



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:34 PM GMT

PDB ID : 3U3I
Title : A RNA binding protein from Crimean-Congo hemorrhagic fever virus
Authors : Guo, Y.; Wang, W.M.; Ji, W.; Deng, M.; Sun, Y.N.; Lou, Z.Y.; Rao, Z.H.
Deposited on : 2011-10-06
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

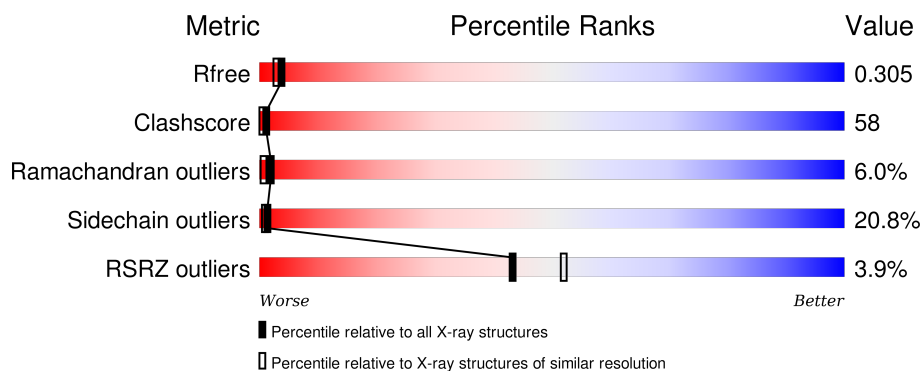
1 Overall quality at a glance

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	482	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3995 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 Nucleocapsid protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	460	Total	C	N	O	S	0	0	0
			3626	2308	615	685	18			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	369	Total	O	0	0
			369	369		

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	58.34Å 67.90Å 131.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.64 – 2.30 43.64 – 2.30	Depositor EDS
% Data completeness (in resolution range)	89.1 (43.64-2.30) 89.3 (43.64-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.62 (at 2.29Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.1_357)	Depositor
R, R_{free}	0.224 , 0.257 0.252 , 0.305	Depositor DCC
R_{free} test set	1077 reflections (5.06%)	DCC
Wilson B-factor (Å ²)	38.5	Xtriage
Anisotropy	0.697	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 62.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	2 of 22493 reflections (0.009%)	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	3995	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.03% 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 [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	0.94	6/3699 (0.2%)	0.96	5/4989 (0.1%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	108	GLU	CG-CD	5.96	1.60	1.51
1	A	74	CYS	CB-SG	-5.64	1.72	1.81
1	A	404	ALA	CA-CB	5.61	1.64	1.52
1	A	464	SER	C-O	5.36	1.33	1.23
1	A	124	ALA	CA-CB	5.19	1.63	1.52
1	A	392	PHE	CD1-CE1	5.10	1.49	1.39

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	27	VAL	N-CA-C	-5.46	96.25	111.00
1	A	269	ASP	CB-CG-OD2	-5.44	113.40	118.30
1	A	348	LEU	CA-CB-CG	5.34	127.58	115.30
1	A	298	ARG	N-CA-CB	-5.26	101.14	110.60
1	A	408	GLY	N-CA-C	5.06	125.76	113.10

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	3626	0	3614	417	0
2	A	369	0	0	21	0
All	All	3995	0	3614	417	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 58.

