



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:19 PM UTC

PDB ID : 2CSD / pdb_00002csd
Title : Crystal structure of Topoisomerase V (61 kDa fragment)
Authors : Taneja, B.; Patel, A.; Slesarev, A.; Mondragon, A.
Deposited on : 2005-05-21
Resolution : 2.90 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Xtrriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

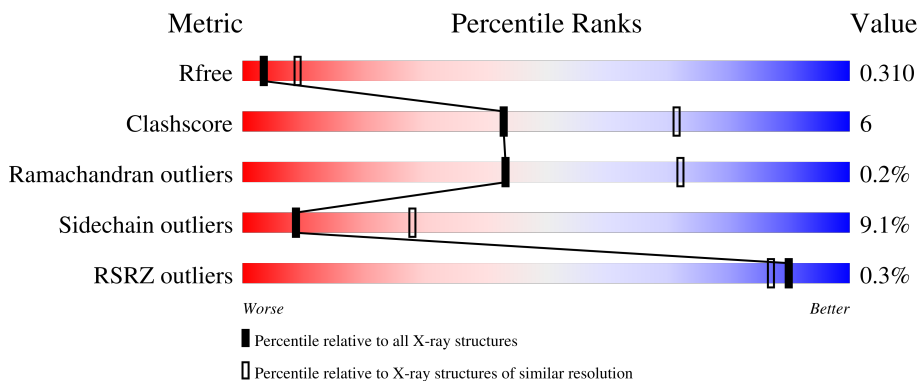
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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}	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	519	 77% 19% ..
1	B	519	 79% 18% ..

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 8390 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.

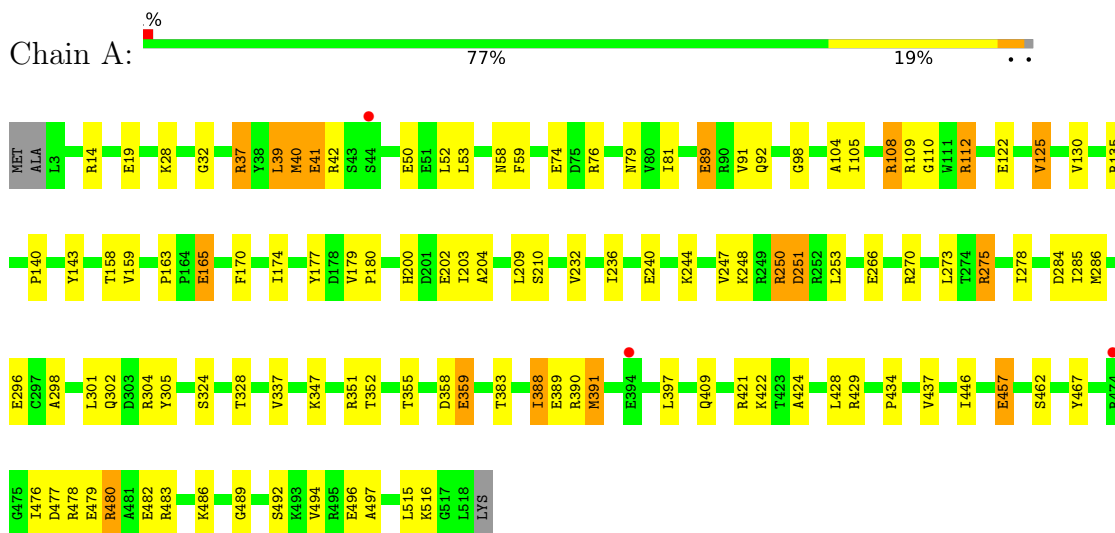
- Molecule 1 is a protein called Topoisomerase V.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	516	Total 4195	C 2625	N 753	O 807	S 10	0	0	0
1	B	516	Total 4195	C 2625	N 753	O 807	S 10	0	0	0

