



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 18, 2026 – 12:54 PM UTC

PDB ID : 2P8R / pdb_00002p8r
Title : Crystal structure of the C-terminal domain of C. elegans pre-mRNA splicing factor Prp8 carrying R2303K mutant
Authors : Zhang, L.; Shen, J.; Guarnieri, M.T.; Heroux, A.; Yang, K.; Zhao, R.
Deposited on : 2007-03-22
Resolution : 2.10 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

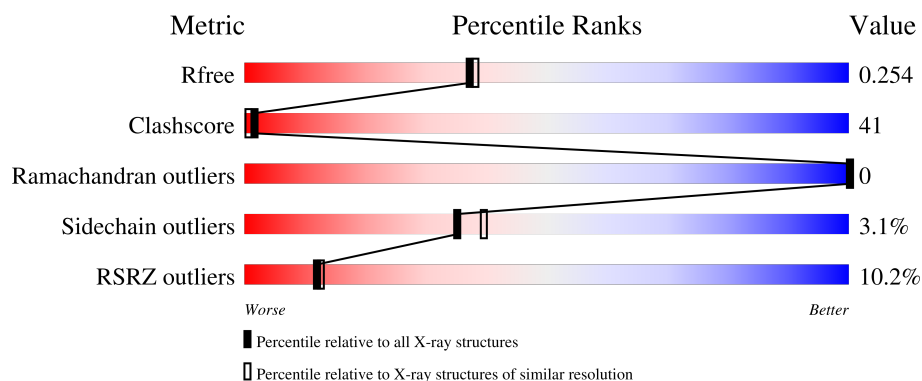
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	273	9% 51% 37% 10%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2162 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 Pre-mRNA-splicing factor Prp8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	246	1995	1274	341	370	10	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2303	LYS	ARG	engineered mutation	UNP P34369

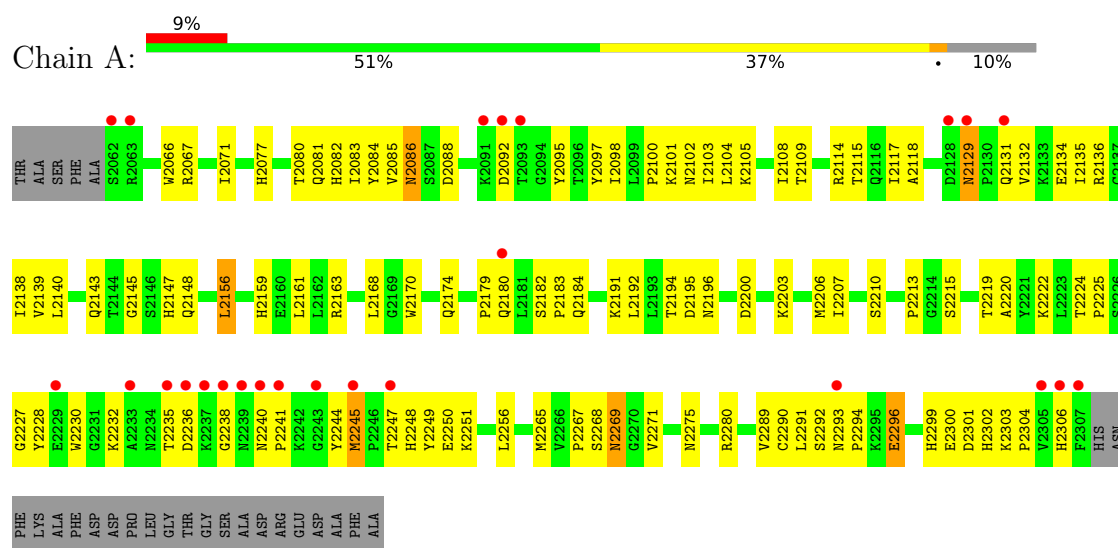
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	167	Total	O	0	0
			167	167		

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: Pre-mRNA-splicing factor Prp8



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	65.22Å 65.22Å 136.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.10 50.00 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.4 (50.00-2.10) 98.4 (50.00-2.10)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.21 (at 2.10Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.230 , 0.248 0.233 , 0.254	Depositor DCC
R_{free} test set	1678 reflections (9.37%)	wwPDB-VP
Wilson B-factor (Å ²)	27.4	Xtriage
Anisotropy	0.205	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 36.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	2162	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.73% 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	0.43	0/2056	0.96	5/2802 (0.2%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2131	GLN	OE1-CD-NE2	-9.78	112.82	122.60
1	A	2131	GLN	CG-CD-NE2	6.66	126.40	116.40
1	A	2129	ASN	CA-C-N	6.02	125.70	119.56
1	A	2129	ASN	C-N-CA	6.02	125.70	119.56
1	A	2081	GLN	N-CA-C	-5.20	106.78	113.23

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	1995	0	1938	163	0
2	A	167	0	0	97	0
All	All	2162	0	1938	163	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 41.

