



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 21, 2021 – 12:04 PM EST

PDB ID : 6WM9
Title : Plasmodium vivax reticulocyte binding protein 2b (PvRBP2b) bound to human monoclonal antibody 237235
Authors : Chan, L.J.; Dietrich, M.H.; Tham, W.H.
Deposited on : 2020-04-20
Resolution : 2.45 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	:	2.16
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

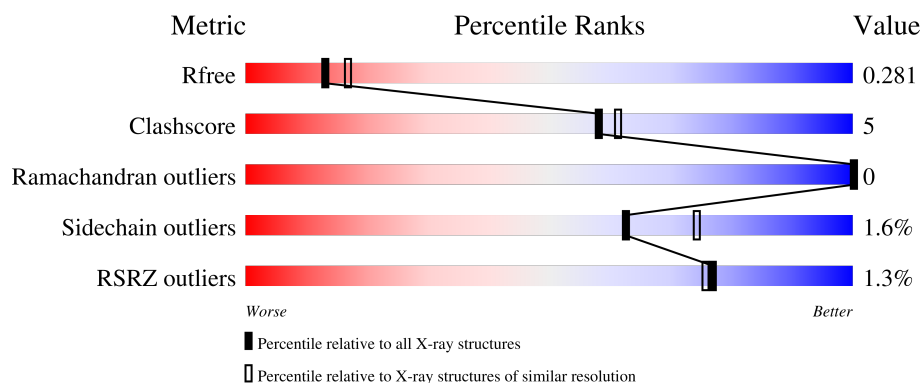
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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	1544 (2.48-2.44)
Clashscore	141614	1613 (2.48-2.44)
Ramachandran outliers	138981	1598 (2.48-2.44)
Sidechain outliers	138945	1598 (2.48-2.44)
RSRZ outliers	127900	1523 (2.48-2.44)

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>%</div> <div>88% 8% .</div> </div>
1	D	307	<div> <div>2%</div> <div>87% 9% .</div> </div>
2	B	235	<div> <div>%</div> <div>78% 17% . .</div> </div>
2	E	235	<div> <div>2%</div> <div>80% 14% 6%</div> </div>
3	C	221	<div> <div>%</div> <div>83% 13% .</div> </div>

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Mol	Chain	Length	Quality of chain
3	F	221	<div><div>%</div><div><div></div><div>85%</div><div>11%</div><div>.</div></div></div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11810 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	A	296	Total	C	N	O	S	0	0	0
			2413	1551	400	454	8			
1	D	295	Total	C	N	O	S	0	0	0
			2414	1551	401	453	9			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
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
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

- Molecule 2 is a protein called 237235 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	225	Total	C	N	O	S	0	0	0
			1650	1038	276	327	9			
2	E	222	Total	C	N	O	S	0	0	0
			1635	1027	276	324	8			

- Molecule 3 is a protein called 237235 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	212	Total	C	N	O	S	0	0	0
			1565	982	260	317	6			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	F	212	Total	C	N	O	S	0	0	0
			1574	990	259	319	6			

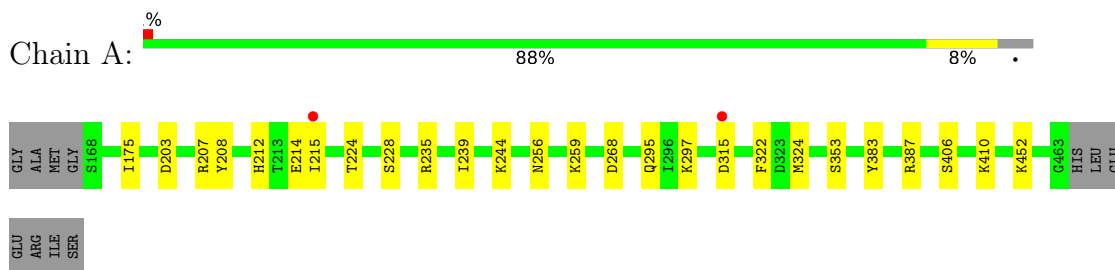
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	112	Total	O	0	0
			112	112		
4	B	88	Total	O	0	0
			88	88		
4	E	81	Total	O	0	0
			81	81		
4	C	81	Total	O	0	0
			81	81		
4	F	92	Total	O	0	0
			92	92		
4	D	105	Total	O	0	0
			105	105		

