



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 03:34 PM UTC

PDB ID : 4CJA / pdb_00004cja
Title : BurrH DNA-binding protein from Burkholderia rhizoxinica in complex with its target DNA
Authors : Stella, S.; Molina, R.; Lopez-Mendez, B.; Campos-Olivas, R.; Duchateau, P.; Montoya, G.
Deposited on : 2013-12-19
Resolution : 2.65 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
Xtriage (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

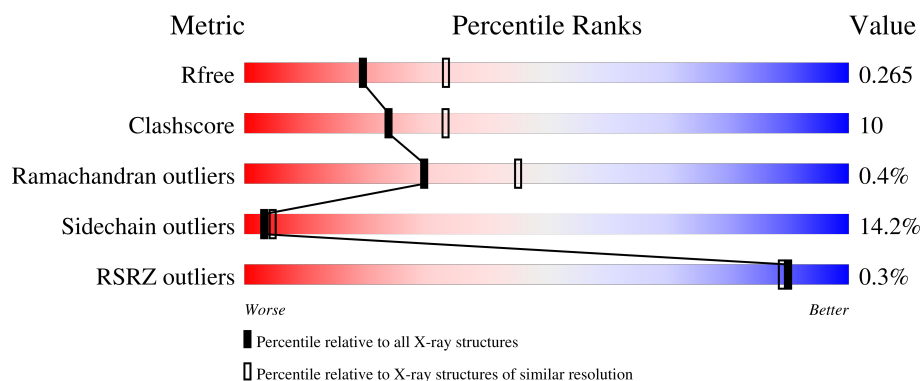
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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	1110 (2.66-2.66)
Clashscore	190562	1141 (2.66-2.66)
Ramachandran outliers	187476	1126 (2.66-2.66)
Sidechain outliers	187428	1126 (2.66-2.66)
RSRZ outliers	180081	1110 (2.66-2.66)

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	794	 66% 25% 5%
2	B	23	 87% 13%
3	C	23	 57% 30% 13%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6553 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 BURRH.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	753	Total	C	N	O	S	0	0	0
			5491	3414	1020	1042	15			

- Molecule 2 is a DNA chain called 5'-D(*DTP*TP*AP*AP*GP*AP*GP*AP*AP*GP*CP*AP*AP*DP *TP*AP*CP*GP*TP*TP*AP*TP*AP)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	23	Total	C	N	O	P	0	0	0
			474	228	93	131	22			

- Molecule 3 is a DNA chain called 5'-D(*DTP*AP*TP*AP*AP*CP*GP*TP*AP*TP*TP*TP*GP*CP *TP*TP*CP*TP*CP*TP*TP*AP*AP)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	23	Total	C	N	O	P	0	0	0
			463	226	74	141	22			

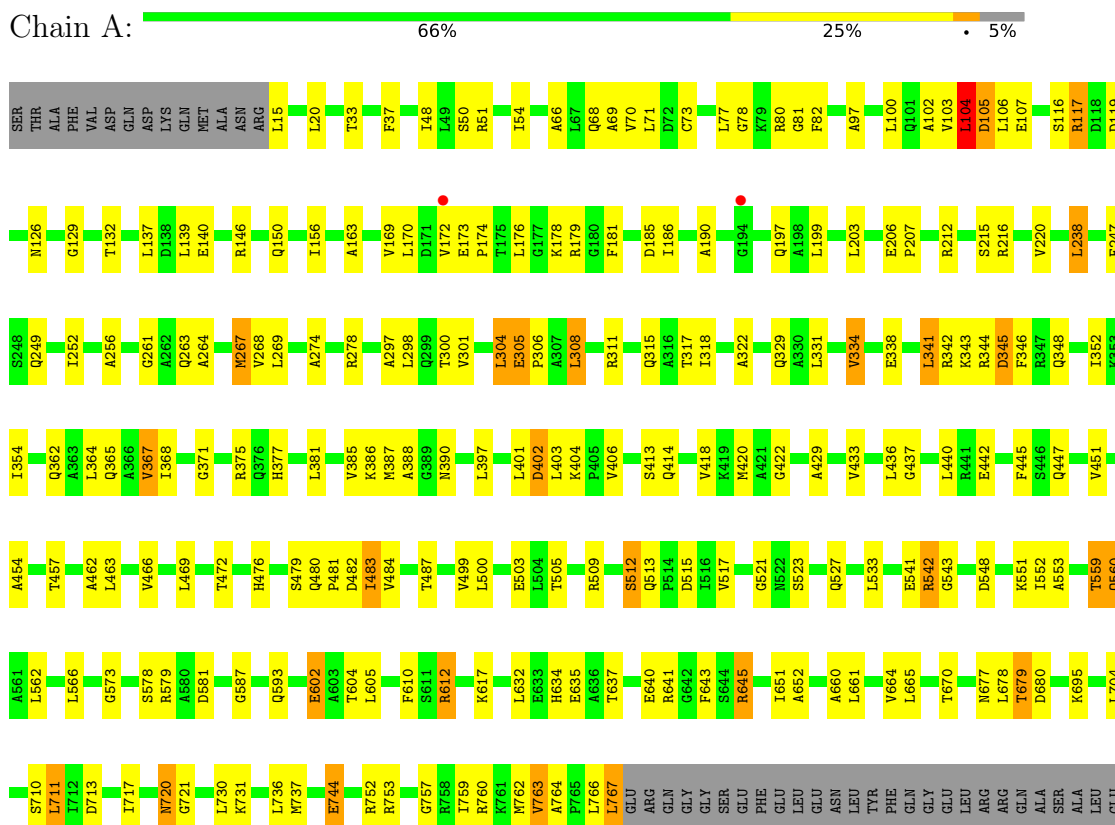
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	105	Total	O	0	0
			105	105		
4	B	10	Total	O	0	0
			10	10		
4	C	10	Total	O	0	0
			10	10		

