



Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 08:33 pm BST

PDB ID : 1U8I
Title : Crystal structure of the HIV-1 Cross Neutralizing Monoclonal Antibody 2F5
in complex with gp41 Peptide ELDKWAN
Authors : Bryson, S.; Julien, J.-P.; Hynes, R.C.; Pai, E.F.
Deposited on : 2004-08-06
Resolution : 2.00 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

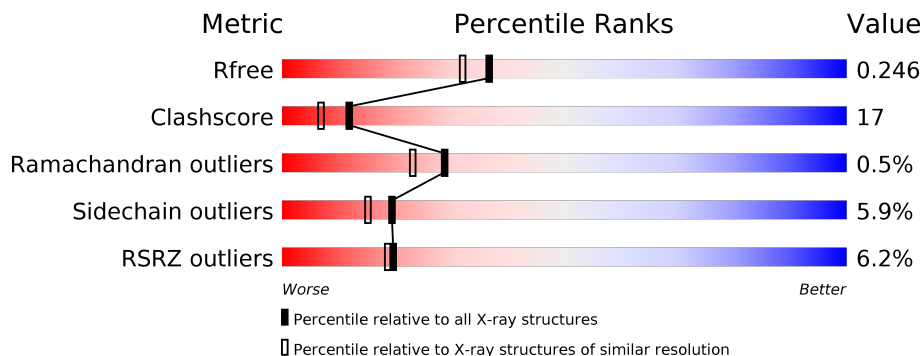
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION




The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	214	
2	B	235	
3	C	7	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3589 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 ANTIBODY 2F5 (LIGHT CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	214	1644	1025	281	333	5	0	0	0

- Molecule 2 is a protein called ANTIBODY 2F5 (HEAVY CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	227	1705	1084	289	325	7	0	0	0

- Molecule 3 is a protein called GP41 PEPTIDE.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	C	7	62	39	10	13	0	0	0

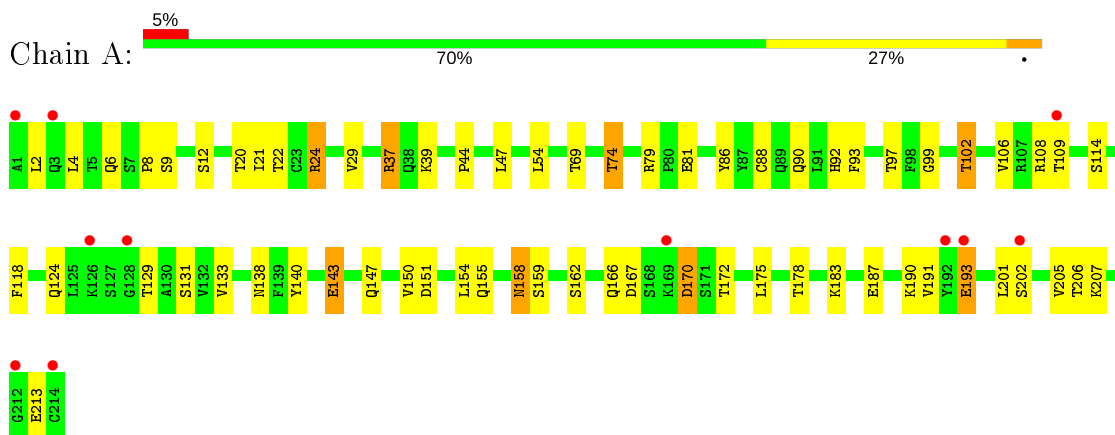
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	84	Total 84	O 84	0	0
4	B	91	Total 91	O 91	0	0
4	C	3	Total 3	O 3	0	0