All (163) 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:2083:ILE:HG22	2:A:2481:HOH:O	1.26	1.34
1:A:2108:ILE:HD13	2:A:2442:HOH:O	1.37	1.23
1:A:2100:PRO:HB2	2:A:2408:HOH:O	1.44	1.16
1:A:2180:GLN:HG2	2:A:2475:HOH:O	1.48	1.14
1:A:2098:ILE:HG13	2:A:2431:HOH:O	1.45	1.14
1:A:2241:PRO:HD3	2:A:2467:HOH:O	1.59	1.03
1:A:2179:PRO:HG2	2:A:2475:HOH:O	1.60	1.01
1:A:2134:GLU:HB3	2:A:2421:HOH:O	1.64	0.98
1:A:2135:ILE:HG13	2:A:2469:HOH:O	1.65	0.97
1:A:2280:ARG:HD3	2:A:2471:HOH:O	1.68	0.94
1:A:2082:HIS:HB2	2:A:2435:HOH:O	1.69	0.92
1:A:2299:HIS:HD2	1:A:2301:ASP:H	1.16	0.92
1:A:2108:ILE:HA	2:A:2442:HOH:O	1.69	0.91
1:A:2220:ALA:HB2	2:A:2460:HOH:O	1.68	0.91
1:A:2136:ARG:HA	2:A:2441:HOH:O	1.70	0.90
1:A:2145:GLY:H	1:A:2275:ASN:HD21	1.20	0.88
1:A:2095:TYR:CD1	2:A:2450:HOH:O	2.30	0.84
1:A:2244:TYR:CE2	2:A:2474:HOH:O	2.30	0.84
1:A:2115:THR:HA	2:A:2456:HOH:O	1.78	0.83
1:A:2182:SER:HB2	2:A:2385:HOH:O	1.79	0.83
1:A:2191:LYS:HD3	1:A:2191:LYS:C	2.03	0.83
1:A:2118:ALA:H	1:A:2143:GLN:HE22	1.26	0.81
1:A:2290:CYS:HB3	2:A:2485:HOH:O	1.79	0.80
1:A:2207:ILE:HG12	2:A:2460:HOH:O	1.79	0.80
1:A:2280:ARG:CD	2:A:2471:HOH:O	2.23	0.80
1:A:2244:TYR:HE2	2:A:2474:HOH:O	1.63	0.80
1:A:2238:GLY:C	2:A:2467:HOH:O	2.26	0.79
1:A:2191:LYS:HE2	1:A:2195:ASP:OD2	1.82	0.79
1:A:2236:ASP:OD1	1:A:2241:PRO:HB3	1.83	0.77
1:A:2180:GLN:N	2:A:2475:HOH:O	2.14	0.77
1:A:2232:LYS:CE	2:A:2415:HOH:O	2.32	0.77
1:A:2250:GLU:HB3	2:A:2492:HOH:O	1.86	0.75
1:A:2184:GLN:HB2	2:A:2385:HOH:O	1.85	0.75
1:A:2182:SER:CB	2:A:2385:HOH:O	2.34	0.74
1:A:2299:HIS:CD2	1:A:2301:ASP:H	2.04	0.74
1:A:2135:ILE:N	2:A:2469:HOH:O	2.19	0.74
1:A:2290:CYS:CB	2:A:2485:HOH:O	2.33	0.73
1:A:2102:ASN:OD1	2:A:2408:HOH:O	2.04	0.73
1:A:2293:ASN:HD22	1:A:2294:PRO:CD	2.01	0.73
1:A:2097:TYR:C	2:A:2431:HOH:O	2.32	0.72
1:A:2293:ASN:HD22	1:A:2294:PRO:HD2	1.54	0.72
1:A:2210:SER:CB	2:A:2490:HOH:O	2.39	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2101:LYS:HE3	2:A:2465:HOH:O	1.92	0.69
1:A:2225:PRO:HG2	2:A:2395:HOH:O	1.93	0.68
1:A:2086:ASN:HD21	1:A:2088:ASP:HB2	1.59	0.68
1:A:2086:ASN:C	1:A:2086:ASN:HD22	2.02	0.67