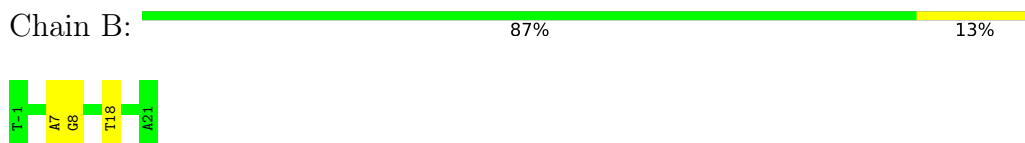
3 Residue-property plots

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: BURRH

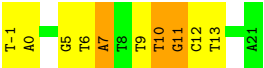


• Molecule 2: 5'-D(*DTP*TP*AP*AP*GP*AP*GP*AP*AP*GP*CP*AP*AP*DP *TP*AP*CP *GP*TP*TP*AP*TP*AP)-3'



• Molecule 3: 5'-D(*DTP*AP*TP*AP*AP*CP*GP*TP*AP*TP*TP*GP*CP *TP*TP*CP *TP*CP*TP*TP*AP*AP)-3'





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	70.24Å 95.95Å 76.45Å 90.00° 109.50° 90.00°	Depositor
Resolution (Å)	38.66 – 2.65 38.66 – 2.65	Depositor EDS
% Data completeness (in resolution range)	99.6 (38.66-2.65) 99.6 (38.66-2.65)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.83 (at 2.65Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.203 , 0.268 0.205 , 0.265	Depositor DCC
R_{free} test set	1396 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	65.5	Xtriage
Anisotropy	0.336	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 34.1	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	0.96	EDS
Total number of atoms	6553	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.58% 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

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	0.54	0/5548	0.95	8/7480 (0.1%)
2	B	0.38	0/534	1.15	1/823 (0.1%)
3	C	0.38	0/516	1.19	3/794 (0.4%)
All	All	0.52	0/6598	0.99	12/9097 (0.1%)

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	185	ASP	N-CA-C	-8.07	103.26	113.43
1	A	720	ASN	N-CA-C	7.62	122.48	112.72
3	C	10	DT	C5'-C4'-C3'	-7.41	103.79	114.90
1	A	542	ARG	N-CA-C	7.41	123.45	113.97
1	A	483	ILE	N-CA-C	-6.92	105.86	111.81
3	C	7	DA	P-O5'-C5'	-6.66	110.01	120.00
2	B	18	DT	P-O5'-C5'	-6.30	110.55	120.00
1	A	140	GLU	N-CA-C	-6.21	105.53	113.23
3	C	11	DG	C2'-C3'-O3'	6.07	120.60	111.50
1	A	78	GLY	N-CA-C	-5.44	106.08	113.37
1	A	560	GLN	N-CA-C	-5.20	105.52	111.14
1	A	573	GLY	N-CA-C	-5.17	108.54	115.32

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	5491	0	5622	116	1
2	B	474	0	261	2	0
3	C	463	0	266	10	0
4	A	105	0	0	12	0
4	B	10	0	0	0	0
4	C	10	0	0	4	0
All	All	6553	0	6149	126	1

