



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:40 PM GMT

PDB ID : 4U0R
Title : Plasmodium falciparum reticulocyte-binding protein homologue 5 (PfRH5) bound to monoclonal antibody 9AD4
Authors : Wright, K.E.; Hjerrild, K.A.; Bartlett, J.; Douglas, A.D.; Jin, J.; Brown, R.E.; Ashfield, R.; Clemmensen, S.B.; de Jongh, W.A.; Draper, S.J.; Higgins, M.K.
Deposited on : 2014-07-14
Resolution : 2.30 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
<http://wwpdb.org/validation/2016/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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

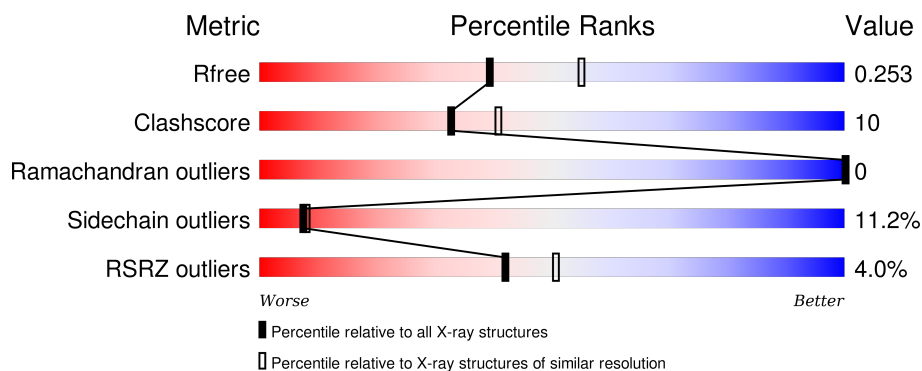
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	91344	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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. 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	526	 3% 42% 11% • 45%
2	B	258	 3% 67% 15% • 14%
3	C	238	 2% 70% 18% • 9%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6005 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 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	288	Total	C	N	O	S	0	0	0
			2450	1584	410	441	15			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	216	ALA	THR	conflict	UNP B2L3N7

- Molecule 2 is a protein called Monoclonal antibody 9AD4 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	221	Total	C	N	O	S	0	0	0
			1668	1060	272	327	9			

- Molecule 3 is a protein called Monoclonal antibody 9AD4 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	217	Total	C	N	O	S	0	0	0
			1677	1046	286	338	7			

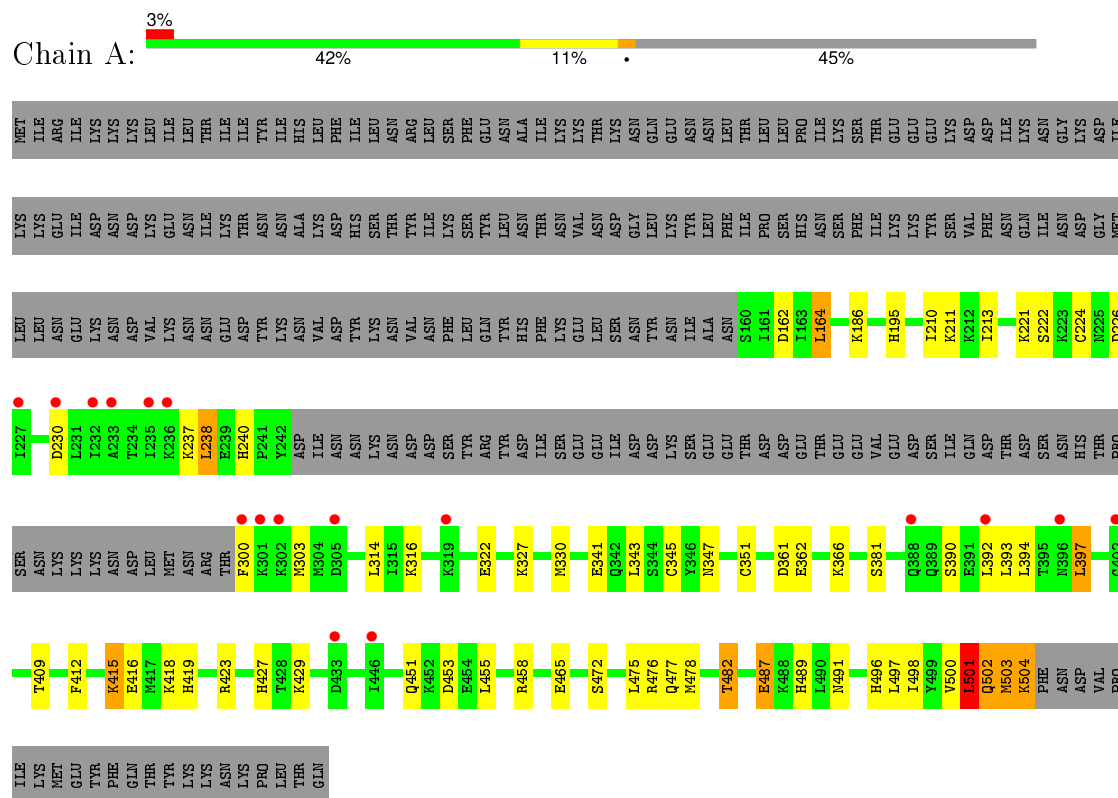
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	45	Total	O	0	0
			45	45		
4	B	100	Total	O	0	0
			100	100		
4	C	65	Total	O	0	0
			65	65		

