



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 21, 2021 – 12:11 PM EST

PDB ID : 6WTY
Title : Plasmodium vivax reticulocyte binding protein 2b (PvRBP2b) bound to human monoclonal antibody 253245
Authors : Chan, L.J.; Dietrich, M.H.; Tham, W.H.
Deposited on : 2020-05-04
Resolution : 3.48 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

<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	:	2.16
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)	:	2.16

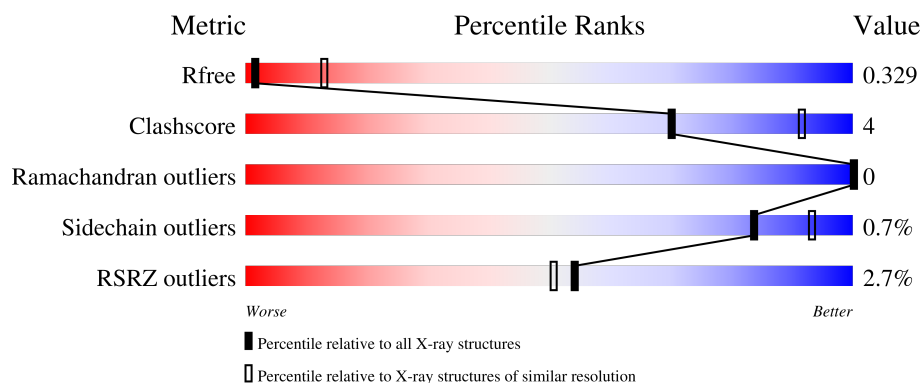
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.48 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	1379 (3.56-3.40)
Clashscore	141614	1461 (3.56-3.40)
Ramachandran outliers	138981	1424 (3.56-3.40)
Sidechain outliers	138945	1425 (3.56-3.40)
RSRZ outliers	127900	1289 (3.56-3.40)

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 ≥ 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	307	<div> <div>2%</div> <div>91% 5% 5%</div> </div>
1	D	307	<div> <div>2%</div> <div>83% 12% 5%</div> </div>
1	G	307	<div> <div>4%</div> <div>93% 6%</div> </div>
1	J	307	<div> <div>2%</div> <div>90% 6%</div> </div>
2	C	221	<div> <div>0%</div> <div>86% 10% 5%</div> </div>

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Mol	Chain	Length	Quality of chain
2	F	221	<div><div></div><div>%</div><div>90%</div><div>6%</div><div></div></div>
2	I	221	<div><div></div><div>3%</div><div>90%</div><div>6%</div><div></div></div>
2	L	221	<div><div></div><div>3%</div><div>86%</div><div>9%</div><div>5%</div></div>
3	B	241	<div><div></div><div>2%</div><div>84%</div><div>8%</div><div>8%</div></div>
3	E	241	<div><div></div><div>2%</div><div>82%</div><div>11%</div><div>7%</div></div>
3	H	241	<div><div></div><div>3%</div><div>74%</div><div>16%</div><div>10%</div></div>
3	K	241	<div><div></div><div>5%</div><div>80%</div><div>10%</div><div>10%</div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 19922 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 reticulocyte binding protein 2b.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	292	Total	C	N	O	S	0	0	0
			2209	1409	361	430	9			
1	J	289	Total	C	N	O	S	0	0	0
			1862	1157	327	373	5			
1	G	290	Total	C	N	O	S	0	0	0
			1881	1168	323	383	7			
1	A	293	Total	C	N	O	S	0	0	0
			2188	1394	364	422	8			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	164	GLY	-	expression tag	UNP A5K736
D	165	ALA	-	expression tag	UNP A5K736
D	166	MET	-	expression tag	UNP A5K736
D	167	GLY	-	expression tag	UNP A5K736
D	168	SER	-	expression tag	UNP A5K736
J	164	GLY	-	expression tag	UNP A5K736
J	165	ALA	-	expression tag	UNP A5K736
J	166	MET	-	expression tag	UNP A5K736
J	167	GLY	-	expression tag	UNP A5K736
J	168	SER	-	expression tag	UNP A5K736
G	164	GLY	-	expression tag	UNP A5K736
G	165	ALA	-	expression tag	UNP A5K736
G	166	MET	-	expression tag	UNP A5K736
G	167	GLY	-	expression tag	UNP A5K736
G	168	SER	-	expression tag	UNP A5K736
A	164	GLY	-	expression tag	UNP A5K736
A	165	ALA	-	expression tag	UNP A5K736
A	166	MET	-	expression tag	UNP A5K736
A	167	GLY	-	expression tag	UNP A5K736
A	168	SER	-	expression tag	UNP A5K736