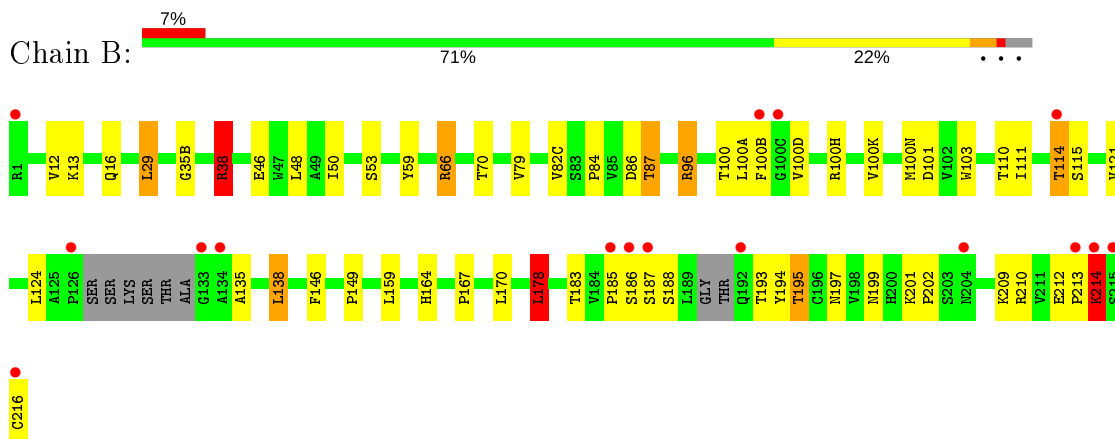
3 Residue-property plots [i](#)

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

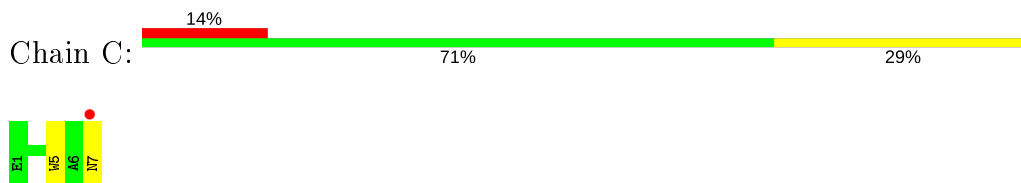
- Molecule 1: ANTIBODY 2F5 (LIGHT CHAIN)



- Molecule 2: ANTIBODY 2F5 (HEAVY CHAIN)



- Molecule 3: GP41 PEPTIDE



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	58.20Å 64.90Å 175.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	17.00 – 2.00 16.91 – 1.99	Depositor EDS
% Data completeness (in resolution range)	93.3 (17.00-2.00) 92.7 (16.91-1.99)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.48 (at 1.99Å)	Xtrriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.233 , 0.247 0.233 , 0.246	Depositor DCC
R_{free} test set	2140 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	30.6	Xtrriage
Anisotropy	0.065	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 50.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3589	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.90% 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	1.01	4/1681 (0.2%)	0.98	5/2284 (0.2%)
2	B	0.94	2/1746 (0.1%)	1.08	9/2385 (0.4%)
3	C	1.03	0/63	0.67	0/83
All	All	0.98	6/3490 (0.2%)	1.03	14/4752 (0.3%)

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
1	A	0	1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	108	ARG	C-N	-15.55	0.98	1.34
2	B	216	CYS	CB-SG	10.06	1.99	1.82
1	A	109	THR	C-N	9.94	1.56	1.34
1	A	193	GLU	CG-CD	8.60	1.64	1.51
2	B	59	TYR	CD1-CE1	5.33	1.47	1.39
1	A	193	GLU	CB-CG	5.05	1.61	1.52

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	38	ARG	NE-CZ-NH2	-12.80	113.90	120.30
2	B	38	ARG	NE-CZ-NH1	12.80	126.70	120.30
2	B	66	ARG	NE-CZ-NH1	8.76	124.68	120.30
1	A	213	GLU	O-C-N	-6.91	111.65	122.70
2	B	66	ARG	NE-CZ-NH2	-6.42	117.09	120.30
1	A	108	ARG	O-C-N	6.30	132.78	122.70
2	B	216	CYS	CA-CB-SG	6.01	124.82	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	178	LEU	CA-CB-CG	5.80	128.63	115.30
2	B	100(N)	MET	N-CA-C	-5.73	95.52	111.00
1	A	37	ARG	NE-CZ-NH2	-5.57	117.51	120.30
2	B	114	THR	O-C-N	5.20	131.03	122.70
1	A	114	SER	N-CA-C	-5.20	96.96	111.00
1	A	108	ARG	CA-C-N	-5.16	105.84	117.20
2	B	38	ARG	CB-CG-CD	5.12	124.91	111.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	86	TYR	Sidechain

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	1644	0	1587	57	0
2	B	1705	0	1721	66	0
3	C	62	0	57	5	0
4	A	84	0	0	3	0
4	B	91	0	0	4	0
4	C	3	0	0	0	0
All	All	3589	0	3365	117	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 17.