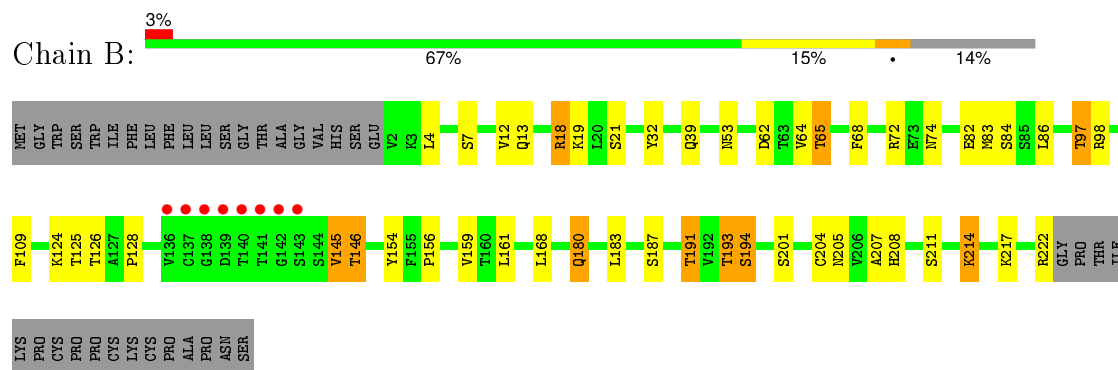
3 Residue-property plots

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

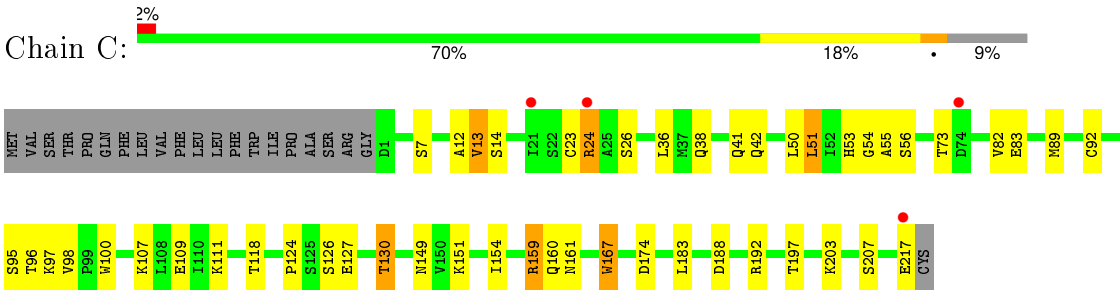
- Molecule 1: Reticulocyte binding protein 5