1:A:2136:ARG:HD2	2:A:2441:HOH:O	1.95	0.66
1:A:2159:HIS:HD2	1:A:2161:LEU:H	1.42	0.66
1:A:2184:GLN:CD	2:A:2385:HOH:O	2.38	0.66
1:A:2228:TYR:CZ	1:A:2232:LYS:HD2	2.30	0.66
1:A:2095:TYR:HD1	2:A:2450:HOH:O	1.75	0.66
1:A:2086:ASN:ND2	1:A:2088:ASP:H	1.93	0.66
1:A:2191:LYS:HD2	2:A:2491:HOH:O	1.96	0.66
1:A:2289:VAL:C	2:A:2485:HOH:O	2.39	0.66
1:A:2136:ARG:CD	2:A:2441:HOH:O	2.44	0.65
1:A:2245:MET:HE2	1:A:2247:THR:CG2	2.27	0.65
1:A:2086:ASN:HD22	1:A:2088:ASP:H	1.43	0.65
1:A:2136:ARG:NE	2:A:2441:HOH:O	2.29	0.65
1:A:2084:TYR:N	2:A:2481:HOH:O	2.29	0.64
1:A:2145:GLY:H	1:A:2275:ASN:ND2	1.94	0.64
1:A:2200:ASP:HB3	1:A:2203:LYS:HG2	1.79	0.64
1:A:2135:ILE:CG1	2:A:2469:HOH:O	2.35	0.62
1:A:2238:GLY:N	2:A:2439:HOH:O	2.32	0.62
1:A:2245:MET:HE2	1:A:2247:THR:HG21	1.80	0.62
1:A:2098:ILE:N	2:A:2431:HOH:O	2.31	0.62
1:A:2084:TYR:C	2:A:2481:HOH:O	2.43	0.61
1:A:2245:MET:H	1:A:2248:HIS:CD2	2.19	0.61
1:A:2232:LYS:HE2	2:A:2415:HOH:O	1.98	0.61
1:A:2083:ILE:HG21	1:A:2256:LEU:HD22	1.81	0.60
1:A:2191:LYS:HD3	1:A:2192:LEU:N	2.15	0.60
1:A:2134:GLU:CB	2:A:2421:HOH:O	2.35	0.60
1:A:2168:LEU:CD1	2:A:2469:HOH:O	2.49	0.60
1:A:2220:ALA:CA	2:A:2460:HOH:O	2.50	0.60
1:A:2194:THR:HG23	1:A:2195:ASP:OD1	2.03	0.59
1:A:2082:HIS:O	1:A:2215:SER:HB2	2.03	0.58
1:A:2067:ARG:O	1:A:2071:ILE:HG13	2.03	0.57
1:A:2183:PRO:HD3	2:A:2474:HOH:O	2.05	0.57
1:A:2269:ASN:C	1:A:2269:ASN:HD22	2.12	0.57
1:A:2159:HIS:CD2	1:A:2161:LEU:H	2.23	0.57
1:A:2180:GLN:HA	2:A:2484:HOH:O	2.05	0.57
1:A:2145:GLY:N	1:A:2275:ASN:HD21	1.96	0.57
1:A:2174:GLN:HG2	2:A:2373:HOH:O	2.06	0.56
1:A:2095:TYR:CB	2:A:2450:HOH:O	2.52	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2115:THR:HG23	2:A:2456:HOH:O	2.06	0.56
1:A:2182:SER:OG	2:A:2385:HOH:O	2.16	0.55
1:A:2115:THR:CB	2:A:2456:HOH:O	2.55	0.55
1:A:2174:GLN:HB3	2:A:2490:HOH:O	2.07	0.54
1:A:2156:LEU:HD22	1:A:2196:ASN:CG	2.32	0.54
1:A:2222:LYS:C	2:A:2492:HOH:O	2.50	0.54
1:A:2269:ASN:C	1:A:2269:ASN:ND2	2.66	0.54
1:A:2134:GLU:C	2:A:2469:HOH:O	2.50	0.53
1:A:2086:ASN:C	1:A:2086:ASN:ND2	2.62	0.53
1:A:2118:ALA:N	1:A:2143:GLN:HE22	2.02	0.53
1:A:2168:LEU:HD13	2:A:2469:HOH:O	2.06	0.52