- Molecule 2 is a protein called 253245 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	211	Total	C	N	O	S	0	0	0
			1449	902	239	303	5			
2	F	212	Total	C	N	O	S	0	0	0
			1476	921	244	306	5			
2	L	211	Total	C	N	O	S	0	0	0
			1420	884	235	296	5			
2	I	212	Total	C	N	O	S	0	0	0
			1435	889	236	305	5			

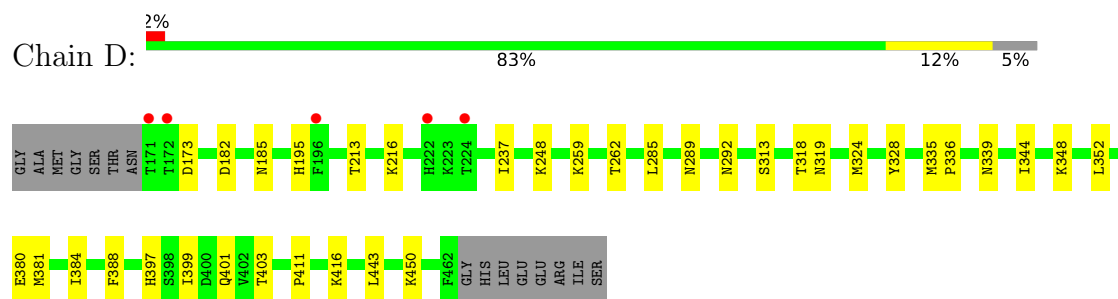
- Molecule 3 is a protein called 253245 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	B	222	Total	C	N	O	S	0	0	0
			1538	976	255	302	5			
3	H	218	Total	C	N	O	S	0	0	0
			1492	948	243	296	5			
3	K	217	Total	C	N	O	S	0	0	0
			1434	899	235	295	5			
3	E	224	Total	C	N	O	S	0	0	0
			1538	968	253	310	7			

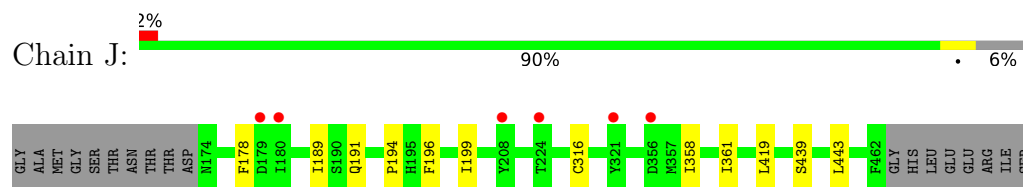
3 Residue-property plots [i](#)

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.

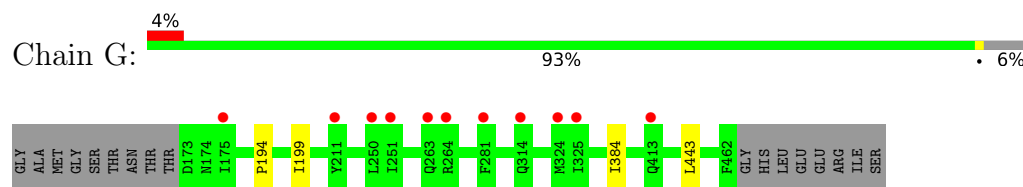
- Molecule 1: reticulocyte binding protein 2b