- Molecule 2: Monoclonal antibody 9AD4 heavy chain



- Molecule 3: Monoclonal antibody 9AD4 light chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	39.79 Å 86.66 Å 324.04 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.83 – 2.30 40.83 – 2.30	Depositor EDS
% Data completeness (in resolution range)	96.1 (40.83-2.30) 96.1 (40.83-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.75 (at 2.29 Å)	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
R, R_{free}	0.221 , 0.258 0.236 , 0.253	Depositor DCC
R_{free} test set	2462 reflections (5.25%)	DCC
Wilson B-factor (Å ²)	41.1	Xtriage
Anisotropy	0.603	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 41.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 49336 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6005	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.70% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.52	0/2502	0.70	2/3354 (0.1%)
2	B	0.55	1/1714 (0.1%)	0.82	0/2343
3	C	0.60	2/1717 (0.1%)	0.73	1/2332 (0.0%)
All	All	0.55	3/5933 (0.1%)	0.75	3/8029 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	51	LEU	C-N	-7.71	1.16	1.34
3	C	50	LEU	C-N	-7.60	1.16	1.34
2	B	204	CYS	CB-SG	-6.51	1.71	1.82

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	51	LEU	O-C-N	-6.90	111.66	122.70
1	A	501	LEU	N-CA-CB	-5.95	98.51	110.40
1	A	503	MET	N-CA-CB	-5.09	101.43	110.60

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	2450	0	2481	61	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1668	0	1612	35	0
3	C	1677	0	1605	24	0
4	A	45	0	0	15	0
4	B	100	0	0	14	0
4	C	65	0	0	5	0
All	All	6005	0	5698	116	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 10.