All (417) 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:157:LYS:CG	1:A:420:THR:HG22	1.17	1.55
1:A:148:LEU:CA	1:A:149:SER:HB2	1.45	1.40
1:A:157:LYS:CG	1:A:420:THR:CG2	2.04	1.36
1:A:1:MET:HA	1:A:2:GLU:CB	1.44	1.35
1:A:29:THR:CG2	1:A:30:PHE:CE2	2.14	1.30
1:A:157:LYS:HG2	1:A:420:THR:CG2	1.60	1.27
1:A:148:LEU:HA	1:A:149:SER:CB	1.60	1.26
1:A:157:LYS:CB	1:A:420:THR:CG2	2.15	1.24
1:A:29:THR:HG21	1:A:30:PHE:CE2	1.70	1.23
1:A:4:LYS:HE2	1:A:398:ALA:O	1.40	1.18
1:A:1:MET:CA	1:A:2:GLU:HB2	1.75	1.16
1:A:1:MET:CA	1:A:2:GLU:CB	2.22	1.15
1:A:228:ILE:HG12	1:A:283:HIS:CE1	1.80	1.15
1:A:373:ILE:HG12	1:A:374:TYR:N	1.50	1.13
1:A:424:ASN:OD1	1:A:428:LYS:HD2	1.49	1.12
1:A:373:ILE:CG1	1:A:374:TYR:H	1.56	1.12
1:A:58:GLN:HG2	1:A:61:SER:HB2	1.18	1.12
1:A:235:LEU:HD12	1:A:290:LEU:HB3	1.19	1.10
1:A:3:ASN:HA	1:A:397:VAL:HG13	1.27	1.10
1:A:157:LYS:HB3	1:A:420:THR:HG23	1.33	1.09
1:A:424:ASN:N	1:A:425:PRO:HD3	1.65	1.08
1:A:157:LYS:HB3	1:A:420:THR:CG2	1.78	1.07
1:A:235:LEU:CD1	1:A:290:LEU:HB3	1.83	1.07
1:A:58:GLN:N	1:A:59:LYS:HB2	1.69	1.07
1:A:1:MET:HA	1:A:2:GLU:HB2	1.30	1.07
1:A:58:GLN:HA	1:A:60:ASP:N	1.69	1.07
1:A:45:ARG:HG3	1:A:45:ARG:HH11	1.12	1.06
1:A:26:LEU:N	1:A:26:LEU:CD2	2.12	1.05
1:A:420:THR:O	1:A:421:GLU:HB2	1.55	1.05
1:A:58:GLN:HG2	1:A:61:SER:CB	1.88	1.03
1:A:1:MET:HA	1:A:2:GLU:HB3	1.09	1.03
1:A:2:GLU:HB3	1:A:4:LYS:NZ	1.74	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:225:ARG:O	1:A:226:SER:HB2	1.55	1.02
1:A:29:THR:HG21	1:A:30:PHE:HE2	1.19	1.01
1:A:29:THR:HG22	1:A:30:PHE:CD2	1.96	1.00
1:A:3:ASN:HA	1:A:397:VAL:CG1	1.92	1.00
1:A:29:THR:CG2	1:A:30:PHE:CD2	2.47	0.98
1:A:475:ASN:ND2	1:A:476:ALA:N	2.11	0.98
1:A:164:MET:HA	1:A:164:MET:HE3	1.45	0.98
1:A:157:LYS:HG3	1:A:420:THR:HG22	1.41	0.98
1:A:419:ASN:H	1:A:419:ASN:HD22	1.06	0.98
1:A:26:LEU:HD22	1:A:26:LEU:N	1.78	0.98
1:A:234:GLY:HA3	2:A:864:HOH:O	1.62	0.98
1:A:419:ASN:N	1:A:419:ASN:HD22	1.60	0.96
1:A:475:ASN:ND2	1:A:476:ALA:H	1.63	0.96
1:A:45:ARG:NH1	1:A:45:ARG:HG3	1.73	0.95
1:A:419:ASN:ND2	1:A:419:ASN:H	1.64	0.95
1:A:30:PHE:HD2	1:A:30:PHE:N	1.65	0.94
1:A:475:ASN:CG	1:A:476:ALA:H	1.71	0.94
1:A:159:PRO:HD2	1:A:162:ILE:HD11	1.49	0.94
1:A:228:ILE:CG1	1:A:283:HIS:CE1	2.50	0.94
1:A:18:GLU:HA	1:A:18:GLU:OE2	1.68	0.93
1:A:58:GLN:HG3	1:A:61:SER:H	1.33	0.93
1:A:228:ILE:CG2	1:A:231:VAL:HG23	1.97	0.93
1:A:228:ILE:HG12	1:A:283:HIS:HE1	1.26	0.92
1:A:2:GLU:HB3	1:A:4:LYS:HZ3	1.28	0.92
1:A:220:ILE:HG12	1:A:280:LEU:HD21	1.52	0.92
1:A:169:MET:O	1:A:173:MET:HG2	1.70	0.92
1:A:120:ILE:HG22	2:A:591:HOH:O	1.68	0.92
1:A:29:THR:HG22	1:A:30:PHE:CE2	2.02	0.91
1:A:58:GLN:HG3	1:A:61:SER:N	1.86	0.91
1:A:1:MET:N	1:A:2:GLU:HB2	1.84	0.91
1:A:373:ILE:HG12	1:A:374:TYR:H	0.76	0.91
1:A:424:ASN:N	1:A:425:PRO:CD	2.34	0.90
1:A:231:VAL:HG13	1:A:287:ALA:N	1.87	0.90
1:A:30:PHE:N	1:A:30:PHE:CD2	2.36	0.90
1:A:390:VAL:HG21	1:A:411:LYS:HB2	1.54	0.90
1:A:58:GLN:CG	1:A:61:SER:H	1.85	0.89
1:A:26:LEU:HD23	1:A:26:LEU:H	1.36	0.89
1:A:228:ILE:HG22	1:A:231:VAL:HG23	1.51	0.88
1:A:249:GLU:O	1:A:253:THR:HG23	1.72	0.88
1:A:45:ARG:CG	1:A:45:ARG:HH11	1.87	0.87
1:A:164:MET:HA	1:A:164:MET:CE	2.04	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:148:LEU:CB	1:A:149:SER:HB2	2.04	0.87
1:A:157:LYS:CB	1:A:420:THR:HG22	1.89	0.87
1:A:35:SER:HB3	1:A:37:CYS:H	1.41	0.86
1:A:262:ASN:O	1:A:265:LYS:HG2	1.76	0.86
1:A:339:ARG:HD3	1:A:339:ARG:N	1.89	0.86
1:A:58:GLN:HA	1:A:60:ASP:H	1.37	0.85
1:A:231:VAL:HG12	1:A:290:LEU:HD12	1.57	0.84
1:A:26:LEU:HD23	1:A:26:LEU:N	1.90	0.84
1:A:148:LEU:CA	1:A:149:SER:CB	2.30	0.83
1:A:238:LEU:HD23	1:A:246:VAL:HB	1.61	0.83