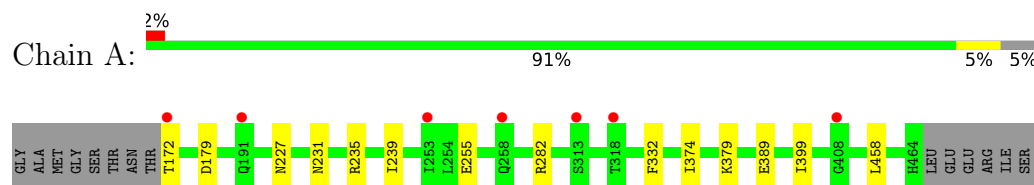
- Molecule 1: reticulocyte binding protein 2b



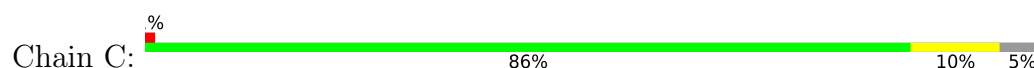
- Molecule 1: reticulocyte binding protein 2b



- Molecule 1: reticulocyte binding protein 2b

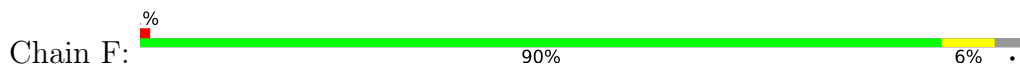


- Molecule 2: 253245 Fab light chain

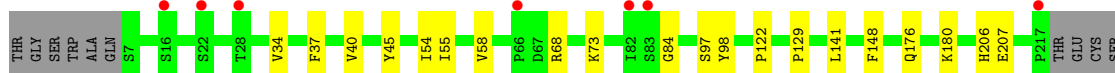
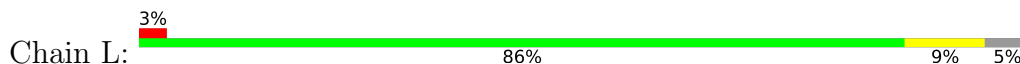




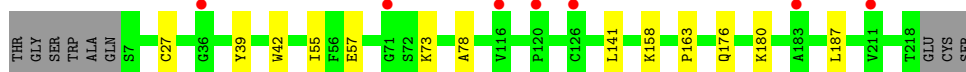
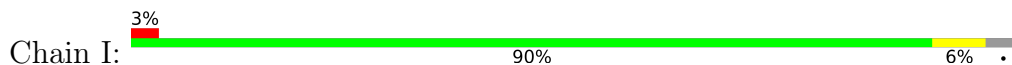
- Molecule 2: 253245 Fab light chain