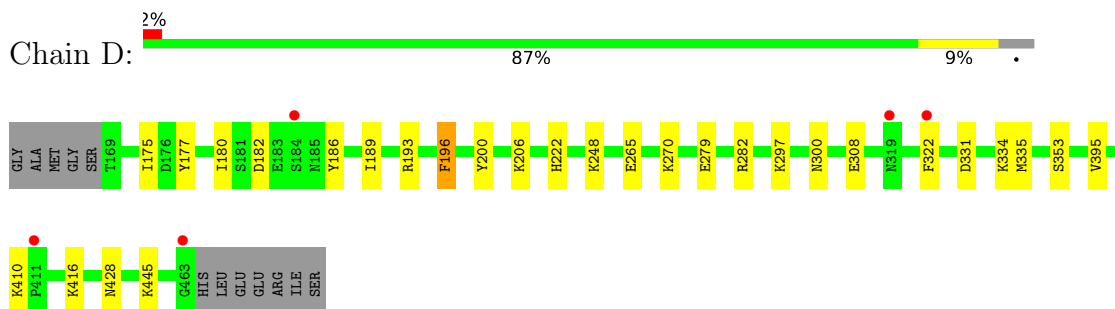
3 Residue-property plots [i](#)

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.

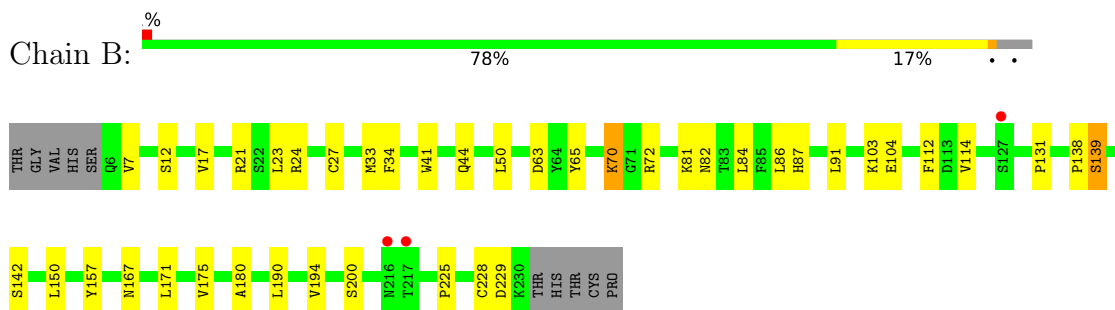
- Molecule 1: Reticulocyte binding protein 2b



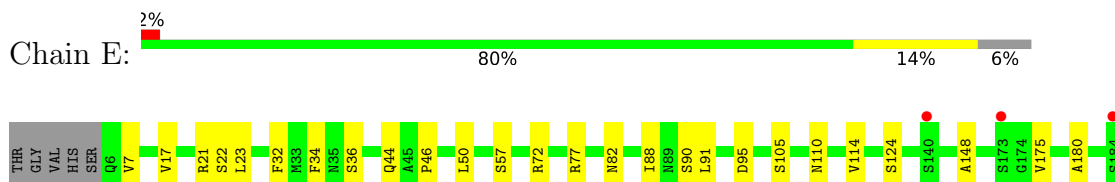
- Molecule 1: Reticulocyte binding protein 2b



- Molecule 2: 237235 Fab heavy chain

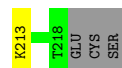
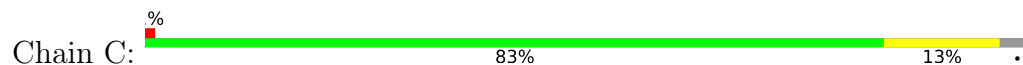


- Molecule 2: 237235 Fab heavy chain

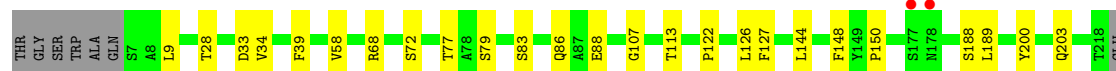
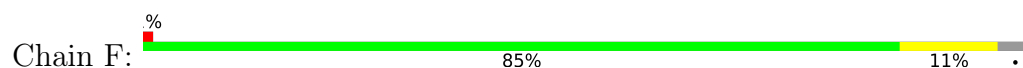