1:A:1:MET:H1	1:A:2:GLU:HB2	1.43	0.82
1:A:58:GLN:CA	1:A:59:LYS:HB2	2.10	0.81
1:A:228:ILE:HG22	1:A:231:VAL:H	1.44	0.81
1:A:238:LEU:HD22	1:A:247:PHE:CE2	2.16	0.81
1:A:58:GLN:N	1:A:59:LYS:CB	2.44	0.81
1:A:205:VAL:HG13	1:A:249:GLU:HB3	1.61	0.81
1:A:162:ILE:O	1:A:166:VAL:HG23	1.79	0.81
1:A:423:ASN:C	1:A:425:PRO:HD3	2.02	0.81
1:A:421:GLU:O	1:A:422:THR:OG1	1.98	0.80
1:A:25:GLY:C	1:A:26:LEU:HD22	2.02	0.80
1:A:29:THR:HB	1:A:30:PHE:CD2	2.16	0.80
1:A:201:CYS:O	1:A:205:VAL:HG23	1.83	0.79
1:A:235:LEU:HD12	1:A:290:LEU:CB	2.08	0.78
1:A:157:LYS:HG2	1:A:420:THR:HG22	0.78	0.78
1:A:95:TRP:HZ2	1:A:132:LYS:HG2	1.49	0.78
1:A:29:THR:CB	1:A:30:PHE:CD2	2.68	0.77
1:A:298:ARG:CG	1:A:298:ARG:HH11	1.98	0.77
1:A:103:ILE:HG23	1:A:106:TRP:CH2	2.18	0.77
1:A:435:GLU:O	1:A:439:THR:HG22	1.84	0.77
1:A:220:ILE:CG1	1:A:280:LEU:HD21	2.15	0.77
1:A:428:LYS:O	1:A:432:LYS:HG3	1.84	0.76
1:A:174:ILE:O	1:A:177:ARG:HB3	1.85	0.76
1:A:170:LEU:HA	1:A:173:MET:HG3	1.68	0.75
1:A:157:LYS:CB	1:A:420:THR:HG21	2.15	0.75
1:A:366:ASP:HB3	2:A:731:HOH:O	1.85	0.74
1:A:205:VAL:CG1	1:A:249:GLU:HB3	2.17	0.74
1:A:300:GLN:HG2	1:A:470:TYR:CE1	2.23	0.74
1:A:103:ILE:HG22	1:A:107:ASP:HB2	1.69	0.74
1:A:57:ALA:C	1:A:59:LYS:HB2	2.08	0.74
1:A:90:LYS:HD3	2:A:785:HOH:O	1.87	0.73
1:A:202:ARG:HA	1:A:237:LYS:NZ	2.03	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:121:GLU:H	1:A:121:GLU:CD	1.88	0.73
1:A:220:ILE:HG12	1:A:280:LEU:CD2	2.19	0.72
1:A:174:ILE:HG22	1:A:175:ARG:N	2.05	0.72
1:A:29:THR:CB	1:A:30:PHE:CE2	2.73	0.72
1:A:152:VAL:HG21	1:A:475:ASN:O	1.88	0.72
1:A:422:THR:HG23	2:A:589:HOH:O	1.87	0.72
1:A:142:ASN:O	1:A:146:THR:HG23	1.89	0.71
1:A:385:ILE:HD13	1:A:388:MET:HE3	1.72	0.71
1:A:337:GLN:HB3	1:A:339:ARG:CD	2.20	0.71
1:A:339:ARG:HD3	1:A:339:ARG:H	1.53	0.71
1:A:35:SER:OG	1:A:74:CYS:HA	1.91	0.70
1:A:363:PHE:CE1	1:A:380:LEU:HD13	2.26	0.70
1:A:453:HIS:HB2	2:A:803:HOH:O	1.90	0.69
1:A:103:ILE:HG23	1:A:106:TRP:CZ2	2.25	0.69
1:A:119:LYS:HB2	1:A:122:GLN:HG3	1.74	0.69
1:A:235:LEU:O	1:A:235:LEU:HD23	1.91	0.69
1:A:221:ASN:HD21	1:A:279:ASN:ND2	1.90	0.69
1:A:169:MET:HG2	1:A:434:PHE:CE2	2.28	0.68
1:A:306:THR:HG22	1:A:391:CYS:SG	2.33	0.68
1:A:419:ASN:ND2	1:A:419:ASN:N	2.30	0.68
1:A:29:THR:HB	1:A:30:PHE:HD2	1.54	0.68
1:A:339:ARG:HB3	1:A:343:LYS:HD3	1.75	0.68
1:A:148:LEU:HA	1:A:149:SER:HB2	0.72	0.68
1:A:30:PHE:HD2	1:A:30:PHE:H	1.39	0.68
1:A:375:MET:O	1:A:376:HIS:CB	2.42	0.68
1:A:164:MET:CE	1:A:164:MET:CA	2.72	0.67
1:A:335:GLY:HA3	1:A:407:SER:OG	1.94	0.67
1:A:228:ILE:CG2	1:A:230:LEU:HB3	2.24	0.67
1:A:334:LEU:HD11	1:A:344:MET:HG2	1.76	0.67
1:A:148:LEU:HB3	1:A:149:SER:CB	2.25	0.66
1:A:79:GLU:HB3	1:A:466:PHE:CD2	2.31	0.66
1:A:117:VAL:HG13	1:A:118:PRO:HD2	1.77	0.66
1:A:55:ASP:C	1:A:57:ALA:H	1.99	0.66
1:A:238:LEU:HD22	1:A:247:PHE:CZ	2.31	0.65
1:A:169:MET:O	1:A:173:MET:CG	2.44	0.65
1:A:304:ILE:N	1:A:304:ILE:HD12	2.11	0.65
1:A:55:ASP:O	1:A:57:ALA:N	2.30	0.65
1:A:3:ASN:CA	1:A:397:VAL:HG13	2.17	0.64
1:A:111:THR:O	1:A:114:LYS:HB2	1.97	0.64
1:A:337:GLN:OE1	1:A:339:ARG:HG2	1.96	0.64
1:A:58:GLN:CG	1:A:61:SER:N	2.50	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:424:ASN:OD1	1:A:428:LYS:CD	2.38	0.64
1:A:234:GLY:C	1:A:238:LEU:HD12	2.17	0.63
1:A:18:GLU:OE2	1:A:21:LYS:HE3	1.97	0.63
1:A:317:ALA:O	1:A:358:LYS:HD3	1.99	0.62
1:A:158:VAL:HG13	1:A:162:ILE:CD1	2.29	0.62
1:A:375:MET:O	1:A:376:HIS:HB2	2.00	0.62
1:A:202:ARG:HA	1:A:237:LYS:HZ2	1.61	0.62
1:A:169:MET:HE3	1:A:455:LEU:HD22	1.81	0.62
1:A:95:TRP:CZ2	1:A:132:LYS:HG2	2.34	0.62
1:A:325:PRO:HB3	1:A:397:VAL:HG12	1.82	0.62
1:A:251:LYS:NZ	2:A:627:HOH:O	2.25	0.62
1:A:399:ASN:HB3	2:A:543:HOH:O	2.00	0.61
