



Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2020 – 11:22 am BST

PDB ID : 2P24
Title : I-Au/MBP125-135
Authors : McBeth, C.; Strong, R.K.
Deposited on : 2007-03-06
Resolution : 2.15 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/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
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

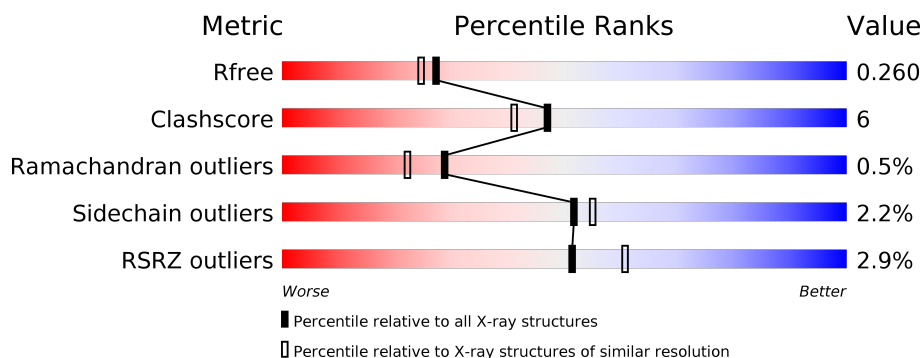
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	1479 (2.16-2.16)
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (2.16-2.16)

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 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	A	236	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: -5px; left: 0; width: 100%; height: 100%; background: linear-gradient(to right, red 0%, red 1%, orange 1%, orange 68%, yellow 68%, yellow 69%, green 69%, green 99%, grey 99%, grey 100%);"></div> <div style="position: absolute; top: 5px; left: 0; width: 100%; height: 100%; background: linear-gradient(to right, red 0%, red 1%, orange 1%, orange 68%, yellow 68%, yellow 69%, green 69%, green 99%, grey 99%, grey 100%);"></div> </div> <div> 68% 9% 23% </div> </div>
2	B	259	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: -5px; left: 0; width: 100%; height: 100%; background: linear-gradient(to right, red 0%, red 3%, orange 3%, orange 66%, yellow 66%, yellow 73%, green 73%, green 99%, grey 99%, grey 100%);"></div> <div style="position: absolute; top: 5px; left: 0; width: 100%; height: 100%; background: linear-gradient(to right, red 0%, red 3%, orange 3%, orange 66%, yellow 66%, yellow 73%, green 73%, green 99%, grey 99%, grey 100%);"></div> </div> <div> 66% 7% 25% </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3203 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 II histocompatibility antigen, A-U alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	182	Total	C	N	O	S	0	0	0
			1424	923	227	271	3			

There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-32	MET	-	EXPRESSION TAG	UNP P14438
A	-31	ALA	-	EXPRESSION TAG	UNP P14438
A	-30	ILE	-	EXPRESSION TAG	UNP P14438
A	-29	MET	-	EXPRESSION TAG	UNP P14438
A	-28	ALA	-	EXPRESSION TAG	UNP P14438
A	-27	PRO	-	EXPRESSION TAG	UNP P14438
A	-26	ARG	-	EXPRESSION TAG	UNP P14438
A	-25	THR	-	EXPRESSION TAG	UNP P14438
A	-24	LEU	-	EXPRESSION TAG	UNP P14438
A	-23	VAL	-	EXPRESSION TAG	UNP P14438
A	-22	LEU	-	EXPRESSION TAG	UNP P14438
A	-21	LEU	-	EXPRESSION TAG	UNP P14438
A	-20	LEU	-	EXPRESSION TAG	UNP P14438
A	-19	SER	-	EXPRESSION TAG	UNP P14438
A	-18	GLY	-	EXPRESSION TAG	UNP P14438
A	-17	ALA	-	EXPRESSION TAG	UNP P14438
A	-16	LEU	-	EXPRESSION TAG	UNP P14438
A	-15	ALA	-	EXPRESSION TAG	UNP P14438
A	-14	LEU	-	EXPRESSION TAG	UNP P14438
A	-13	THR	-	EXPRESSION TAG	UNP P14438
A	-12	GLN	-	EXPRESSION TAG	UNP P14438
A	-11	THR	-	EXPRESSION TAG	UNP P14438
A	-10	TRP	-	EXPRESSION TAG	UNP P14438
A	-9	ALA	-	EXPRESSION TAG	UNP P14438
A	-8	GLY	-	EXPRESSION TAG	UNP P14438
A	-7	SER	-	EXPRESSION TAG	UNP P14438
A	-6	HIS	-	EXPRESSION TAG	UNP P14438