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 (126) 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:206:GLU:OE1	1:A:216:ARG:NH2	2.15	0.78
1:A:635:GLU:HG2	1:A:645:ARG:HH21	1.47	0.78
1:A:146:ARG:NH1	1:A:173:GLU:OE1	2.23	0.72
1:A:345:ASP:N	1:A:345:ASP:OD1	2.22	0.72
1:A:278:ARG:NH1	1:A:305:GLU:OE2	2.23	0.71
1:A:634:HIS:N	4:A:2080:HOH:O	2.24	0.71
1:A:710:SER:HB2	1:A:713:ASP:H	1.55	0.71
1:A:172:VAL:HG21	1:A:199:LEU:HB3	1.73	0.70
1:A:602:GLU:OE2	1:A:612:ARG:NH2	2.26	0.68
1:A:132:THR:HA	1:A:163:ALA:HB2	1.76	0.68
1:A:736:LEU:HD13	1:A:762:MET:HE2	1.75	0.67
1:A:342:ARG:HH22	1:A:348:GLN:HB2	1.61	0.66
1:A:651:ILE:HD13	1:A:664:VAL:HG21	1.79	0.65
3:C:13:DT:OP1	4:C:2007:HOH:O	2.15	0.65
1:A:420:MET:HE3	1:A:451:VAL:HG13	1.80	0.64
1:A:146:ARG:NH2	1:A:170:LEU:O	2.33	0.61
1:A:480:GLN:O	1:A:484:VAL:HG23	2.01	0.59
1:A:390:ASN:ND2	1:A:422:GLY:O	2.29	0.59
1:A:513:GLN:NE2	4:A:2052:HOH:O	2.36	0.58
1:A:652:ALA:HB2	1:A:661:LEU:HD11	1.85	0.57
1:A:454:ALA:HB2	1:A:463:LEU:HD11	1.86	0.57
1:A:479:SER:OG	1:A:482:ASP:OD1	2.24	0.56
1:A:757:GLY:HA2	1:A:760:ARG:HG2	1.87	0.56
1:A:190:ALA:HB2	1:A:199:LEU:HD21	1.88	0.56
1:A:172:VAL:HG12	1:A:203:LEU:HD22	1.88	0.55
1:A:116:SER:OG	1:A:117:ARG:N	2.38	0.55
1:A:542:ARG:H	1:A:543:GLY:HA2	1.72	0.54
1:A:308:LEU:HB3	1:A:318:ILE:HD11	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:635:GLU:N	4:A:2080:HOH:O	2.31	0.54
1:A:542:ARG:N	1:A:543:GLY:HA2	2.22	0.54
3:C:11:DG:N7	4:C:2006:HOH:O	2.33	0.54
1:A:462:ALA:O	1:A:466:VAL:HG23	2.09	0.53
1:A:387:MET:HE3	1:A:418:VAL:HG22	1.90	0.53
1:A:527:GLN:HB3	1:A:559:THR:HG21	1.91	0.52
1:A:197:GLN:NE2	4:A:2012:HOH:O	2.19	0.52
1:A:80:ARG:O	1:A:117:ARG:NH1	2.43	0.52
3:C:5:DG:H2''	3:C:6:DT:H5''	1.91	0.52
1:A:509:ARG:NH2	1:A:533:LEU:O	2.42	0.52
1:A:587:GLY:O	4:A:2069:HOH:O	2.19	0.52
1:A:37:PHE:CZ	1:A:68:GLN:HG2	2.45	0.51
1:A:610:PHE:CE1	1:A:645:ARG:HG3	2.46	0.51
3:C:9:DT:H2''	3:C:10:DT:H5''	1.91	0.51
1:A:371:GLY:C	1:A:375:ARG:HH21	2.19	0.51
1:A:720:ASN:H	1:A:721:GLY:HA3	1.74	0.51
1:A:552:ILE:O	4:A:2061:HOH:O	2.19	0.50
1:A:479:SER:O	1:A:483:ILE:HG13	2.11	0.50
1:A:763:VAL:HB	1:A:767:LEU:HD11	1.94	0.49
1:A:386:LYS:HD2	1:A:418:VAL:HG12	1.94	0.49
1:A:103:VAL:HG13	1:A:107:GLU:HB3	1.95	0.49
3:C:10:DT:OP2	4:C:2003:HOH:O	2.19	0.49
1:A:102:ALA:HA	1:A:105:ASP:HB2	1.95	0.49
1:A:103:VAL:C	1:A:105:ASP:H	2.21	0.48
1:A:643:PHE:CZ	1:A:678:LEU:HD22	2.48	0.48
1:A:81:GLY:O	1:A:117:ARG:HG2	2.13	0.48
1:A:66:ALA:O	1:A:70:VAL:HG23	2.13	0.48
1:A:238:LEU:HB3	1:A:269:LEU:HD11	1.95	0.48
1:A:429:ALA:O	1:A:433:VAL:HG13	2.13	0.48
1:A:753:ARG:NH1	4:A:2101:HOH:O	2.45	0.48
1:A:216:ARG:O	1:A:220:VAL:HG23	2.14	0.48
1:A:176:LEU:HB2	1:A:181:PHE:HD2	1.78	0.47
1:A:274:ALA:O	1:A:278:ARG:HG2	2.14	0.47
1:A:548:ASP:O	1:A:552:ILE:HG13	2.14	0.47
1:A:247:PHE:N	4:A:2015:HOH:O	2.48	0.47