1:A:230:LEU:HD12	1:A:230:LEU:O	2.00	0.61
1:A:93:LEU:HD21	1:A:314:LEU:HB3	1.83	0.61
1:A:424:ASN:N	1:A:424:ASN:ND2	2.49	0.61
1:A:159:PRO:O	1:A:162:ILE:HD13	2.01	0.60
1:A:109:SER:O	1:A:113:LEU:HG	2.00	0.60
1:A:169:MET:HG2	1:A:434:PHE:CD2	2.37	0.60
1:A:159:PRO:HG3	1:A:424:ASN:HB3	1.82	0.60
1:A:29:THR:CB	1:A:30:PHE:HD2	2.12	0.60
1:A:164:MET:CA	1:A:164:MET:HE3	2.26	0.60
1:A:220:ILE:CD1	1:A:280:LEU:HD21	2.32	0.60
1:A:249:GLU:O	1:A:250:ALA:C	2.39	0.60
1:A:230:LEU:HD21	1:A:280:LEU:CD2	2.32	0.60
1:A:148:LEU:HB3	1:A:149:SER:HB3	1.83	0.59
1:A:35:SER:HG	1:A:74:CYS:HA	1.68	0.59
1:A:158:VAL:HG13	1:A:162:ILE:HD11	1.82	0.59
1:A:29:THR:CG2	1:A:30:PHE:HE2	1.81	0.59
1:A:109:SER:O	1:A:113:LEU:CG	2.51	0.59
1:A:159:PRO:HG3	1:A:424:ASN:CB	2.32	0.59
1:A:167:LYS:HA	1:A:170:LEU:HB2	1.83	0.59
1:A:421:GLU:C	1:A:422:THR:HG1	2.00	0.59
1:A:109:SER:O	1:A:113:LEU:HB2	2.03	0.59
1:A:225:ARG:O	1:A:226:SER:CB	2.39	0.58
1:A:450:ALA:HA	2:A:803:HOH:O	2.02	0.58
1:A:151:LYS:HG3	1:A:473:LYS:O	2.03	0.58
1:A:58:GLN:HA	1:A:59:LYS:C	2.21	0.58
1:A:29:THR:HB	1:A:30:PHE:CE2	2.38	0.58
1:A:420:THR:O	1:A:421:GLU:CB	2.40	0.58
1:A:197:HIS:HB3	1:A:217:TRP:CZ3	2.39	0.58
1:A:333:GLU:HG2	2:A:608:HOH:O	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:449:VAL:HG12	1:A:452:GLU:H	1.67	0.57
1:A:238:LEU:CD2	1:A:247:PHE:CZ	2.87	0.57
1:A:298:ARG:HG3	1:A:298:ARG:HH11	1.68	0.57
1:A:363:PHE:HE1	1:A:380:LEU:CD1	2.18	0.57
1:A:148:LEU:CB	1:A:149:SER:CB	2.73	0.57
1:A:207:GLY:HA2	1:A:253:THR:HB	1.85	0.57
1:A:230:LEU:HD23	1:A:283:HIS:CD2	2.40	0.56
1:A:237:LYS:O	1:A:237:LYS:HG3	2.03	0.56
1:A:238:LEU:CD2	1:A:246:VAL:HB	2.32	0.56
1:A:230:LEU:C	1:A:230:LEU:HD12	2.25	0.56
1:A:30:PHE:HD1	1:A:40:VAL:HG23	1.70	0.56
1:A:411:LYS:HB3	1:A:465:PRO:HB3	1.87	0.56
1:A:30:PHE:CD1	1:A:40:VAL:HG23	2.41	0.56
1:A:372:ARG:O	1:A:373:ILE:C	2.43	0.56
1:A:442:ASN:HB3	1:A:445:ASP:OD2	2.06	0.55
1:A:230:LEU:CD2	1:A:280:LEU:HD23	2.36	0.55
1:A:298:ARG:HG2	1:A:298:ARG:NH1	2.21	0.55
1:A:157:LYS:HD2	1:A:158:VAL:H	1.72	0.55
1:A:376:HIS:CE1	1:A:378:ALA:HB3	2.41	0.55
1:A:159:PRO:HD2	1:A:162:ILE:CD1	2.31	0.55
1:A:159:PRO:CD	1:A:162:ILE:HD11	2.30	0.55
1:A:180:ILE:O	1:A:180:ILE:HG23	2.06	0.55
1:A:238:LEU:HD23	1:A:242:GLU:O	2.07	0.55
1:A:282:LYS:HD2	2:A:791:HOH:O	2.07	0.55
1:A:103:ILE:CG2	1:A:107:ASP:HB2	2.37	0.54
1:A:177:ARG:NH2	1:A:475:ASN:ND2	2.56	0.54
1:A:385:ILE:HD13	1:A:388:MET:CE	2.37	0.54
1:A:228:ILE:HG13	1:A:283:HIS:CE1	2.42	0.54
1:A:363:PHE:HE1	1:A:380:LEU:HD13	1.67	0.54
1:A:49:GLN:O	1:A:52:SER:HB2	2.06	0.54
1:A:58:GLN:N	1:A:59:LYS:CG	2.71	0.54
1:A:17:PHE:CE2	1:A:21:LYS:HD3	2.43	0.54
1:A:58:GLN:HG3	1:A:60:ASP:HB2	1.89	0.53
1:A:201:CYS:SG	1:A:233:THR:HB	2.48	0.53
1:A:58:GLN:HA	1:A:59:LYS:HB2	1.88	0.53
1:A:228:ILE:HG21	1:A:283:HIS:ND1	2.24	0.53
1:A:253:THR:O	1:A:256:ALA:HB3	2.07	0.53
1:A:390:VAL:HG21	1:A:411:LYS:CB	2.31	0.53
1:A:300:GLN:HG2	1:A:470:TYR:HE1	1.71	0.53
1:A:215:PRO:HB2	1:A:218:GLY:O	2.09	0.53
1:A:228:ILE:CG1	1:A:283:HIS:HE1	2.02	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:475:ASN:HD22	1:A:476:ALA:N	2.03	0.53
1:A:423:ASN:C	1:A:425:PRO:CD	2.76	0.52
1:A:364:ALA:O	1:A:365:ASP:HB2	2.09	0.52
1:A:332:PHE:CG	1:A:396:PRO:HG3	2.45	0.52
1:A:419:ASN:ND2	2:A:681:HOH:O	2.42	0.52
1:A:42:ASN:ND2	1:A:44:ASP:H	2.07	0.52
1:A:366:ASP:N	1:A:366:ASP:OD2	2.43	0.52
1:A:304:ILE:N	1:A:304:ILE:CD1	2.73	0.52
1:A:109:SER:O	1:A:113:LEU:CB	2.58	0.52
1:A:43:LEU:CD2	1:A:69:GLU:HB3	2.39	0.52
1:A:305:ASP:HA	2:A:826:HOH:O	2.10	0.52
1:A:157:LYS:HD2	1:A:158:VAL:N	2.24	0.52
1:A:79:GLU:HB3	1:A:466:PHE:HD2	1.73	0.51