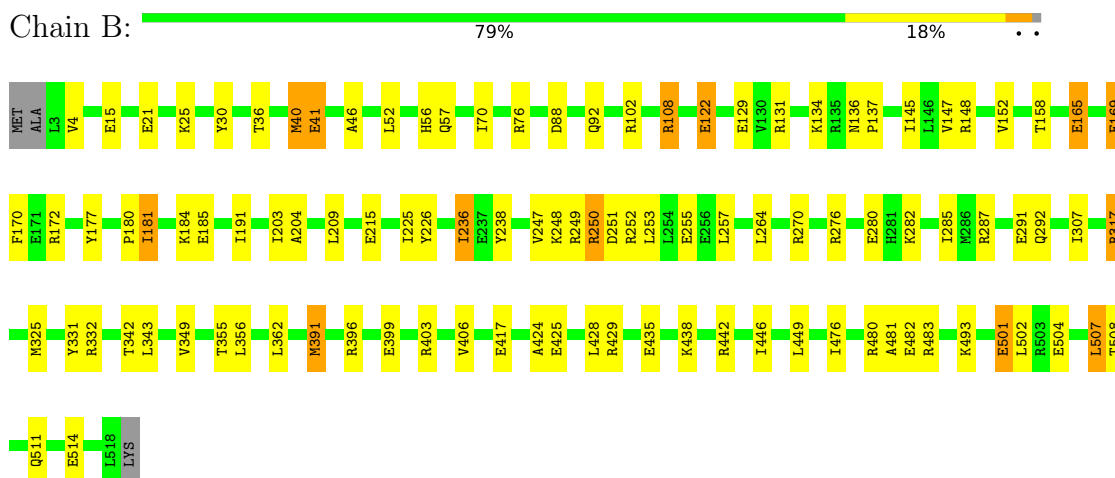
3 Residue-property plots [i](#)

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: Topoisomerase V



- Molecule 1: Topoisomerase V



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	75.50Å 86.40Å 175.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.80 – 2.90 28.80 – 2.90	Depositor EDS
% Data completeness (in resolution range)	98.9 (28.80-2.90) 98.9 (28.80-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.01 (at 2.90Å)	Xtrriage
Refinement program	REFMAC 5.0, CNS	Depositor
R, R_{free}	0.236 , 0.308 0.235 , 0.310	Depositor DCC
R_{free} test set	1319 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	56.4	Xtrriage
Anisotropy	0.134	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 34.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	8390	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.60% 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	0.52	0/4260	0.97	0/5745
1	B	0.50	0/4260	0.96	0/5745
All	All	0.51	0/8520	0.96	0/11490

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	4195	0	4198	57	0
1	B	4195	0	4198	49	0
All	All	8390	0	8396	104	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 6.