- Molecule 3: 237235 Fab light chain



- Molecule 3: 237235 Fab light chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	61.90Å 86.78Å 90.77Å 91.62° 109.98° 99.88°	Depositor
Resolution (Å)	42.46 – 2.45 43.67 – 2.45	Depositor EDS
% Data completeness (in resolution range)	97.5 (42.46-2.45) 97.5 (43.67-2.45)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.63 (at 2.45Å)	Xtriage
Refinement program	PHENIX 1.15_3459	Depositor
R, R_{free}	0.223 , 0.279 0.224 , 0.281	Depositor DCC
R_{free} test set	3120 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	29.8	Xtriage
Anisotropy	0.772	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 47.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	11810	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.33% 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	0.24	0/2461	0.35	0/3318
1	D	0.24	0/2462	0.35	0/3318
2	B	0.26	0/1691	0.47	0/2305
2	E	0.26	0/1676	0.47	0/2288
3	C	0.25	0/1608	0.45	0/2203
3	F	0.25	0/1617	0.45	0/2213
All	All	0.25	0/11515	0.42	0/15645

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	2413	0	2335	13	0
1	D	2414	0	2342	18	0
2	B	1650	0	1535	23	0
2	E	1635	0	1528	22	0
3	C	1565	0	1460	17	0
3	F	1574	0	1482	18	0
4	A	112	0	0	2	0
4	B	88	0	0	1	0
4	C	81	0	0	2	0
4	D	105	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	E	81	0	0	0	0
4	F	92	0	0	3	0
All	All	11810	0	10682	106	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 5.