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	SER	-	EXPRESSION TAG	UNP P14438
A	-4	ARG	-	EXPRESSION TAG	UNP P14438
A	-3	GLY	-	EXPRESSION TAG	UNP P14438
A	-2	GLU	-	EXPRESSION TAG	UNP P14438
A	-1	ASP	-	EXPRESSION TAG	UNP P14438
A	0	ASP	-	EXPRESSION TAG	UNP P14438
A	1	ILE	-	EXPRESSION TAG	UNP P14438
A	2	GLU	-	EXPRESSION TAG	UNP P14438
A	3	ALA	-	EXPRESSION TAG	UNP P14438
A	193	SER	-	EXPRESSION TAG	UNP P14438
A	194	GLY	-	EXPRESSION TAG	UNP P14438
A	195	SER	-	EXPRESSION TAG	UNP P14438
A	196	ARG	-	EXPRESSION TAG	UNP P14438
A	197	LEU	-	EXPRESSION TAG	UNP P14438
A	198	GLU	-	EXPRESSION TAG	UNP P14438
A	199	VAL	-	EXPRESSION TAG	UNP P14438
A	200	LEU	-	EXPRESSION TAG	UNP P14438
A	201	PHE	-	EXPRESSION TAG	UNP P14438
A	202	GLN	-	EXPRESSION TAG	UNP P14438

- Molecule 2 is a protein called H-2 class II histocompatibility antigen, A-U beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	194	Total	C	N	O	S	0	0	0
			1573	994	272	301	6			

There are 62 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-31	MET	-	SEE REMARK 999	UNP P06344
B	-30	ALA	-	SEE REMARK 999	UNP P06344
B	-29	ILE	-	SEE REMARK 999	UNP P06344
B	-28	MET	-	SEE REMARK 999	UNP P06344
B	-27	ALA	-	SEE REMARK 999	UNP P06344
B	-26	PRO	-	SEE REMARK 999	UNP P06344
B	-25	ARG	-	SEE REMARK 999	UNP P06344
B	-24	THR	-	SEE REMARK 999	UNP P06344
B	-23	LEU	-	SEE REMARK 999	UNP P06344
B	-22	VAL	-	SEE REMARK 999	UNP P06344
B	-21	LEU	-	SEE REMARK 999	UNP P06344
B	-20	LEU	-	SEE REMARK 999	UNP P06344
B	-19	LEU	-	SEE REMARK 999	UNP P06344

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	SER	-	SEE REMARK 999	UNP P06344
B	-17	GLY	-	SEE REMARK 999	UNP P06344
B	-16	ALA	-	SEE REMARK 999	UNP P06344
B	-15	LEU	-	SEE REMARK 999	UNP P06344
B	-14	ALA	-	SEE REMARK 999	UNP P06344
B	-13	LEU	-	SEE REMARK 999	UNP P06344
B	-12	THR	-	SEE REMARK 999	UNP P06344
B	-11	GLN	-	SEE REMARK 999	UNP P06344
B	-10	THR	-	SEE REMARK 999	UNP P06344
B	-9	TRP	-	SEE REMARK 999	UNP P06344
B	-8	ALA	-	SEE REMARK 999	UNP P06344
B	-7	GLY	-	SEE REMARK 999	UNP P06344
B	-6	SER	-	SEE REMARK 999	UNP P06344
B	-5	HIS	-	SEE REMARK 999	UNP P06344
B	-4	SER	-	SEE REMARK 999	UNP P06344
B	-3	ARG	-	SEE REMARK 999	UNP P06344
B	-2	GLY	-	SEE REMARK 999	UNP P06344
B	-1	TYR	-	SEE REMARK 999	UNP P06344
B	0	GLY	-	SEE REMARK 999	UNP P06344
B	1	GLY	-	SEE REMARK 999	UNP P06344
B	2	ARG	-	SEE REMARK 999	UNP P06344
B	3	ALA	-	SEE REMARK 999	UNP P06344
B	4	SER	-	SEE REMARK 999	UNP P06344
B	5	ASP	-	SEE REMARK 999	UNP P06344
B	6	TYR	-	SEE REMARK 999	UNP P06344
B	7	LYS	-	SEE REMARK 999	UNP P06344
B	8	SER	-	SEE REMARK 999	UNP P06344
B	9	ALA	-	SEE REMARK 999	UNP P06344
B	10	HIS	-	SEE REMARK 999	UNP P06344
B	91	LYS	-	linker	UNP P06344
B	92	GLY	-	linker	UNP P06344
B	93	GLY	-	linker	UNP P06344
B	94	THR	-	linker	UNP P06344
B	95	GLY	-	linker	UNP P06344
B	96	SER	-	linker	UNP P06344
B	97	GLY	-	linker	UNP P06344
B	98	SER	-	linker	UNP P06344
B	99	GLY	-	linker	UNP P06344
B	100	SER	-	linker	UNP P06344
B	299	SER	-	EXPRESSION TAG	UNP P06344
B	300	GLY	-	EXPRESSION TAG	UNP P06344
B	301	SER	-	EXPRESSION TAG	UNP P06344