All (104) 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:479:GLU:HG2	1:A:483:ARG:NH1	1.71	1.05
1:A:479:GLU:HG2	1:A:483:ARG:HH12	1.19	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:508:THR:H	1:B:511:GLN:HE21	1.28	0.82
1:A:28:LYS:HG3	1:A:275:ARG:NH2	2.03	0.73
1:A:58:ASN:OD1	1:A:159:VAL:HG23	1.91	0.70
1:B:331:TYR:HE1	1:B:343:LEU:HA	1.57	0.69
1:B:88:ASP:O	1:B:92:GLN:HG2	1.96	0.65
1:B:331:TYR:CE1	1:B:343:LEU:HA	2.32	0.65
1:B:102:ARG:HD2	1:B:147:VAL:O	1.97	0.64
1:A:479:GLU:CG	1:A:483:ARG:HH12	2.04	0.64
1:B:108:ARG:HB3	1:B:325:MET:HE2	1.80	0.64
1:B:247:VAL:HA	1:B:250:ARG:HD2	1.80	0.64
1:A:163:PRO:HB2	1:A:165:GLU:HG3	1.81	0.62
1:B:501:GLU:O	1:B:504:GLU:HB2	1.99	0.61
1:A:109:ARG:O	1:A:112:ARG:HG2	2.01	0.61
1:B:435:GLU:OE1	1:B:438:LYS:HD2	2.01	0.60
1:B:145:ILE:HD11	1:B:226:TYR:HD2	1.66	0.60
1:A:250:ARG:HG2	1:A:251:ASP:N	2.17	0.59
1:B:424:ALA:O	1:B:428:LEU:HG	2.03	0.58
1:B:502:LEU:O	1:B:507:LEU:HB2	2.04	0.58
1:B:282:LYS:O	1:B:285:ILE:HG22	2.03	0.58
1:A:275:ARG:O	1:A:275:ARG:HD3	2.05	0.56
1:B:36:THR:HG21	1:B:56:HIS:HB2	1.85	0.56
1:B:287:ARG:O	1:B:291:GLU:HB2	2.06	0.55
1:A:200:HIS:HA	1:A:203:ILE:HD12	1.89	0.55
1:A:177:TYR:CZ	1:A:236:ILE:HG13	2.42	0.54
1:B:508:THR:H	1:B:511:GLN:NE2	2.02	0.54
1:B:250:ARG:HG2	1:B:251:ASP:N	2.22	0.54
1:A:298:ALA:O	1:A:302:GLN:HG3	2.07	0.54
1:A:247:VAL:HA	1:A:250:ARG:HD2	1.90	0.54
1:B:36:THR:O	1:B:40:MET:HG2	2.08	0.53
1:B:425:GLU:O	1:B:429:ARG:HG2	2.09	0.52
1:B:276:ARG:O	1:B:280:GLU:HG2	2.10	0.52
1:B:476:ILE:HG22	1:B:481:ALA:HB2	1.91	0.52
1:A:109:ARG:HH11	1:A:112:ARG:HH21	1.57	0.51
1:A:41:GLU:O	1:A:41:GLU:HG2	2.09	0.51
1:A:140:PRO:O	1:A:143:TYR:HB3	2.11	0.50
1:A:383:THR:O	1:A:409:GLN:NE2	2.44	0.50
1:B:46:ALA:O	1:B:52:LEU:HD23	2.12	0.49
1:B:264:LEU:C	1:B:264:LEU:HD23	2.38	0.48
1:A:492:SER:O	1:A:496:GLU:HG3	2.14	0.48
1:A:174:ILE:HD13	1:A:232:VAL:HG21	1.95	0.48
1:A:477:ASP:OD1	1:A:480:ARG:HB2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:15:GLU:HB3	1:B:76:ARG:HD3	1.96	0.47
1:B:446:ILE:HB	1:B:482:GLU:OE1	2.14	0.47
1:A:482:GLU:HG2	1:A:486:LYS:HD2	1.96	0.47
1:A:424:ALA:O	1:A:428:LEU:HG	2.14	0.47
1:A:446:ILE:HB	1:A:482:GLU:OE1	2.14	0.47
1:B:41:GLU:HG3	1:B:292:GLN:HE22	1.79	0.47
1:A:89:GLU:HA	1:A:92:GLN:HG2	1.96	0.47
1:B:204:ALA:HB1	1:B:209:LEU:O	2.15	0.47
1:B:317:ARG:HH11	1:B:317:ARG:HB3	1.79	0.47
1:B:180:PRO:HB3	1:B:442:ARG:O	2.15	0.46
1:A:79:ASN:O	1:A:81:ILE:HD12	2.16	0.46
1:A:457:GLU:OE1	1:A:478:ARG:NH1	2.48	0.46
1:B:253:LEU:O	1:B:257:LEU:HG	2.16	0.46
1:A:301:LEU:O	1:A:305:TYR:HB2	2.16	0.45
1:B:181:ILE:HG22	1:B:185:GLU:HB2	1.99	0.45
1:B:41:GLU:HG2	1:B:41:GLU:O	2.16	0.45
1:A:497:ALA:O	1:A:516:LYS:NZ	2.50	0.44
1:B:122:GLU:H	1:B:122:GLU:HG2	1.40	0.44
1:A:204:ALA:HB1	1:A:209:LEU:O	2.17	0.44
1:B:145:ILE:HD11	1:B:226:TYR:CD2	2.49	0.44
1:A:39:LEU:O	1:A:42:ARG:HB2	2.17	0.44
1:A:324:SER:O	1:A:328:THR:HG23	2.17	0.44
1:A:109:ARG:O	1:A:112:ARG:CG	2.66	0.44
1:A:14:ARG:NH1	1:B:238:TYR:HD2	2.16	0.43
1:B:391:MET:HG3	1:B:396:ARG:HH11	1.83	0.43
1:B:57:GLN:HG2	1:B:137:PRO:HD3	2.00	0.43
1:A:32:GLY:HA3	1:A:59:PHE:CD2	2.53	0.43
1:A:275:ARG:HD3	1:A:275:ARG:C	2.44	0.43
1:A:210:SER:HB3	1:A:351:ARG:HD3	1.99	0.43
1:A:355:THR:HA	1:A:359:GLU:HG3	2.00	0.43
1:A:494:VAL:HG12	1:A:515:LEU:HD21	1.99	0.43
1:B:21:GLU:O	1:B:25:LYS:HG3	2.18	0.43
1:A:40:MET:HE3	1:A:40:MET:HB3	1.82	0.43
1:A:165:GLU:O	1:A:170:PHE:HA	2.18	0.43
1:A:391:MET:HE3	1:A:391:MET:HB2	1.84	0.43
1:B:215:GLU:HB3	1:B:226:TYR:CD1	2.53	0.42
1:A:125:VAL:HG11	1:A:286:MET:HE1	2.00	0.42
1:A:434:PRO:O	1:A:437:VAL:HB	2.19	0.42
1:A:14:ARG:HH11	1:B:238:TYR:HD2	1.68	0.42
1:A:347:LYS:NZ	1:A:358:ASP:OD1	2.52	0.42
1:B:30:TYR:CZ	1:B:129:GLU:HB2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:191:ILE:HG21	1:B:203:ILE:HG12	2.02	0.42
1:A:179:VAL:HA	1:A:180:PRO:HD2	1.86	0.42
1:B:165:GLU:HA	1:B:169:GLU:O	2.20	0.42
1:A:19:GLU:HG2	1:A:76:ARG:HH11	1.85	0.42
1:B:165:GLU:O	1:B:170:PHE:HA	2.20	0.42
1:A:91:VAL:HG11	1:A:98:GLY:O	2.20	0.41
1:A:244:LYS:O	1:A:248:LYS:HG2	2.20	0.41
1:A:476:ILE:HG23	1:A:480:ARG:HB3	2.02	0.41
1:B:177:TYR:CZ	1:B:236:ILE:HG13	2.55	0.41
1:B:356:LEU:HD22	1:B:362:LEU:HD12	2.02	0.41
1:A:37:ARG:HD2	1:A:37:ARG:HA	1.77	0.41
1:A:388:ILE:HG22	1:A:389:GLU:N	2.35	0.41
1:A:108:ARG:O	1:A:109:ARG:HB2	2.21	0.41
1:A:40:MET:HE3	1:A:52:LEU:HG	2.03	0.41
1:A:104:ALA:O	1:A:110:GLY:HA3	2.20	0.41
1:A:421:ARG:HE	1:A:421:ARG:HB3	1.77	0.41
1:B:102:ARG:NH1	1:B:148:ARG:O	2.54	0.41
1:B:399:GLU:O	1:B:403:ARG:HG3	2.21	0.40
1:B:136:ASN:HA	1:B:137:PRO:HD2	1.98	0.40
1:A:467:TYR:OH	1:A:478:ARG:HG2	2.21	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	514/519 (99%)	493 (96%)	20 (4%)	1 (0%)	43 72
1	B	514/519 (99%)	480 (93%)	33 (6%)	1 (0%)	43 72
All	All	1028/1038 (99%)	973 (95%)	53 (5%)	2 (0%)	43 72