All (116) 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:238:LEU:CD2	1:A:300:PHE:HE2	1.45	1.29
1:A:238:LEU:CD2	1:A:300:PHE:CE2	2.17	1.27
1:A:496:HIS:O	1:A:501:LEU:HD13	1.32	1.23
2:B:21:SER:HB2	4:B:309:HOH:O	1.35	1.22
1:A:501:LEU:HD12	1:A:501:LEU:N	1.59	1.16
1:A:496:HIS:O	1:A:501:LEU:CD1	1.95	1.14
1:A:238:LEU:HD21	1:A:300:PHE:CE2	1.79	1.13
1:A:238:LEU:HD23	1:A:300:PHE:HE2	1.15	1.10
1:A:300:PHE:CE2	1:A:409:THR:HG22	1.87	1.09
1:A:500:VAL:C	1:A:501:LEU:HD12	1.75	1.06
3:C:217:GLU:HG2	4:C:352:HOH:O	1.62	0.98
2:B:97:THR:HG21	2:B:109:PHE:HB3	1.45	0.98
1:A:501:LEU:N	1:A:501:LEU:CD1	2.30	0.91
3:C:23:CYS:HG	3:C:92:CYS:HG	1.15	0.89
1:A:451:GLN:HE22	1:A:453:ASP:HB3	1.44	0.83
1:A:478:MET:O	1:A:482:THR:HG23	1.78	0.82
1:A:238:LEU:HD23	1:A:300:PHE:CE2	2.02	0.82
3:C:188:ASP:OD2	3:C:192:ARG:NH1	2.12	0.81
2:B:128:PRO:HB3	2:B:154:TYR:HB3	1.66	0.77
2:B:39:GLN:HE22	3:C:42:GLN:HE22	1.33	0.76
1:A:500:VAL:CA	1:A:501:LEU:HD12	2.17	0.75
1:A:476:ARG:NH2	4:A:623:HOH:O	1.86	0.75
2:B:97:THR:CG2	2:B:109:PHE:HB3	2.17	0.73
3:C:154:ILE:HD11	3:C:183:LEU:HD21	1.72	0.71
1:A:366:LYS:HE3	4:A:636:HOH:O	1.91	0.70
1:A:164:LEU:HD22	1:A:478:MET:HB3	1.74	0.70
1:A:503:MET:O	1:A:504:LYS:C	2.30	0.70
1:A:238:LEU:HD21	1:A:300:PHE:CZ	2.26	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:13:GLN:NE2	4:B:301:HOH:O	2.26	0.68
2:B:65:THR:HG21	4:B:397:HOH:O	1.92	0.68
2:B:64:VAL:HG13	2:B:68:PHE:HB2	1.80	0.63
2:B:156:PRO:O	2:B:208:HIS:HE1	1.82	0.62
2:B:7:SER:HB2	4:B:309:HOH:O	1.99	0.61
1:A:381:SER:HB3	4:A:640:HOH:O	2.00	0.61
2:B:193:THR:HG23	4:B:315:HOH:O	2.00	0.61
2:B:222:ARG:NH2	3:C:124:PRO:O	2.34	0.61
1:A:345:CYS:HG	1:A:351:CYS:HG	0.69	0.60
1:A:300:PHE:CD2	1:A:409:THR:HG22	2.36	0.60
2:B:124:LYS:HD3	4:B:301:HOH:O	2.02	0.60
2:B:72:ARG:HD3	2:B:74:ASN:OD1	2.02	0.60
1:A:238:LEU:CD2	1:A:300:PHE:CZ	2.82	0.59
1:A:300:PHE:HE1	1:A:412:PHE:HB2	1.66	0.59
2:B:145:VAL:HG22	2:B:194:SER:HA	1.84	0.59
1:A:498:ILE:O	1:A:502:GLN:HA	2.02	0.59
3:C:54:GLY:O	3:C:55:ALA:HB3	2.02	0.59
2:B:39:GLN:NE2	3:C:42:GLN:HE22	1.99	0.59
1:A:487:GLU:CG	4:A:603:HOH:O	2.51	0.58
1:A:501:LEU:H	1:A:501:LEU:HD12	1.63	0.58
1:A:211:LYS:HD3	4:A:643:HOH:O	2.03	0.58
1:A:427:HIS:ND1	1:A:472:SER:HB2	2.19	0.57
1:A:491:ASN:O	4:A:601:HOH:O	2.17	0.57
1:A:366:LYS:HG3	4:A:636:HOH:O	2.05	0.57
1:A:429:LYS:HG3	4:A:639:HOH:O	2.06	0.56
3:C:83:GLU:OE2	4:C:360:HOH:O	2.18	0.56
3:C:36:LEU:HD12	3:C:96:THR:HA	1.89	0.55
1:A:341:GLU:HG2	2:B:53:ASN:HB2	1.89	0.54
3:C:26:SER:HB3	4:C:326:HOH:O	2.08	0.54
3:C:217:GLU:CG	4:C:352:HOH:O	2.35	0.54
2:B:124:LYS:CE	4:B:301:HOH:O	2.57	0.53
3:C:127:GLU:HB2	4:C:321:HOH:O	2.09	0.53
1:A:393:LEU:O	1:A:397:LEU:HB2	2.08	0.53
1:A:186:LYS:HG3	1:A:210:ILE:HD13	1.91	0.53
3:C:41:GLN:HB2	3:C:51:LEU:HD11	1.91	0.53
1:A:300:PHE:CE2	1:A:409:THR:CG2	2.78	0.52