All (106) 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:B:138:PRO:HG3	2:B:150:LEU:HB3	1.66	0.75
3:F:33:ASP:OD2	3:F:34:VAL:HG23	1.91	0.70
3:C:38:ASN:OD1	3:C:73:LYS:NZ	2.26	0.68
2:E:23:LEU:HB2	2:E:91:LEU:HD11	1.75	0.68
2:B:228:CYS:SG	2:B:229:ASP:N	2.66	0.67
1:A:203:ASP:O	1:A:207:ARG:NH1	2.29	0.65
3:F:203:GLN:NE2	4:F:301:HOH:O	2.28	0.65
3:F:113:THR:HG21	3:F:150:PRO:HB3	1.82	0.62
2:E:200:SER:HA	2:E:203:THR:HG22	1.83	0.60
1:D:248:LYS:NZ	4:D:503:HOH:O	2.32	0.60
2:E:193:VAL:HG21	3:F:144:LEU:HD13	1.84	0.59
2:E:36:SER:HB3	1:D:445:LYS:HD3	1.84	0.58
2:E:180:ALA:HA	2:E:190:LEU:HB3	1.85	0.58
2:E:180:ALA:HB2	2:E:190:LEU:HD23	1.85	0.57
1:A:256:ASN:HB3	1:A:259:LYS:HB2	1.86	0.57
2:E:175:VAL:HG22	2:E:194:VAL:HG22	1.89	0.55
3:C:40:VAL:HG22	3:C:58:VAL:HA	1.88	0.54
2:E:57:SER:O	2:E:77:ARG:NH1	2.41	0.53
3:F:126:LEU:HD23	3:F:127:PHE:N	2.23	0.53
1:D:335:MET:CE	1:D:395:VAL:HG11	2.39	0.53
2:B:7:VAL:HG12	2:B:114:VAL:HG11	1.90	0.53
2:B:23:LEU:HB2	2:B:91:LEU:HD11	1.90	0.53
3:C:122:PRO:HB3	3:C:148:PHE:HB3	1.90	0.53
3:C:41:SER:N	3:C:96:CYS:O	2.35	0.53
1:D:331:ASP:HA	1:D:334:LYS:HE2	1.90	0.53
3:C:171:THR:HG22	3:C:184:SER:H	1.74	0.53
1:D:428:ASN:ND2	4:D:504:HOH:O	2.34	0.53
3:C:45:HIS:ND1	4:C:302:HOH:O	2.34	0.52
2:B:180:ALA:HB2	2:B:190:LEU:HD23	1.91	0.52
2:B:131:PRO:HB3	2:B:157:TYR:HB3	1.91	0.52
2:E:110:ASN:OD1	1:D:193:ARG:NH2	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:315:ASP:OD1	1:A:315:ASP:N	2.42	0.51
1:A:175:ILE:HD11	1:A:244:LYS:HG3	1.92	0.51
3:F:33:ASP:CG	3:F:34:VAL:H	2.10	0.51
2:B:103:LYS:NZ	2:B:104:GLU:O	2.44	0.50
2:B:27:CYS:HB3	2:B:84:LEU:HB3	1.92	0.50
1:D:279:GLU:OE1	1:D:282:ARG:NH1	2.40	0.50
2:B:44:GLN:HB2	2:B:50:LEU:HD23	1.94	0.50
3:C:158:LYS:HG2	3:C:201:SER:HB2	1.93	0.50
2:E:7:VAL:HG12	2:E:114:VAL:HG11	1.93	0.50
2:E:23:LEU:HD23	2:E:88:ILE:HD12	1.93	0.50
1:D:308:GLU:OE1	1:D:416:LYS:NZ	2.45	0.50
3:F:86:GLN:NE2	3:F:88:GLU:OE2	2.41	0.49
3:C:203:GLN:HG3	3:C:212:GLU:HG3	1.94	0.49
2:B:24:ARG:HG3	2:B:87:HIS:CE1	2.49	0.48
2:E:7:VAL:HG11	2:E:114:VAL:HG21	1.95	0.48
3:F:72:SER:HA	4:F:304:HOH:O	2.14	0.48
1:A:452:LYS:NZ	4:A:517:HOH:O	2.46	0.48
2:B:63:ASP:N	2:B:63:ASP:OD1	2.46	0.48
2:E:148:ALA:N	2:E:196:VAL:O	2.44	0.48
2:B:41:TRP:CE2	2:B:86:LEU:HB2	2.49	0.48
2:B:72:ARG:NH1	4:B:303:HOH:O	2.44	0.47
2:B:65:TYR:HB2	2:B:70:LYS:HD2	1.96	0.47
2:E:17:VAL:HG11	2:E:23:LEU:HD13	1.96	0.47
3:C:40:VAL:HG22	3:C:58:VAL:HG22	1.97	0.47
2:B:17:VAL:HG11	2:B:23:LEU:HD13	1.97	0.47
2:B:34:PHE:CD2	2:B:82:ASN:HA	2.50	0.47
1:D:335:MET:HE1	1:D:395:VAL:HG11	1.96	0.46
2:B:139:SER:H	2:B:142:SER:HB3	1.80	0.46
2:B:175:VAL:HG22	2:B:194:VAL:HG22	1.98	0.46
2:B:180:ALA:HA	2:B:190:LEU:HB3	1.97	0.45
1:A:214:GLU:N	1:A:214:GLU:OE1	2.42	0.45
3:F:33:ASP:OD2	3:F:34:VAL:N	2.35	0.45
3:F:58:VAL:HG12	4:F:304:HOH:O	2.16	0.45
2:B:167:ASN:HB2	2:B:171:LEU:HD12	1.98	0.45
1:A:212:HIS:HB2	1:A:215:ILE:HG12	1.99	0.44
3:C:127:PHE:CE1	3:C:144:LEU:HD23	2.52	0.44
1:D:265:GLU:HB2	1:D:270:LYS:HD3	2.00	0.44
1:A:235:ARG:O	1:A:239:ILE:HG12	2.17	0.44
3:F:188:SER:O	3:F:189:LEU:HD23	2.17	0.44
2:B:142:SER:OG	2:B:142:SER:O	2.36	0.43
1:A:295:GLN:NE2	4:A:502:HOH:O	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:175:ILE:HA	1:D:177:TYR:CE2	2.54	0.43
1:D:297:LYS:HA	1:D:300:ASN:HB2	2.01	0.43
1:D:180:ILE:O	1:D:189:ILE:HG12	2.18	0.43
3:F:68:ARG:HB3	3:F:83:SER:O	2.19	0.43
2:B:81:LYS:HA	2:E:82:ASN:HD21	1.83	0.42
3:C:17:GLY:O	3:C:114:VAL:HA	2.18	0.42
3:F:9:LEU:HB2	3:F:107:GLY:HA2	2.01	0.42
3:C:213:LYS:HA	3:C:213:LYS:HD3	1.89	0.42
3:F:189:LEU:HD11	3:F:200:TYR:CE2	2.55	0.42
3:C:87:ALA:HA	3:C:114:VAL:HG21	2.01	0.42
3:F:122:PRO:HB3	3:F:148:PHE:HB3	2.02	0.42
1:D:189:ILE:HG22	1:D:196:PHE:CD1	2.55	0.42
3:F:72:SER:OG	3:F:79:SER:HB2	2.19	0.42
3:C:18:SER:O	3:C:21:GLN:HG2	2.19	0.41
3:F:28:THR:HG22	3:F:77:THR:OG1	2.20	0.41
1:A:224:THR:O	1:A:228:SER:OG	2.23	0.41
1:A:383:TYR:O	1:A:387:ARG:HG2	2.20	0.41
2:E:200:SER:O	2:E:204:GLN:HB2	2.20	0.41
2:E:21:ARG:HG3	2:E:22:SER:H	1.86	0.41
3:C:150:PRO:HG2	4:C:304:HOH:O	2.20	0.41
1:D:335:MET:HE3	1:D:395:VAL:HG11	2.03	0.41
2:E:44:GLN:HB2	2:E:50:LEU:HD23	2.03	0.41
2:E:34:PHE:CD2	2:E:82:ASN:HA	2.55	0.41
2:E:110:ASN:HB3	3:F:39:PHE:HB3	2.03	0.41
3:C:23:VAL:HG13	3:C:85:LEU:HD11	2.02	0.41
1:D:206:LYS:HD3	1:D:222:HIS:CG	2.56	0.41
2:E:72:ARG:NH2	2:E:95:ASP:OD1	2.54	0.41
2:B:138:PRO:HD2	2:B:225:PRO:HA	2.03	0.40
1:D:182:ASP:HB3	1:D:186:TYR:N	2.36	0.40
2:E:7:VAL:HG13	2:E:32:PHE:CD1	2.56	0.40
1:A:208:TYR:CE1	1:A:324:MET:HG3	2.56	0.40
3:C:58:VAL:HG12	3:C:59:THR:HG23	2.03	0.40
1:A:322:PHE:CZ	1:A:410:LYS:HA	2.56	0.40
1:D:322:PHE:CZ	1:D:410:LYS:HA	2.57	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	294/307 (96%)	286 (97%)	8 (3%)	0	100	100
1	D	293/307 (95%)	286 (98%)	7 (2%)	0	100	100
2	B	223/235 (95%)	219 (98%)	4 (2%)	0	100	100
2	E	220/235 (94%)	214 (97%)	6 (3%)	0	100	100
3	C	210/221 (95%)	202 (96%)	8 (4%)	0	100	100
3	F	210/221 (95%)	206 (98%)	4 (2%)	0	100	100
All	All	1450/1526 (95%)	1413 (97%)	37 (3%)	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	258/286 (90%)	254 (98%)	4 (2%)	62	74
1	D	259/286 (91%)	256 (99%)	3 (1%)	71	81
2	B	175/199 (88%)	168 (96%)	7 (4%)	31	41
2	E	177/199 (89%)	173 (98%)	4 (2%)	50	63
3	C	171/187 (91%)	170 (99%)	1 (1%)	86	91
3	F	174/187 (93%)	174 (100%)	0	100	100
All	All	1214/1344 (90%)	1195 (98%)	19 (2%)	62	74