1:A:448:ILE:HG23	1:A:449:VAL:N	2.24	0.51
1:A:299:ALA:O	1:A:302:ALA:HB3	2.11	0.51
1:A:385:ILE:CD1	1:A:388:MET:CE	2.89	0.51
1:A:235:LEU:C	1:A:235:LEU:CD2	2.78	0.51
1:A:205:VAL:HB	1:A:237:LYS:NZ	2.26	0.51
1:A:453:HIS:O	1:A:456:HIS:HB3	2.11	0.51
1:A:228:ILE:HG21	1:A:231:VAL:HG23	1.86	0.51
1:A:43:LEU:HD22	1:A:69:GLU:HB3	1.93	0.51
1:A:320:THR:HB	1:A:322:GLU:OE2	2.11	0.51
1:A:10:LYS:HB3	1:A:141:VAL:CG2	2.41	0.51
1:A:327:VAL:HG22	1:A:355:TRP:CE2	2.46	0.51
1:A:97:GLU:CG	1:A:97:GLU:O	2.58	0.50
1:A:373:ILE:CG1	1:A:374:TYR:N	2.30	0.50
1:A:174:ILE:CG2	1:A:175:ARG:N	2.75	0.50
1:A:235:LEU:C	1:A:235:LEU:HD23	2.31	0.50
1:A:298:ARG:HG2	1:A:298:ARG:HH11	1.70	0.50
1:A:103:ILE:HG22	1:A:103:ILE:O	2.11	0.50
1:A:347:ALA:O	1:A:351:THR:HG22	2.10	0.50
1:A:424:ASN:ND2	1:A:424:ASN:H	2.09	0.50
1:A:58:GLN:CA	1:A:59:LYS:CB	2.74	0.50
1:A:120:ILE:O	1:A:123:LEU:HB2	2.11	0.50
1:A:337:GLN:HB3	1:A:339:ARG:HD3	1.93	0.50
1:A:205:VAL:HB	1:A:237:LYS:HZ1	1.77	0.50
1:A:58:GLN:CG	1:A:61:SER:CB	2.77	0.50
1:A:1:MET:HB3	2:A:594:HOH:O	2.11	0.49
1:A:42:ASN:HD22	1:A:43:LEU:N	2.10	0.49
1:A:238:LEU:O	1:A:242:GLU:HA	2.11	0.49
1:A:345:LYS:HE2	2:A:560:HOH:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:357:LYS:HD3	2:A:600:HOH:O	2.12	0.49
1:A:230:LEU:O	1:A:233:THR:OG1	2.30	0.49
1:A:46:PHE:CE2	1:A:66:ALA:HA	2.46	0.49
1:A:152:VAL:HG12	1:A:474:GLY:HA3	1.93	0.49
1:A:321:PRO:O	1:A:323:THR:N	2.44	0.49
1:A:43:LEU:HB3	1:A:46:PHE:HD2	1.77	0.49
1:A:337:GLN:HB3	1:A:339:ARG:CG	2.42	0.49
1:A:244:LYS:HD2	1:A:244:LYS:N	2.28	0.49
1:A:376:HIS:CG	1:A:377:PRO:HD2	2.48	0.49
1:A:164:MET:HE3	1:A:167:LYS:HB2	1.95	0.49
1:A:35:SER:CB	1:A:37:CYS:H	2.18	0.49
1:A:339:ARG:CD	1:A:339:ARG:N	2.69	0.49
1:A:332:PHE:CD2	1:A:396:PRO:HG3	2.48	0.49
1:A:230:LEU:CD2	1:A:280:LEU:CD2	2.91	0.48
1:A:205:VAL:HG21	1:A:237:LYS:CE	2.43	0.48
1:A:161:GLU:HG2	1:A:162:ILE:HG23	1.94	0.48
1:A:55:ASP:C	1:A:57:ALA:N	2.65	0.48
1:A:235:LEU:HD12	1:A:290:LEU:HD13	1.95	0.48
1:A:436:ILE:HG22	1:A:437:GLN:N	2.28	0.48
1:A:285:ALA:O	1:A:289:GLU:HG3	2.14	0.48
1:A:452:GLU:O	1:A:456:HIS:HB2	2.14	0.48
1:A:63:TYR:CE1	1:A:437:GLN:HG3	2.48	0.48
1:A:58:GLN:HG2	1:A:61:SER:H	1.72	0.48
1:A:337:GLN:HG2	1:A:339:ARG:HE	1.77	0.48
1:A:158:VAL:HG13	1:A:162:ILE:HG12	1.96	0.48
1:A:96:PHE:C	1:A:98:LYS:H	2.17	0.48
1:A:203:GLU:HB3	1:A:211:MET:SD	2.54	0.48
1:A:38:GLU:HA	1:A:38:GLU:OE1	2.14	0.48
1:A:58:GLN:H	1:A:59:LYS:CG	2.27	0.47
1:A:337:GLN:HB3	1:A:339:ARG:NE	2.29	0.47
1:A:157:LYS:HB2	1:A:420:THR:HG21	1.94	0.47
1:A:238:LEU:HD21	1:A:247:PHE:CD1	2.50	0.47
1:A:422:THR:O	1:A:423:ASN:C	2.53	0.47
1:A:337:GLN:CG	1:A:339:ARG:HE	2.27	0.47
1:A:49:GLN:O	1:A:52:SER:CB	2.63	0.47
1:A:97:GLU:HG3	1:A:97:GLU:O	2.15	0.47
1:A:42:ASN:HD21	1:A:44:ASP:CG	2.18	0.47
1:A:152:VAL:HG11	1:A:475:ASN:N	2.30	0.47
1:A:176:ARG:NH1	1:A:446:MET:O	2.43	0.47
1:A:205:VAL:O	1:A:249:GLU:CG	2.63	0.47
1:A:238:LEU:HD22	1:A:247:PHE:CD2	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:383:GLY:CA	2:A:626:HOH:O	2.62	0.47
1:A:199:GLU:O	1:A:202:ARG:N	2.47	0.47
1:A:205:VAL:CG1	1:A:249:GLU:CB	2.92	0.47
1:A:220:ILE:HD11	1:A:280:LEU:HD21	1.97	0.47
1:A:248:ASP:O	1:A:251:LYS:HB2	2.14	0.47
1:A:29:THR:CB	1:A:30:PHE:HE2	2.24	0.46
1:A:138:GLY:C	1:A:140:ARG:H	2.19	0.46
1:A:394:THR:HG22	1:A:409:HIS:HD2	1.80	0.46
1:A:1:MET:HA	1:A:4:LYS:NZ	2.31	0.46
1:A:351:THR:HA	1:A:352:PRO:HD3	1.79	0.46
1:A:202:ARG:HA	1:A:237:LYS:HZ3	1.78	0.46
1:A:203:GLU:CB	1:A:211:MET:SD	3.04	0.46
1:A:205:VAL:O	1:A:249:GLU:HG2	2.15	0.46
1:A:204:PHE:CD2	1:A:204:PHE:C	2.89	0.46
1:A:383:GLY:HA2	2:A:626:HOH:O	2.15	0.45
1:A:98:LYS:HE3	1:A:98:LYS:HB3	1.52	0.45