2:B:207:ALA:HB2	2:B:214:LYS:HD3	1.90	0.52
1:A:361:ASP:O	4:A:636:HOH:O	2.19	0.52
1:A:300:PHE:CE1	1:A:412:PHE:HB2	2.45	0.51
2:B:191:THR:HG23	4:B:347:HOH:O	2.10	0.51
2:B:62:ASP:CB	4:B:397:HOH:O	2.59	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:208:HIS:HD2	2:B:211:SER:OG	1.95	0.49
2:B:62:ASP:HB3	4:B:397:HOH:O	2.11	0.49
1:A:419:HIS:HB3	1:A:423:ARG:NH2	2.27	0.49
3:C:154:ILE:HD12	3:C:159:ARG:HG3	1.95	0.49
1:A:381:SER:CB	4:A:640:HOH:O	2.60	0.49
1:A:362:GLU:O	1:A:362:GLU:HG3	2.11	0.49
1:A:501:LEU:C	1:A:502:GLN:NE2	2.66	0.48
1:A:186:LYS:CE	4:A:638:HOH:O	2.62	0.48
3:C:38:GLN:OE1	3:C:53:HIS:O	2.32	0.48
3:C:95:SER:HA	3:C:100:TRP:CD1	2.49	0.48
1:A:500:VAL:CB	1:A:501:LEU:HD12	2.43	0.48
1:A:504:LYS:HB2	1:A:504:LYS:HE3	1.75	0.46
1:A:300:PHE:CD2	1:A:409:THR:CG2	2.97	0.46
3:C:126:SER:O	3:C:130:THR:HG23	2.16	0.46
2:B:62:ASP:HA	4:B:397:HOH:O	2.16	0.45
1:A:186:LYS:NZ	4:A:638:HOH:O	2.25	0.45
1:A:501:LEU:H	1:A:501:LEU:CD1	2.23	0.45
3:C:167:TRP:CD1	3:C:167:TRP:N	2.84	0.45
2:B:12:VAL:CG2	2:B:18:ARG:HG3	2.47	0.44
2:B:124:LYS:HE2	4:B:301:HOH:O	2.17	0.44
1:A:419:HIS:HB2	4:A:628:HOH:O	2.18	0.44
1:A:237:LYS:HB2	1:A:303:MET:HE1	1.99	0.44
3:C:149:ASN:HD21	3:C:151:LYS:HE3	1.83	0.44
1:A:477:GLN:HG2	4:A:611:HOH:O	2.18	0.44
2:B:65:THR:CG2	4:B:397:HOH:O	2.56	0.44
2:B:191:THR:CG2	4:B:347:HOH:O	2.66	0.43
1:A:500:VAL:HB	1:A:501:LEU:CD1	2.48	0.43
3:C:54:GLY:C	3:C:56:SER:H	2.22	0.43
2:B:83:MET:HB3	2:B:86:LEU:HD21	2.00	0.43
2:B:146:THR:HB	2:B:191:THR:HG22	2.01	0.43
2:B:128:PRO:CB	2:B:154:TYR:HB3	2.43	0.43
2:B:32:TYR:O	2:B:72:ARG:NH2	2.49	0.43
1:A:497:LEU:O	1:A:503:MET:HG3	2.19	0.42
1:A:419:HIS:HB3	1:A:423:ARG:HH22	1.83	0.42
1:A:195:HIS:CB	1:A:343:LEU:HD11	2.49	0.42
3:C:24:ARG:HA	3:C:73:THR:O	2.20	0.42
2:B:180:GLN:O	2:B:180:GLN:HG2	2.19	0.42
2:B:146:THR:HB	2:B:191:THR:HB	2.02	0.42
1:A:500:VAL:C	1:A:501:LEU:CD1	2.66	0.41
3:C:12:ALA:HB1	3:C:111:LYS:HG3	2.03	0.41
1:A:415:LYS:HE3	1:A:415:LYS:HB3	1.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:419:HIS:CB	4:A:628:HOH:O	2.68	0.41
3:C:13:VAL:HG11	3:C:82:VAL:HG21	2.03	0.41
1:A:451:GLN:NE2	1:A:453:ASP:HB3	2.25	0.41
2:B:19:LYS:HG3	2:B:82:GLU:HG2	2.03	0.41
1:A:240:HIS:HE2	1:A:489:HIS:HE2	1.69	0.41
1:A:300:PHE:CE1	1:A:412:PHE:CB	3.04	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	284/526 (54%)	274 (96%)	10 (4%)	0	100	100
2	B	219/258 (85%)	212 (97%)	7 (3%)	0	100	100
3	C	215/238 (90%)	208 (97%)	7 (3%)	0	100	100
All	All	718/1022 (70%)	694 (97%)	24 (3%)	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	279/511 (55%)	248 (89%)	31 (11%)	8	8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	185/216 (86%)	162 (88%)	23 (12%)	6	6
3	C	190/209 (91%)	171 (90%)	19 (10%)	9	11
All	All	654/936 (70%)	581 (89%)	73 (11%)	7	8