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	268	ASP
1	A	297	LYS
1	A	353	SER
1	A	406	SER
2	B	12	SER
2	B	21	ARG
2	B	33	MET
2	B	70	LYS
2	B	112	PHE
2	B	139	SER
2	B	200	SER
2	E	46	PRO
2	E	90	SER
2	E	105	SER
2	E	124	SER
3	C	33	ASP
1	D	196	PHE
1	D	200	TYR
1	D	353	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	417	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 monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

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	296/307 (96%)	0.02	2 (0%) 87 88	20, 31, 49, 59	0
1	D	295/307 (96%)	-0.07	5 (1%) 70 67	20, 31, 48, 56	0
2	B	225/235 (95%)	0.21	3 (1%) 77 76	19, 34, 54, 73	0
2	E	222/235 (94%)	0.19	5 (2%) 60 56	21, 35, 55, 66	0
3	C	212/221 (95%)	-0.01	2 (0%) 84 85	22, 31, 49, 62	0
3	F	212/221 (95%)	-0.04	2 (0%) 84 85	21, 32, 50, 57	0
All	All	1462/1526 (95%)	0.05	19 (1%) 77 76	19, 32, 51, 73	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	216	ASN	3.3
3	C	116	GLY	3.3
2	B	217	THR	3.2
2	E	184	SER	3.1
3	F	177	SER	2.6
1	A	215	ILE	2.5
1	D	411	PRO	2.5
1	D	319	ASN	2.4
2	E	140	SER	2.4
2	E	196	VAL	2.4
2	B	127	SER	2.2
1	D	322	PHE	2.2
1	D	184	SER	2.2
3	F	178	ASN	2.2
3	C	7	SER	2.2
1	A	315	ASP	2.1
1	D	463	GLY	2.1
2	E	173	SER	2.1
2	E	199	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 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.