1:A:513:GLN:O	1:A:517:VAL:HG23	2.15	0.47
1:A:445:PHE:CZ	1:A:480:GLN:HG2	2.50	0.47
1:A:447:GLN:O	1:A:451:VAL:HG23	2.15	0.46
1:A:126:ASN:HB2	4:A:2008:HOH:O	2.13	0.46
1:A:73:CYS:HB3	1:A:104:LEU:HG	1.97	0.46
1:A:660:ALA:O	1:A:664:VAL:HG23	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:77:LEU:HD22	1:A:82:PHE:CD2	2.50	0.46
1:A:173:GLU:N	1:A:174:PRO:HD2	2.30	0.46
1:A:341:LEU:HD21	1:A:367:VAL:HG11	1.96	0.46
1:A:767:LEU:H	1:A:767:LEU:HG	1.46	0.46
3:C:6:DT:H2''	3:C:7:DA:C8	2.51	0.46
1:A:760:ARG:HA	1:A:763:VAL:HG23	1.98	0.46
1:A:264:ALA:O	1:A:268:VAL:HG23	2.16	0.46
1:A:635:GLU:HG2	1:A:645:ARG:NH2	2.25	0.46
1:A:551:LYS:HD3	1:A:587:GLY:HA3	1.98	0.46
1:A:711:LEU:HD22	1:A:711:LEU:HA	1.83	0.46
1:A:256:ALA:HA	1:A:261:GLY:HA3	1.98	0.46
1:A:341:LEU:HG	1:A:346:PHE:CD2	2.51	0.46
1:A:365:GLN:NE2	4:A:2030:HOH:O	2.49	0.46
1:A:553:ALA:HB2	1:A:562:LEU:HD11	1.98	0.46
1:A:66:ALA:HA	1:A:97:ALA:HB2	1.98	0.45
1:A:717:ILE:O	1:A:721:GLY:HA3	2.16	0.45
1:A:305:GLU:OE1	1:A:306:PRO:HD3	2.17	0.45
1:A:354:ILE:HD11	1:A:385:VAL:HG22	1.98	0.45
1:A:414:GLN:O	1:A:418:VAL:HG23	2.17	0.45
1:A:311:ARG:HD3	1:A:338:GLU:OE1	2.17	0.45
1:A:402:ASP:N	1:A:402:ASP:OD1	2.49	0.44
1:A:354:ILE:HG23	1:A:388:ALA:HB1	1.99	0.44
1:A:635:GLU:CG	1:A:645:ARG:HH21	2.23	0.44
1:A:437:GLY:HA2	1:A:440:LEU:HB2	1.99	0.44
1:A:297:ALA:O	1:A:301:VAL:HG23	2.17	0.44
3:C:-1:DT:H2''	3:C:0:DA:C8	2.52	0.44
1:A:212:ARG:O	1:A:249:GLN:NE2	2.30	0.44
3:C:7:DA:H5'	3:C:7:DA:H8	1.82	0.44
1:A:677:ASN:O	1:A:680:ASP:HB2	2.17	0.44
1:A:322:ALA:HB2	1:A:331:LEU:HD11	1.99	0.44
1:A:263:GLN:O	1:A:267:MET:HB2	2.18	0.43
1:A:362:GLN:HG3	2:B:8:DG:H5''	2.00	0.43
1:A:156:ILE:HD13	1:A:169:VAL:HG21	2.00	0.43
1:A:69:ALA:O	1:A:100:LEU:HD23	2.18	0.43
1:A:48:ILE:HD12	1:A:71:LEU:HD23	2.01	0.43
1:A:304:LEU:HA	1:A:304:LEU:HD13	1.80	0.43
1:A:612:ARG:HD2	1:A:612:ARG:HA	1.65	0.43
3:C:10:DT:O2	4:C:2005:HOH:O	2.21	0.43
1:A:759:ILE:HD13	1:A:759:ILE:HA	1.90	0.43
1:A:329:GLN:NE2	2:B:7:DA:OP1	2.46	0.42
1:A:77:LEU:HD21	1:A:103:VAL:HG12	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:334:VAL:HG23	1:A:364:LEU:HD11	2.01	0.42
1:A:512:SER:O	1:A:515:ASP:HB2	2.19	0.42
1:A:300:THR:HG23	1:A:304:LEU:HD23	2.00	0.42
1:A:481:PRO:HG3	4:A:2011:HOH:O	2.18	0.42
1:A:206:GLU:N	1:A:207:PRO:HD2	2.35	0.42
1:A:578:SER:O	1:A:581:ASP:HB2	2.20	0.41
1:A:116:SER:HB3	1:A:119:ASP:HB2	2.02	0.41
1:A:348:GLN:O	1:A:352:ILE:HG13	2.21	0.41
1:A:764:ALA:C	1:A:766:LEU:H	2.28	0.41
1:A:305:GLU:CD	1:A:306:PRO:HD3	2.46	0.41
1:A:15:LEU:HB3	1:A:51:ARG:NH1	2.36	0.41
1:A:404:LYS:HE2	4:A:2036:HOH:O	2.20	0.41
1:A:737:MET:HE3	1:A:737:MET:HB3	1.77	0.41
1:A:50:SER:O	1:A:54:ILE:HG13	2.21	0.40
1:A:744:GLU:H	1:A:744:GLU:HG2	1.52	0.40
3:C:12:DC:H2''	3:C:13:DT:H5'	2.04	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:541:GLU:OE2	1:A:679:THR:OG1[2_756]	2.09	0.11