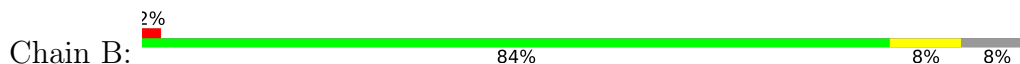
- Molecule 2: 253245 Fab light chain



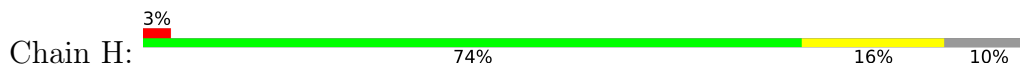
- Molecule 2: 253245 Fab light chain



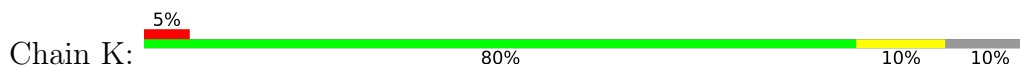
- Molecule 3: 253245 Fab heavy chain

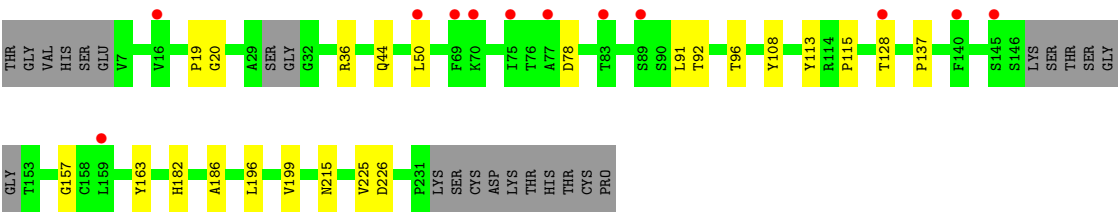


- Molecule 3: 253245 Fab heavy chain

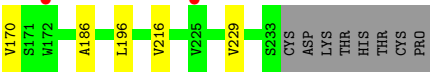
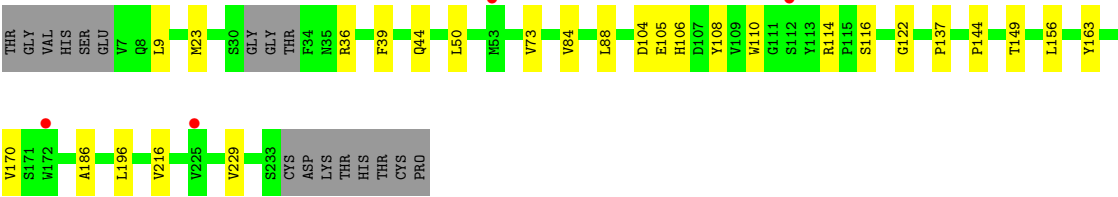
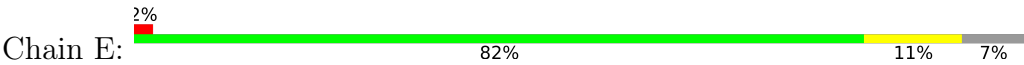


- Molecule 3: 253245 Fab heavy chain





● Molecule 3: 253245 Fab heavy chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	70.56Å 78.19Å 312.08Å 90.00° 94.16° 90.00°	Depositor
Resolution (Å)	48.70 – 3.48 48.70 – 3.48	Depositor EDS
% Data completeness (in resolution range)	98.3 (48.70-3.48) 98.3 (48.70-3.48)	Depositor EDS
R_{merge}	0.77	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.03 (at 3.48Å)	Xtriage
Refinement program	PHENIX 1.15_3459	Depositor
R, R_{free}	0.262 , 0.301 0.283 , 0.329	Depositor DCC
R_{free} test set	1997 reflections (4.61%)	wwPDB-VP
Wilson B-factor (Å ²)	86.2	Xtriage
Anisotropy	0.053	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 63.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.37$, $\langle L^2 \rangle = 0.20$	Xtriage
Estimated twinning fraction	0.088 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.84	EDS
Total number of atoms	19922	wwPDB-VP
Average B, all atoms (Å ²)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.91% 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 [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	0.23	0/2230	0.34	0/3039
1	D	0.23	0/2252	0.33	0/3067
1	G	0.22	0/1910	0.33	0/2628
1	J	0.22	0/1892	0.34	0/2600
2	C	0.25	0/1484	0.44	0/2042
2	F	0.25	0/1513	0.44	0/2080
2	I	0.24	0/1469	0.45	0/2023
2	L	0.25	0/1455	0.44	0/2006
3	B	0.24	0/1577	0.44	0/2169
3	E	0.24	0/1577	0.45	0/2171
3	H	0.25	0/1531	0.46	0/2112
3	K	0.26	0/1466	0.46	0/2020
All	All	0.24	0/20356	0.41	0/27957

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	2188	0	1916	7	0
1	D	2209	0	1939	20	0
1	G	1881	0	1334	2	0
1	J	1862	0	1312	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	1449	0	1270	12	0
2	F	1476	0	1298	8	0
2	I	1435	0	1224	8	0
2	L	1420	0	1210	13	0
3	B	1538	0	1366	11	0
3	E	1538	0	1349	15	0
3	H	1492	0	1312	27	0
3	K	1434	0	1209	13	0
All	All	19922	0	16739	132	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 4.