All (73) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	162	ASP
1	A	164	LEU
1	A	213	ILE
1	A	221	LYS
1	A	222	SER
1	A	224	CYS
1	A	226	ASP
1	A	230	ASP
1	A	238	LEU
1	A	314	LEU
1	A	316	LYS
1	A	322	GLU
1	A	327	LYS
1	A	330	MET
1	A	347	ASN
1	A	390	SER
1	A	392	LEU
1	A	394	LEU
1	A	397	LEU
1	A	415	LYS
1	A	416	GLU
1	A	418	LYS
1	A	455	LEU
1	A	458	ARG
1	A	465	GLU
1	A	475	LEU
1	A	482	THR
1	A	487	GLU
1	A	501	LEU
1	A	502	GLN
1	A	504	LYS
2	B	4	LEU
2	B	18	ARG
2	B	65	THR

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Mol	Chain	Res	Type
2	B	84	SER
2	B	97	THR
2	B	98	ARG
2	B	125	THR
2	B	126	THR
2	B	145	VAL
2	B	146	THR
2	B	159	VAL
2	B	161	LEU
2	B	168	LEU
2	B	180	GLN
2	B	183	LEU
2	B	187	SER
2	B	191	THR
2	B	193	THR
2	B	194	SER
2	B	201	SER
2	B	205	ASN
2	B	214	LYS
2	B	217	LYS
3	C	7	SER
3	C	13	VAL
3	C	14	SER
3	C	24	ARG
3	C	89	MET
3	C	97	LYS
3	C	98	VAL
3	C	107	LYS
3	C	109	GLU
3	C	118	THR
3	C	130	THR
3	C	159	ARG
3	C	160	GLN
3	C	161	ASN
3	C	167	TRP
3	C	174	ASP
3	C	197	THR
3	C	203	LYS
3	C	207	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	165	GLN
1	A	195	HIS
1	A	342	GLN
1	A	347	ASN
1	A	365	HIS
1	A	439	GLN
1	A	451	GLN
1	A	502	GLN
2	B	39	GLN
2	B	180	GLN
2	B	208	HIS
3	C	17	GLN
3	C	38	GLN
3	C	57	ASN
3	C	149	ASN
3	C	160	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 ⓘ

There are no carbohydrates 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 ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
3	C	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	50:LEU	C	51:LEU	N	1.16
1	C	51:LEU	C	52:ILE	N	1.16

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	288/526 (54%)	0.54	17 (5%) 26 34	24, 67, 93, 117	0
2	B	221/258 (85%)	0.53	8 (3%) 46 55	10, 41, 61, 72	8 (3%)
3	C	217/238 (91%)	0.33	4 (1%) 71 78	29, 46, 66, 106	0
All	All	726/1022 (71%)	0.47	29 (3%) 42 51	10, 49, 87, 117	8 (1%)

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	140	THR	15.7
2	B	138	GLY	12.4
2	B	142	GLY	11.9
2	B	137	CYS	9.2
1	A	300	PHE	7.8
2	B	141	THR	6.2
1	A	301	LYS	6.0
3	C	217	GLU	3.8
1	A	230	ASP	3.6
1	A	446	ILE	3.5
2	B	139	ASP	3.4
1	A	433	ASP	3.3
1	A	396	ASN	3.2
3	C	24	ARG	3.2
2	B	143	SER	3.2
1	A	302	LYS	3.0
2	B	136	VAL	2.8
1	A	236	LYS	2.6
1	A	392	LEU	2.6
1	A	233	ALA	2.5
1	A	227	ILE	2.5
1	A	235	ILE	2.4
3	C	21	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	388	GLN	2.3
3	C	74	ASP	2.2
1	A	402	GLY	2.1
1	A	319	LYS	2.1
1	A	305	ASP	2.1
1	A	232	ILE	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.