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Chain	Residue	Modelled	Actual	Comment	Reference
B	302	ARG	-	EXPRESSION TAG	UNP P06344
B	303	LEU	-	EXPRESSION TAG	UNP P06344
B	304	GLU	-	EXPRESSION TAG	UNP P06344
B	305	VAL	-	EXPRESSION TAG	UNP P06344
B	306	LEU	-	EXPRESSION TAG	UNP P06344
B	307	PHE	-	EXPRESSION TAG	UNP P06344
B	308	GLN	-	EXPRESSION TAG	UNP P06344

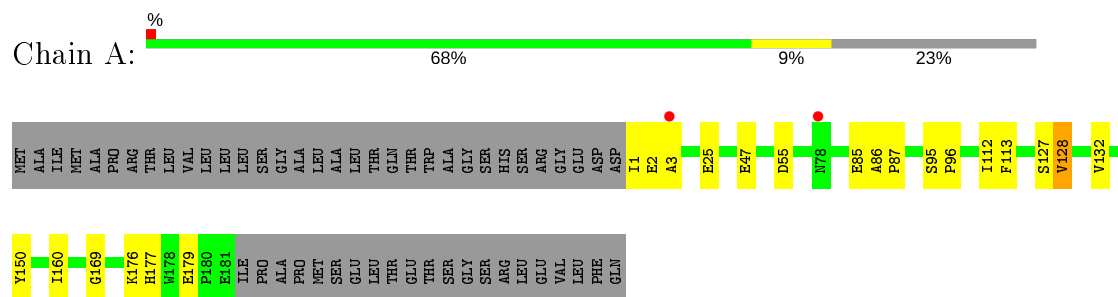
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	110	Total	O	0	0
			110	110		
3	B	96	Total	O	0	0
			96	96		

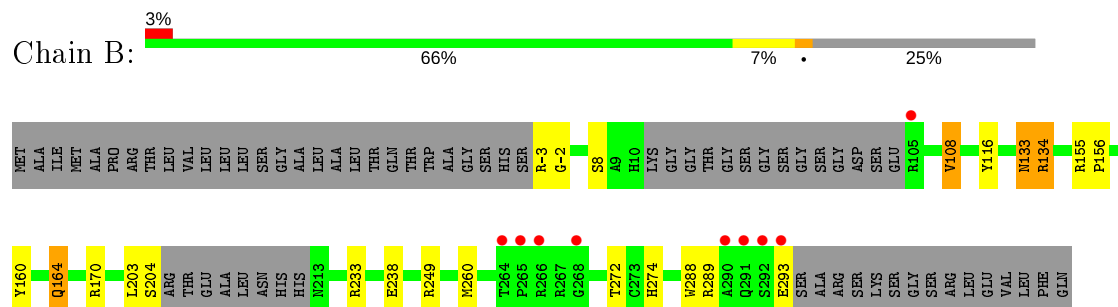
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: H-2 class II histocompatibility antigen, A-U alpha chain



- Molecule 2: H-2 class II histocompatibility antigen, A-U beta chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	103.66 Å 103.66 Å 97.25 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.37 – 2.15 46.36 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.9 (46.37-2.15) 99.9 (46.36-2.15)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	8.08 (at 2.14 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.209 , 0.260 0.209 , 0.260	Depositor DCC
R_{free} test set	1456 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	28.9	Xtriage
Anisotropy	0.065	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 52.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3203	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.57% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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

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	1.08	2/1469 (0.1%)	0.84	2/2012 (0.1%)
2	B	1.03	0/1611	0.89	0/2190
All	All	1.05	2/3080 (0.1%)	0.87	2/4202 (0.0%)

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
2	B	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	47	GLU	CB-CG	-5.91	1.41	1.52
1	A	25	GLU	CG-CD	5.21	1.59	1.51

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	55	ASP	CB-CG-OD1	6.13	123.82	118.30
1	A	55	ASP	CB-CG-OD2	-6.04	112.86	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	108	VAL	Peptide

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	1424	0	1328	15	0
2	B	1573	0	1466	25	0
3	A	110	0	0	2	0
3	B	96	0	0	1	0
All	All	3203	0	2794	36	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 6.

