:B:27:VAL:HG21	2:B:37:VAL:HG21	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	Allowed	Outliers	Percentiles	
1	A	274/276 (99%)	267 (97%)	7 (3%)	0	100	100
2	B	98/100 (98%)	95 (97%)	3 (3%)	0	100	100
3	C	11/13 (85%)	11 (100%)	0	0	100	100
4	D	199/201 (99%)	196 (98%)	3 (2%)	0	100	100
5	E	240/242 (99%)	233 (97%)	7 (3%)	0	100	100
All	All	822/832 (99%)	802 (98%)	20 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	234/234 (100%)	207 (88%)	27 (12%)	6	19
2	B	95/95 (100%)	85 (90%)	10 (10%)	7	22

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	11/11 (100%)	9 (82%)	2 (18%)	2	5
4	D	178/178 (100%)	151 (85%)	27 (15%)	3	9
5	E	210/210 (100%)	195 (93%)	15 (7%)	16	42
All	All	728/728 (100%)	647 (89%)	81 (11%)	7	20

All (81) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	SER
1	A	12	MET
1	A	14	ARG
1	A	17	ARG
1	A	23	ILE
1	A	34	VAL
1	A	35	ARG
1	A	75	ARG
1	A	76	GLU
1	A	98	MET
1	A	111	ARG
1	A	132	SER
1	A	134	THR
1	A	146	LYS
1	A	156	ARG
1	A	163	LEU
1	A	165	VAL
1	A	176	LYS
1	A	177	GLU
1	A	194	VAL
1	A	216	THR
1	A	222	GLU
1	A	225	THR
1	A	232	GLU
1	A	248	VAL
1	A	251	SER
1	A	273	ARG
2	B	0	MET
2	B	3	ARG
2	B	16	GLU
2	B	20	SER
2	B	40	LEU
2	B	45	ARG

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Mol	Chain	Res	Type
2	B	47	GLU
2	B	48	LYS
2	B	58	LYS
2	B	70	PHE
3	C	3	GLU
3	C	9	GLN
4	D	5	GLU
4	D	10	PHE
4	D	12	SER
4	D	13	MET
4	D	68	GLU
4	D	79	SER
4	D	80	LEU
4	D	122	LEU
4	D	129	GLN
4	D	141	SER
4	D	142	LYS
4	D	143	SER
4	D	144	SER
4	D	162	GLN
4	D	164	LYS
4	D	166	SER
4	D	173	LYS
4	D	174	CYS
4	D	193	ASN
4	D	195	SER
4	D	201	ASN
4	D	208	ILE
4	D	209	PRO
4	D	210	GLU
4	D	211	ASP
4	D	212	THR
4	D	216	SER
5	E	21	LEU
5	E	22	ARG
5	E	40	SER
5	E	46	LEU
5	E	54	PHE
5	E	55	GLN
5	E	75	ARG
5	E	77	SER
5	E	109	THR

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Mol	Chain	Res	Type
5	E	139	VAL
5	E	195	LEU
5	E	205	ARG
5	E	231	GLU
5	E	236	THR
5	E	237	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
4	D	59	ASN
4	D	96	HIS
4	D	162	GLN
5	E	10	HIS
5	E	55	GLN
5	E	92	ASN

### 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 ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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<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	276/276 (100%)	0.13	0 <span>100</span> <span>100</span>	31, 50, 70, 87	25 (9%)
2	B	100/100 (100%)	0.06	0 <span>100</span> <span>100</span>	34, 45, 67, 75	6 (6%)
3	C	13/13 (100%)	0.23	0 <span>100</span> <span>100</span>	34, 51, 72, 73	0
4	D	201/201 (100%)	0.19	1 (0%) <span>90</span> <span>88</span>	27, 42, 78, 91	11 (5%)
5	E	242/242 (100%)	0.08	0 <span>100</span> <span>100</span>	23, 38, 55, 112	14 (5%)
All	All	832/832 (100%)	0.13	1 (0%) <span>95</span> <span>95</span>	23, 44, 72, 112	56 (6%)

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	141	SER	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](#)

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<sup>th</sup> 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	B-factors( $\text{\AA}^2$ )	Q<0.9
6	NA	B	101	1/1	0.88	0.12	44,44,44,44	0
7	MG	B	103	1/1	0.91	0.18	53,53,53,53	0
7	MG	B	102	1/1	0.93	0.11	60,60,60,60	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.