All (117) 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:195:THR:HG22	4:B:303:HOH:O	1.60	1.00
2:B:84:PRO:O	2:B:87:THR:HG23	1.66	0.96
1:A:90:GLN:HE22	1:A:93:PHE:H	1.01	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:20:THR:HG22	1:A:74:THR:HB	1.50	0.92
2:B:100(H):ARG:NH2	3:C:7:ASN:ND2	2.23	0.87
1:A:106:VAL:H	1:A:166:GLN:HE22	1.20	0.85
2:B:86:ASP:HB2	2:B:111:ILE:HD12	1.59	0.84
2:B:38:ARG:HD2	2:B:48:LEU:HD21	1.60	0.80
2:B:100(H):ARG:HH22	3:C:7:ASN:ND2	1.82	0.76
1:A:90:GLN:NE2	1:A:93:PHE:H	1.81	0.75
1:A:90:GLN:NE2	1:A:92:HIS:H	1.84	0.75
1:A:162:SER:HB2	2:B:167:PRO:HG2	1.71	0.71
2:B:210:ARG:NH1	2:B:212:GLU:OE1	2.25	0.70
2:B:100(H):ARG:NH2	3:C:7:ASN:HD21	1.90	0.69
2:B:29:LEU:O	2:B:53:SER:HB2	1.93	0.69
1:A:133:VAL:HG21	2:B:124:LEU:HD22	1.75	0.68
1:A:118:PHE:HB2	1:A:133:VAL:HG22	1.77	0.67
1:A:12:SER:HB3	1:A:140:TYR:OH	1.95	0.66
2:B:46:GLU:OE1	4:B:280:HOH:O	2.15	0.65
1:A:90:GLN:HE21	1:A:92:HIS:H	1.42	0.64
2:B:96:ARG:NH2	4:B:299:HOH:O	2.30	0.64
1:A:190:LYS:HG3	1:A:191:VAL:HG23	1.77	0.64
2:B:214:LYS:N	2:B:214:LYS:HE3	2.13	0.64
1:A:118:PHE:HD2	1:A:133:VAL:HG23	1.61	0.64
2:B:82(C):VAL:HB	2:B:111:ILE:HD13	1.79	0.63
1:A:39:LYS:HE3	4:A:265:HOH:O	2.00	0.61
1:A:8:PRO:O	1:A:102:THR:HB	2.01	0.61
1:A:167:ASP:HB3	1:A:170:ASP:HB2	1.83	0.60
1:A:79:ARG:HB3	1:A:81:GLU:OE2	2.01	0.60
1:A:193:GLU:OE2	4:A:231:HOH:O	2.16	0.60
2:B:82(C):VAL:CG2	2:B:111:ILE:HD13	2.32	0.59
2:B:213:PRO:C	2:B:214:LYS:HE3	2.23	0.59
1:A:29:VAL:HG11	1:A:90:GLN:HG3	1.84	0.59
2:B:213:PRO:HA	2:B:214:LYS:HE3	1.84	0.58
1:A:90:GLN:NE2	1:A:92:HIS:N	2.51	0.57
1:A:29:VAL:HG11	1:A:90:GLN:CG	2.35	0.57
2:B:114:THR:CG2	2:B:115:SER:O	2.52	0.56
2:B:135:ALA:HB1	2:B:183:THR:HG23	1.88	0.56
2:B:114:THR:HG21	2:B:146:PHE:CB	2.35	0.56
1:A:183:LYS:O	1:A:187:GLU:HG2	2.05	0.56
2:B:38:ARG:HD3	2:B:46:GLU:OE1	2.06	0.55
2:B:209:LYS:NZ	4:B:244:HOH:O	2.39	0.55
1:A:133:VAL:CG2	2:B:124:LEU:HD22	2.37	0.55
2:B:121:VAL:O	2:B:209:LYS:HE3	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:86:ASP:HB2	2:B:111:ILE:CD1	2.34	0.55
2:B:96:ARG:HD3	2:B:101:ASP:OD2	2.06	0.55
2:B:38:ARG:HB3	2:B:48:LEU:HD11	1.87	0.54
1:A:4:LEU:HD11	1:A:90:GLN:HB2	1.89	0.54
2:B:185:PRO:O	2:B:187:SER:N	2.40	0.54
1:A:21:ILE:HG23	1:A:102:THR:HG21	1.90	0.53
2:B:100(B):PHE:O	2:B:100(D):VAL:HG23	2.08	0.53
2:B:114:THR:CG2	2:B:115:SER:N	2.71	0.53
1:A:6:GLN:HE21	1:A:99:GLY:HA3	1.74	0.53
1:A:81:GLU:CD	1:A:81:GLU:H	2.13	0.52
2:B:185:PRO:C	2:B:187:SER:H	2.13	0.52
1:A:124:GLN:HE22	1:A:131:SER:HB2	1.75	0.52
1:A:124:GLN:NE2	1:A:131:SER:H	2.07	0.52
1:A:147:GLN:NE2	1:A:154:LEU:HG	2.25	0.52
2:B:213:PRO:C	2:B:214:LYS:HZ2	2.13	0.51
2:B:188:SER:HB3	2:B:194:TYR:OH	2.11	0.51