The worst 5 of 132 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)
2:C:157:TRP:HE1	2:C:185:SER:HG	1.33	0.73
3:H:40:SER:HB2	3:H:117:LEU:HD21	1.72	0.71
3:K:137:PRO:HB3	3:K:163:TYR:HB3	1.73	0.70
3:E:106:HIS:HB2	3:E:110:TRP:HB2	1.75	0.69
1:D:388:PHE:HA	1:D:443:LEU:HD13	1.80	0.64

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	291/307 (95%)	283 (97%)	8 (3%)	0	100	100
1	D	290/307 (94%)	279 (96%)	11 (4%)	0	100	100
1	G	288/307 (94%)	279 (97%)	9 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	J	287/307 (94%)	276 (96%)	11 (4%)	0	100	100
2	C	209/221 (95%)	197 (94%)	12 (6%)	0	100	100
2	F	210/221 (95%)	195 (93%)	15 (7%)	0	100	100
2	I	210/221 (95%)	193 (92%)	17 (8%)	0	100	100
2	L	209/221 (95%)	189 (90%)	20 (10%)	0	100	100
3	B	216/241 (90%)	203 (94%)	13 (6%)	0	100	100
3	E	220/241 (91%)	207 (94%)	13 (6%)	0	100	100
3	H	214/241 (89%)	203 (95%)	11 (5%)	0	100	100
3	K	211/241 (88%)	203 (96%)	8 (4%)	0	100	100
All	All	2855/3076 (93%)	2707 (95%)	148 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	207/286 (72%)	206 (100%)	1 (0%)	88	95
1	D	212/286 (74%)	211 (100%)	1 (0%)	88	95
1	G	128/286 (45%)	128 (100%)	0	100	100
1	J	121/286 (42%)	121 (100%)	0	100	100
2	C	145/188 (77%)	143 (99%)	2 (1%)	67	85
2	F	148/188 (79%)	148 (100%)	0	100	100
2	I	138/188 (73%)	138 (100%)	0	100	100
2	L	134/188 (71%)	133 (99%)	1 (1%)	84	93
3	B	149/206 (72%)	147 (99%)	2 (1%)	69	86
3	E	151/206 (73%)	149 (99%)	2 (1%)	69	86
3	H	143/206 (69%)	141 (99%)	2 (1%)	67	85
3	K	131/206 (64%)	129 (98%)	2 (2%)	65	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	1807/2720 (66%)	1794 (99%)	13 (1%)	84	93

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	H	34	PHE
3	H	182	HIS
3	K	182	HIS
3	B	110	TRP
3	K	113	TYR

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

Mol	Chain	Res	Type
1	A	367	ASN
3	E	189	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 ⓘ

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	293/307 (95%)	0.26	7 (2%) 59 55	52, 68, 88, 106	0
1	D	292/307 (95%)	0.13	5 (1%) 70 66	51, 67, 84, 103	0
1	G	290/307 (94%)	0.28	11 (3%) 40 37	54, 85, 116, 135	0
1	J	289/307 (94%)	0.04	6 (2%) 63 60	67, 86, 100, 119	0
2	C	211/221 (95%)	0.33	3 (1%) 75 71	42, 72, 86, 102	0
2	F	212/221 (95%)	0.31	3 (1%) 75 71	43, 66, 88, 120	0
2	I	212/221 (95%)	0.34	7 (3%) 46 43	57, 75, 93, 108	0
2	L	211/221 (95%)	0.32	7 (3%) 46 43	48, 76, 97, 106	0
3	B	222/241 (92%)	0.22	4 (1%) 68 64	47, 65, 82, 103	0
3	E	224/241 (92%)	0.26	4 (1%) 68 64	41, 68, 82, 99	0
3	H	218/241 (90%)	0.37	8 (3%) 41 39	54, 74, 93, 110	0
3	K	217/241 (90%)	0.51	12 (5%) 25 24	57, 85, 115, 122	0
All	All	2891/3076 (93%)	0.27	77 (2%) 54 51	41, 74, 98, 135	0

The worst 5 of 77 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	224	THR	5.7
3	K	83	THR	4.4
1	G	413	GLN	4.1
3	K	50	LEU	3.6
3	H	199	VAL	3.5

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 [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.