1:A:7:VAL:HG12	2:A:546:HOH:O	2.16	0.45
1:A:234:GLY:O	1:A:238:LEU:HD12	2.17	0.45
1:A:12:GLU:O	1:A:13:MET:C	2.54	0.45
1:A:231:VAL:HG11	1:A:286:LYS:HG3	1.98	0.45
1:A:249:GLU:O	1:A:252:LYS:N	2.49	0.45
1:A:231:VAL:CG1	1:A:287:ALA:N	2.69	0.45
1:A:138:GLY:C	1:A:140:ARG:N	2.70	0.45
1:A:56:ASP:O	1:A:57:ALA:C	2.54	0.45
1:A:385:ILE:HD13	1:A:385:ILE:HA	1.75	0.45
1:A:44:ASP:O	1:A:45:ARG:C	2.55	0.45
1:A:298:ARG:HB3	1:A:299:ALA:H	1.59	0.45
1:A:336:LYS:HE2	1:A:336:LYS:HB3	1.41	0.45
1:A:112:GLU:CD	1:A:112:GLU:H	2.20	0.45
1:A:250:ALA:O	1:A:254:VAL:HG23	2.17	0.45
1:A:15:LYS:HD3	2:A:743:HOH:O	2.15	0.45
1:A:347:ALA:O	1:A:351:THR:CG2	2.65	0.45
1:A:257:LEU:HG	1:A:261:LEU:HD11	1.99	0.44
1:A:294:SER:O	1:A:298:ARG:HB2	2.18	0.44
1:A:244:LYS:N	1:A:244:LYS:CD	2.81	0.44
1:A:228:ILE:O	1:A:228:ILE:HG22	2.17	0.44
1:A:386:SER:O	1:A:390:VAL:HG23	2.17	0.44
1:A:449:VAL:HG11	1:A:452:GLU:CD	2.38	0.44
1:A:231:VAL:HG13	1:A:287:ALA:H	1.80	0.43
1:A:173:MET:HG2	1:A:173:MET:H	1.50	0.43
1:A:230:LEU:HD21	1:A:280:LEU:HD22	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:131:LEU:O	1:A:132:LYS:C	2.55	0.43
1:A:425:PRO:O	1:A:426:CYS:C	2.57	0.43
1:A:27:VAL:C	1:A:29:THR:H	2.21	0.43
1:A:45:ARG:NH2	1:A:69:GLU:OE1	2.52	0.43
1:A:65:SER:O	1:A:68:VAL:HB	2.19	0.43
1:A:106:TRP:N	1:A:106:TRP:CD1	2.87	0.43
1:A:305:ASP:OD2	1:A:305:ASP:C	2.57	0.43
1:A:31:THR:HA	1:A:415:ASN:O	2.18	0.43
1:A:316:LYS:HA	1:A:316:LYS:HD2	1.77	0.43
1:A:462:LYS:HA	1:A:467:GLN:OE1	2.18	0.43
1:A:385:ILE:CD1	1:A:388:MET:HE1	2.48	0.43
1:A:313:TRP:CH2	1:A:380:LEU:HD23	2.54	0.43
1:A:251:LYS:O	1:A:255:GLU:HG3	2.19	0.43
1:A:206:LYS:HE2	1:A:208:LYS:HE3	2.01	0.43
1:A:140:ARG:H	1:A:140:ARG:HG3	1.46	0.42
1:A:1:MET:CG	1:A:1:MET:O	2.67	0.42
1:A:158:VAL:HG13	1:A:162:ILE:CG1	2.49	0.42
1:A:30:PHE:HA	1:A:417:ARG:HD2	2.00	0.42
1:A:196:GLU:H	1:A:196:GLU:HG3	1.64	0.42
1:A:424:ASN:H	1:A:425:PRO:HD3	1.69	0.42
1:A:91:LYS:HB3	1:A:137:ILE:HG22	2.01	0.42
1:A:75:ALA:HA	1:A:76:PRO:HD3	1.66	0.42
1:A:205:VAL:HG12	1:A:249:GLU:HB3	1.99	0.42
1:A:18:GLU:CA	1:A:18:GLU:OE2	2.49	0.42
1:A:63:TYR:HE1	1:A:437:GLN:HG3	1.85	0.42
1:A:235:LEU:HG	1:A:291:TYR:N	2.35	0.41
1:A:419:ASN:HB2	1:A:423:ASN:ND2	2.36	0.41
1:A:380:LEU:HD21	1:A:388:MET:CE	2.50	0.41
1:A:83:VAL:O	1:A:83:VAL:HG12	2.20	0.41
1:A:447:ASP:N	1:A:447:ASP:OD1	2.53	0.41
1:A:418:THR:HG22	1:A:426:CYS:HB3	2.02	0.41
1:A:448:ILE:HA	1:A:448:ILE:HD12	1.89	0.41
1:A:230:LEU:HD21	1:A:280:LEU:HD23	1.98	0.41
1:A:174:ILE:O	1:A:177:ARG:N	2.53	0.41
1:A:380:LEU:HD21	1:A:388:MET:HE2	2.01	0.41
1:A:449:VAL:HG11	1:A:452:GLU:OE2	2.20	0.41
1:A:119:LYS:N	1:A:122:GLN:OE1	2.50	0.41
1:A:159:PRO:HG2	1:A:162:ILE:HD12	2.02	0.41
1:A:360:TYR:O	1:A:363:PHE:HB2	2.20	0.41
1:A:324:PHE:O	1:A:327:VAL:N	2.52	0.41
1:A:152:VAL:HG23	1:A:460:VAL:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:120:ILE:H	1:A:120:ILE:HG13	1.39	0.41
1:A:297:LEU:HA	1:A:297:LEU:HD23	1.75	0.41
1:A:385:ILE:CD1	1:A:388:MET:HE3	2.45	0.41
1:A:322:GLU:CD	1:A:322:GLU:H	2.23	0.41
1:A:31:THR:OG1	1:A:35:SER:HB2	2.20	0.41
1:A:449:VAL:O	1:A:449:VAL:HG12	2.22	0.40
1:A:426:CYS:O	1:A:430:ILE:HG13	2.21	0.40
1:A:137:ILE:H	1:A:137:ILE:HG12	1.79	0.40
1:A:179:LEU:HA	1:A:179:LEU:HD23	1.86	0.40
1:A:419:ASN:HB2	1:A:423:ASN:HD22	1.87	0.40
1:A:254:VAL:HG21	1:A:284:ILE:HD11	2.03	0.40
1:A:294:SER:HA	1:A:297:LEU:HB2	2.04	0.40
1:A:453:HIS:CB	2:A:803:HOH:O	2.60	0.40
1:A:43:LEU:O	1:A:44:ASP:C	2.60	0.40
1:A:169:MET:CE	1:A:455:LEU:HD22	2.51	0.40
1:A:103:ILE:HG21	1:A:103:ILE:HD13	1.73	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	452/482 (94%)	360 (80%)	65 (14%)	27 (6%)	2 1