2:B:84:PRO:O	2:B:87:THR:CG2	2.51	0.51
2:B:87:THR:HG22	2:B:111:ILE:H	1.75	0.51
1:A:158:ASN:ND2	1:A:158:ASN:H	2.09	0.51
2:B:193:THR:HG22	2:B:210:ARG:HH21	1.76	0.51
1:A:155:GLN:HB3	1:A:158:ASN:HD21	1.76	0.51
1:A:9:SER:O	1:A:102:THR:HA	2.10	0.50
1:A:118:PHE:HB2	1:A:133:VAL:CG2	2.41	0.50
2:B:12:VAL:O	2:B:111:ILE:HA	2.13	0.49
2:B:87:THR:HB	2:B:110:THR:HA	1.95	0.48
2:B:114:THR:HG22	2:B:115:SER:O	2.12	0.48
1:A:170:ASP:HB3	1:A:172:THR:HG23	1.95	0.48
2:B:82(C):VAL:CB	2:B:111:ILE:HD13	2.43	0.48
1:A:147:GLN:CD	1:A:154:LEU:HD11	2.34	0.48
2:B:82(C):VAL:HB	2:B:111:ILE:CD1	2.42	0.48
2:B:201:LYS:HB2	2:B:202:PRO:HD3	1.96	0.47
1:A:2:LEU:C	1:A:2:LEU:HD23	2.34	0.47
1:A:158:ASN:H	1:A:158:ASN:HD22	1.62	0.47
1:A:90:GLN:HE22	1:A:93:PHE:N	1.87	0.47
1:A:37:ARG:HB2	1:A:47:LEU:HD11	1.96	0.47
1:A:118:PHE:CD2	1:A:133:VAL:HG23	2.47	0.47
2:B:29:LEU:O	2:B:53:SER:CB	2.62	0.47
2:B:13:LYS:H	2:B:16:GLN:NE2	2.13	0.45
2:B:213:PRO:C	2:B:214:LYS:NZ	2.69	0.45
1:A:143:GLU:H	1:A:143:GLU:CD	2.20	0.45
2:B:35(B):GLY:HA2	2:B:50:ILE:HA	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:147:GLN:CG	1:A:154:LEU:HD11	2.47	0.45
2:B:213:PRO:C	2:B:214:LYS:CE	2.86	0.45
1:A:124:GLN:HG2	1:A:129:THR:O	2.16	0.44
2:B:100(H):ARG:HH22	3:C:7:ASN:HD22	1.61	0.44
1:A:138:ASN:OD1	2:B:164:HIS:HE1	2.00	0.44
1:A:201:LEU:HD13	1:A:205:VAL:HG12	1.99	0.44
1:A:206:THR:O	1:A:207:LYS:HD2	2.18	0.44
1:A:175:LEU:HD23	1:A:175:LEU:C	2.38	0.43
1:A:133:VAL:HG21	2:B:124:LEU:CD2	2.44	0.43
1:A:201:LEU:CD1	1:A:205:VAL:HG12	2.49	0.43
2:B:178:LEU:HD12	2:B:178:LEU:C	2.39	0.43
1:A:158:ASN:N	1:A:158:ASN:ND2	2.66	0.43
2:B:100(K):VAL:HG21	3:C:5:TRP:CD1	2.54	0.43
2:B:114:THR:HG21	2:B:146:PHE:HB3	1.99	0.42
1:A:44:PRO:HD2	2:B:103:TRP:CE3	2.55	0.42
2:B:100(H):ARG:O	2:B:100(K):VAL:HG22	2.20	0.42
2:B:70:THR:CG2	2:B:79:VAL:HB	2.50	0.42
1:A:6:GLN:NE2	1:A:88:CYS:H	2.18	0.41
2:B:100(A):LEU:HG	2:B:100(B):PHE:CD1	2.55	0.41
2:B:100:THR:HA	2:B:100(D):VAL:O	2.21	0.41
2:B:138:LEU:N	2:B:138:LEU:CD2	2.83	0.41
1:A:159:SER:HA	1:A:178:THR:O	2.21	0.41
2:B:185:PRO:C	2:B:187:SER:N	2.73	0.41
1:A:74:THR:CG2	4:A:240:HOH:O	2.68	0.41
2:B:114:THR:HG23	2:B:115:SER:O	2.19	0.41
2:B:138:LEU:N	2:B:138:LEU:HD23	2.36	0.41
2:B:87:THR:CG2	2:B:111:ILE:H	2.34	0.41
1:A:150:VAL:O	1:A:151:ASP:C	2.60	0.41
1:A:24:ARG:HA	1:A:69:THR:O	2.21	0.41
1:A:29:VAL:HG11	1:A:90:GLN:HG2	2.03	0.40
2:B:66:ARG:NH2	2:B:86:ASP:OD2	2.53	0.40
2:B:213:PRO:CA	2:B:214:LYS:HE3	2.48	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	212/214 (99%)	204 (96%)	8 (4%)	0	100	100
2	B	221/235 (94%)	212 (96%)	7 (3%)	2 (1%)	17	11
3	C	5/7 (71%)	5 (100%)	0	0	100	100
All	All	438/456 (96%)	421 (96%)	15 (3%)	2 (0%)	29	23