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	751/794 (95%)	702 (94%)	46 (6%)	3 (0%)	30 45

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	129	GLY
1	A	104	LEU
1	A	521	GLY

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	543/577 (94%)	466 (86%)	77 (14%)	3 5

All (77) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	LEU
1	A	33	THR
1	A	104	LEU
1	A	105	ASP
1	A	106	LEU
1	A	117	ARG
1	A	137	LEU
1	A	139	LEU
1	A	150	GLN
1	A	178	LYS
1	A	179	ARG
1	A	186	ILE
1	A	215	SER
1	A	238	LEU
1	A	252	ILE
1	A	267	MET
1	A	298	LEU
1	A	304	LEU
1	A	305	GLU
1	A	308	LEU
1	A	315	GLN
1	A	317	THR
1	A	334	VAL
1	A	341	LEU

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Mol	Chain	Res	Type
1	A	343	LYS
1	A	344	ARG
1	A	345	ASP
1	A	367	VAL
1	A	368	ILE
1	A	377	HIS
1	A	381	LEU
1	A	397	LEU
1	A	401	LEU
1	A	402	ASP
1	A	403	LEU
1	A	406	VAL
1	A	413	SER
1	A	436	LEU
1	A	442	GLU
1	A	457	THR
1	A	469	LEU
1	A	472	THR
1	A	476	HIS
1	A	487	THR
1	A	499	VAL
1	A	500	LEU
1	A	503	GLU
1	A	505	THR
1	A	512	SER
1	A	523	SER
1	A	559	THR
1	A	560	GLN
1	A	566	LEU
1	A	579	ARG
1	A	593	GLN
1	A	602	GLU
1	A	604	THR
1	A	605	LEU
1	A	612	ARG
1	A	617	LYS
1	A	632	LEU
1	A	637	THR
1	A	640	GLU
1	A	641	ARG
1	A	645	ARG
1	A	665	LEU

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Mol	Chain	Res	Type
1	A	670	THR
1	A	679	THR
1	A	695	LYS
1	A	704	LEU
1	A	711	LEU
1	A	730	LEU
1	A	731	LYS
1	A	744	GLU
1	A	752	ARG
1	A	763	VAL
1	A	767	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	101	GLN
1	A	159	ASN
1	A	192	ASN
1	A	263	GLN
1	A	332	GLN
1	A	370	HIS
1	A	377	HIS
1	A	380	ASN
1	A	461	GLN
1	A	494	GLN
1	A	530	GLN
1	A	555	ASN
1	A	589	ASN
1	A	593	GLN
1	A	654	ASN

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 [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	753/794 (94%)	-0.35	2 (0%) 90 89	31, 66, 99, 123	0
2	B	23/23 (100%)	-0.99	0 100 100	33, 41, 90, 101	0
3	C	23/23 (100%)	-0.86	0 100 100	44, 55, 77, 95	0
All	All	799/840 (95%)	-0.38	2 (0%) 90 89	31, 65, 98, 123	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	194	GLY	3.4
1	A	172	VAL	2.4

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.