All (27) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	GLU
1	A	149	SER
1	A	180	ILE
1	A	322	GLU
1	A	365	ASP

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Mol	Chain	Res	Type
1	A	373	ILE
1	A	374	TYR
1	A	376	HIS
1	A	56	ASP
1	A	165	SER
1	A	226	SER
1	A	421	GLU
1	A	423	ASN
1	A	478	SER
1	A	164	MET
1	A	211	MET
1	A	45	ARG
1	A	47	VAL
1	A	250	ALA
1	A	425	PRO
1	A	471	ASN
1	A	6	GLU
1	A	59	LYS
1	A	160	GLY
1	A	422	THR
1	A	207	GLY
1	A	224	GLY

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	389/408 (95%)	308 (79%)	81 (21%)	1 1

All (81) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	LYS
1	A	15	LYS
1	A	18	GLU
1	A	22	LYS

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Mol	Chain	Res	Type
1	A	26	LEU
1	A	30	PHE
1	A	35	SER
1	A	38	GLU
1	A	42	ASN
1	A	45	ARG
1	A	54	THR
1	A	55	ASP
1	A	56	ASP
1	A	61	SER
1	A	67	LEU
1	A	97	GLU
1	A	106	TRP
1	A	111	THR
1	A	114	LYS
1	A	120	ILE
1	A	121	GLU
1	A	128	GLN
1	A	137	ILE
1	A	140	ARG
1	A	141	VAL
1	A	142	ASN
1	A	148	LEU
1	A	162	ILE
1	A	170	LEU
1	A	171	SER
1	A	173	MET
1	A	177	ARG
1	A	180	ILE
1	A	195	ARG
1	A	196	GLU
1	A	198	VAL
1	A	201	CYS
1	A	211	MET
1	A	220	ILE
1	A	225	ARG
1	A	226	SER
1	A	228	ILE
1	A	235	LEU
1	A	237	LYS
1	A	241	THR
1	A	242	GLU