All (36) 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:A:160:ILE:HG22	1:A:179:GLU:HG2	1.50	0.92
2:B:160:TYR:O	2:B:164:GLN:HB2	1.85	0.77
2:B:289:ARG:H	2:B:293:GLU:HA	1.50	0.75
2:B:260:MET:HG3	3:B:328:HOH:O	1.93	0.68
2:B:272:THR:HG22	2:B:274:HIS:CD2	2.31	0.65
2:B:203:LEU:O	2:B:204:SER:HB2	2.00	0.62
3:A:287:HOH:O	2:B:249:ARG:HD3	1.99	0.61
2:B:203:LEU:HD11	2:B:288:TRP:CZ2	2.36	0.61
2:B:233:ARG:HE	2:B:238:GLU:HG2	1.68	0.57
1:A:95:SER:HB2	1:A:96:PRO:HD2	1.87	0.55
2:B:-3:ARG:CG	2:B:-2:GLY:H	2.19	0.55
1:A:160:ILE:HD12	1:A:177:HIS:HE1	1.75	0.52
2:B:272:THR:CG2	2:B:274:HIS:CD2	2.93	0.51
2:B:233:ARG:HG3	2:B:238:GLU:HB2	1.94	0.50
1:A:113:PHE:CZ	2:B:134:ARG:HG3	2.48	0.48
1:A:3:ALA:HB2	2:B:116:TYR:HB3	1.95	0.48
1:A:160:ILE:CG2	1:A:179:GLU:HG2	2.33	0.48
1:A:113:PHE:CE1	2:B:134:ARG:HG2	2.49	0.46
2:B:-3:ARG:CG	2:B:-2:GLY:N	2.79	0.46
2:B:108:VAL:H	2:B:133:ASN:ND2	2.13	0.46
1:A:113:PHE:CZ	2:B:134:ARG:CG	2.99	0.45
1:A:85:GLU:O	1:A:169:GLY:HA3	2.16	0.45
2:B:289:ARG:H	2:B:293:GLU:CA	2.25	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:132:VAL:HA	1:A:150:TYR:O	2.17	0.44
2:B:155:ARG:N	2:B:156:PRO:CD	2.81	0.44
1:A:128:VAL:O	1:A:128:VAL:CG2	2.66	0.44
2:B:289:ARG:N	2:B:293:GLU:HA	2.26	0.44
1:A:86:ALA:HA	1:A:87:PRO:HD2	1.76	0.43
1:A:160:ILE:HD12	1:A:177:HIS:CE1	2.54	0.43
2:B:-3:ARG:HG2	2:B:-2:GLY:N	2.34	0.42
1:A:176:LYS:HA	1:A:176:LYS:HD2	1.83	0.42
2:B:203:LEU:HD11	2:B:288:TRP:HZ2	1.82	0.42
2:B:203:LEU:HD11	2:B:288:TRP:CE2	2.55	0.42
1:A:112:ILE:HA	3:A:218:HOH:O	2.20	0.41
2:B:203:LEU:HD11	2:B:288:TRP:NE1	2.36	0.41
2:B:-3:ARG:HG2	2:B:-2:GLY:H	1.85	0.41

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	180/236 (76%)	174 (97%)	5 (3%)	1 (1%)	25	18
2	B	188/259 (73%)	182 (97%)	5 (3%)	1 (0%)	29	22
All	All	368/495 (74%)	356 (97%)	10 (3%)	2 (0%)	29	22

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	GLU
2	B	133	ASN

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	154/207 (74%)	151 (98%)	3 (2%)	57	61
2	B	168/226 (74%)	164 (98%)	4 (2%)	49	51
All	All	322/433 (74%)	315 (98%)	7 (2%)	52	55

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	ILE
1	A	127	SER
1	A	128	VAL
2	B	8	SER
2	B	134	ARG
2	B	164	GLN
2	B	170	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	88	GLN
1	A	118	ASN
2	B	133	ASN
2	B	250	ASN
2	B	256	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 [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, 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	182/236 (77%)	-0.22	2 (1%) 80 85	12, 26, 41, 50	0
2	B	194/259 (74%)	0.00	9 (4%) 32 42	13, 29, 58, 72	0
All	All	376/495 (75%)	-0.10	11 (2%) 51 61	12, 27, 49, 72	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	292	SER	6.1
2	B	268	GLY	5.9
2	B	265	PRO	4.8
2	B	291	GLN	3.1
2	B	290	ALA	3.1
2	B	264	THR	3.1
2	B	266	ARG	2.7
1	A	78	ASN	2.5
2	B	293	GLU	2.4
2	B	105	ARG	2.3
1	A	3	ALA	2.1

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.