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	214	LYS
2	B	186	SER

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	187/187 (100%)	177 (95%)	10 (5%)	22	18
2	B	197/203 (97%)	184 (93%)	13 (7%)	16	12
3	C	6/6 (100%)	6 (100%)	0	100	100
All	All	390/396 (98%)	367 (94%)	23 (6%)	19	15

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	THR
1	A	24	ARG
1	A	54	LEU
1	A	74	THR
1	A	97	THR
1	A	102	THR
1	A	143	GLU

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Mol	Chain	Res	Type
1	A	158	ASN
1	A	170	ASP
1	A	202	SER
2	B	29	LEU
2	B	38	ARG
2	B	87	THR
2	B	96	ARG
2	B	138	LEU
2	B	149	PRO
2	B	159	LEU
2	B	170	LEU
2	B	178	LEU
2	B	195	THR
2	B	197	ASN
2	B	199	ASN
2	B	214	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	6	GLN
1	A	38	GLN
1	A	90	GLN
1	A	124	GLN
1	A	137	ASN
1	A	147	GLN
1	A	155	GLN
1	A	158	ASN
1	A	166	GLN
1	A	199	GLN
2	B	16	GLN
2	B	39	GLN
2	B	64	ASN
2	B	76	ASN
2	B	164	HIS
2	B	192	GLN
2	B	199	ASN
3	C	7	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 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	108:ARG	C	109:THR	N	0.98

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	214/214 (100%)	0.25	11 (5%) 28 27	21, 35, 51, 67	0
2	B	227/235 (96%)	0.33	16 (7%) 16 15	21, 34, 57, 80	0
3	C	7/7 (100%)	0.12	1 (14%) 2 2	25, 28, 40, 60	0
All	All	448/456 (98%)	0.28	28 (6%) 20 19	21, 35, 54, 80	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	216	CYS	15.6
2	B	133	GLY	7.8
2	B	134	ALA	7.5
2	B	215	SER	6.3
2	B	100(B)	PHE	6.3
1	A	1	ALA	6.1
2	B	214	LYS	5.0
2	B	185	PRO	4.3
1	A	214	CYS	4.0
2	B	187	SER	4.0
2	B	126	PRO	3.7
1	A	126	LYS	3.5
1	A	212	GLY	3.5
2	B	204	ASN	3.2
3	C	7	ASN	3.2
2	B	213	PRO	3.1
2	B	1	ARG	3.1
2	B	186	SER	2.8
1	A	169	LYS	2.6
1	A	192	TYR	2.4
1	A	202	SER	2.4
1	A	128	GLY	2.3
1	A	193	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
2	B	114	THR	2.2
2	B	100(C)	GLY	2.2
1	A	3	GLN	2.1
2	B	192	GLN	2.1
1	A	109	THR	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.