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Mol	Chain	Res	Type
1	A	249	GLU
1	A	253	THR
1	A	263	LYS
1	A	265	LYS
1	A	268	VAL
1	A	272	SER
1	A	278	THR
1	A	295	SER
1	A	298	ARG
1	A	304	ILE
1	A	309	SER
1	A	326	THR
1	A	336	LYS
1	A	339	ARG
1	A	342	LYS
1	A	343	LYS
1	A	350	SER
1	A	351	THR
1	A	366	ASP
1	A	372	ARG
1	A	373	ILE
1	A	380	LEU
1	A	397	VAL
1	A	399	ASN
1	A	413	ILE
1	A	419	ASN
1	A	420	THR
1	A	423	ASN
1	A	424	ASN
1	A	436	ILE
1	A	439	THR
1	A	446	MET
1	A	447	ASP
1	A	448	ILE
1	A	463	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	42	ASN
1	A	279	ASN
1	A	283	HIS

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Mol	Chain	Res	Type
1	A	399	ASN
1	A	409	HIS
1	A	419	ASN
1	A	423	ASN
1	A	444	GLN
1	A	475	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](#)

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	460/482 (95%)	0.17	18 (3%)	43 52	25, 46, 82, 151	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	27	VAL	5.7
1	A	420	THR	5.3
1	A	140	ARG	3.9
1	A	372	ARG	3.6
1	A	244	LYS	3.4
1	A	235	LEU	3.4
1	A	29	THR	3.0
1	A	195	ARG	2.8
1	A	443	ILE	2.5
1	A	338	PRO	2.4
1	A	366	ASP	2.4
1	A	55	ASP	2.2
1	A	238	LEU	2.2
1	A	180	ILE	2.1
1	A	423	ASN	2.1
1	A	421	GLU	2.1
1	A	181	LEU	2.0
1	A	428	LYS	2.0

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 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.