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	489	GLY
1	B	355	THR

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	447/449 (100%)	404 (90%)	43 (10%)	8	26
1	B	447/449 (100%)	409 (92%)	38 (8%)	10	31
All	All	894/898 (100%)	813 (91%)	81 (9%)	9	28

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

Mol	Chain	Res	Type
1	A	37	ARG
1	A	39	LEU
1	A	40	MET
1	A	41	GLU
1	A	50	GLU
1	A	53	LEU
1	A	74	GLU
1	A	89	GLU
1	A	105	ILE
1	A	108	ARG
1	A	112	ARG
1	A	122	GLU
1	A	125	VAL
1	A	130	VAL
1	A	135	ARG
1	A	158	THR
1	A	165	GLU
1	A	202	GLU
1	A	240	GLU
1	A	250	ARG
1	A	251	ASP
1	A	253	LEU

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Mol	Chain	Res	Type
1	A	266	GLU
1	A	270	ARG
1	A	273	LEU
1	A	275	ARG
1	A	278	ILE
1	A	284	ASP
1	A	285	ILE
1	A	296	GLU
1	A	304	ARG
1	A	337	VAL
1	A	352	THR
1	A	359	GLU
1	A	388	ILE
1	A	390	ARG
1	A	391	MET
1	A	397	LEU
1	A	422	LYS
1	A	429	ARG
1	A	457	GLU
1	A	462	SER
1	A	480	ARG
1	B	4	VAL
1	B	40	MET
1	B	41	GLU
1	B	70	ILE
1	B	108	ARG
1	B	122	GLU
1	B	131	ARG
1	B	134	LYS
1	B	152	VAL
1	B	158	THR
1	B	165	GLU
1	B	169	GLU
1	B	172	ARG
1	B	181	ILE
1	B	184	LYS
1	B	225	ILE
1	B	236	ILE
1	B	248	LYS
1	B	249	ARG
1	B	250	ARG
1	B	252	ARG

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Mol	Chain	Res	Type
1	B	255	GLU
1	B	270	ARG
1	B	307	ILE
1	B	317	ARG
1	B	332	ARG
1	B	342	THR
1	B	349	VAL
1	B	391	MET
1	B	406	VAL
1	B	417	GLU
1	B	449	LEU
1	B	480	ARG
1	B	483	ARG
1	B	493	LYS
1	B	501	GLU
1	B	507	LEU
1	B	514	GLU

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

Mol	Chain	Res	Type
1	A	56	HIS
1	A	246	HIS
1	A	433	ASN
1	A	439	GLN
1	B	56	HIS
1	B	292	GLN
1	B	302	GLN
1	B	409	GLN
1	B	511	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 oligosaccharides 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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	516/519 (99%)	-0.18	3 (0%) 85 81	33, 49, 58, 66	1 (0%)
1	B	516/519 (99%)	-0.03	0 100 100	37, 54, 70, 76	0
All	All	1032/1038 (99%)	-0.11	3 (0%) 90 87	33, 52, 68, 76	1 (0%)

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	474	ARG	2.3
1	A	44	SER	2.2
1	A	394	GLU	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 oligosaccharides 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.