1:A:2083:ILE:C	2:A:2481:HOH:O	2.52	0.52
1:A:2220:ALA:CB	2:A:2460:HOH:O	2.39	0.52
1:A:2222:LYS:HG2	2:A:2492:HOH:O	2.10	0.52
1:A:2115:THR:CA	2:A:2456:HOH:O	2.48	0.52
1:A:2280:ARG:HD2	2:A:2471:HOH:O	2.00	0.52
1:A:2134:GLU:CG	2:A:2421:HOH:O	2.56	0.52
1:A:2083:ILE:HG21	1:A:2256:LEU:CD2	2.39	0.51
1:A:2210:SER:HB3	2:A:2490:HOH:O	2.08	0.51
1:A:2222:LYS:CB	2:A:2492:HOH:O	2.58	0.51
1:A:2095:TYR:N	2:A:2450:HOH:O	2.14	0.51
1:A:2129:ASN:ND2	1:A:2132:VAL:HG23	2.26	0.50
1:A:2095:TYR:HB2	2:A:2450:HOH:O	2.10	0.50
1:A:2269:ASN:ND2	1:A:2271:VAL:H	2.09	0.50
1:A:2184:GLN:N	1:A:2184:GLN:OE1	2.45	0.50
1:A:2135:ILE:CA	2:A:2469:HOH:O	2.58	0.50
1:A:2290:CYS:N	2:A:2485:HOH:O	2.45	0.49
1:A:2085:VAL:HG23	2:A:2481:HOH:O	2.12	0.49
1:A:2293:ASN:ND2	1:A:2294:PRO:HD2	2.24	0.48
1:A:2290:CYS:SG	2:A:2485:HOH:O	2.61	0.48
1:A:2296:GLU:H	1:A:2296:GLU:CD	2.20	0.48
1:A:2147:HIS:CD2	1:A:2148:GLN:HG3	2.48	0.48
1:A:2222:LYS:CG	2:A:2492:HOH:O	2.62	0.48
1:A:2140:LEU:O	1:A:2267:PRO:HD3	2.13	0.48
1:A:2291:LEU:O	1:A:2292:SER:HB2	2.14	0.48
1:A:2222:LYS:HB3	2:A:2492:HOH:O	2.14	0.48
1:A:2245:MET:CB	1:A:2247:THR:HG22	2.44	0.47
1:A:2174:GLN:CG	2:A:2490:HOH:O	2.62	0.47
1:A:2300:GLU:O	1:A:2303:LYS:HG2	2.14	0.47
1:A:2080:THR:HB	1:A:2105:LYS:HG2	1.97	0.47
1:A:2224:THR:HB	1:A:2225:PRO:HD2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2066:TRP:CH2	1:A:2303:LYS:HA	2.49	0.47
1:A:2104:LEU:O	1:A:2104:LEU:HG	2.15	0.46
1:A:2174:GLN:NE2	2:A:2490:HOH:O	2.46	0.46
1:A:2227:GLY:HA3	1:A:2248:HIS:O	2.15	0.46
1:A:2100:PRO:C	2:A:2408:HOH:O	2.59	0.46
1:A:2300:GLU:OE2	1:A:2303:LYS:HE3	2.14	0.46
1:A:2159:HIS:O	1:A:2163:ARG:HG3	2.17	0.45
1:A:2077:HIS:HD2	2:A:2423:HOH:O	1.99	0.45
1:A:2245:MET:HB2	1:A:2247:THR:HG22	1.98	0.45
1:A:2238:GLY:CA	2:A:2439:HOH:O	2.64	0.45
1:A:2082:HIS:CB	2:A:2435:HOH:O	2.45	0.45
1:A:2170:TRP:NE1	1:A:2206:MET:HG2	2.32	0.45
1:A:2179:PRO:CG	2:A:2475:HOH:O	2.39	0.44
1:A:2268:SER:HB3	2:A:2485:HOH:O	2.16	0.44
1:A:2139:VAL:HG22	1:A:2265:MET:HB2	1.99	0.44
1:A:2219:THR:C	2:A:2460:HOH:O	2.61	0.44
1:A:2207:ILE:HG23	2:A:2460:HOH:O	2.18	0.44
1:A:2191:LYS:C	1:A:2191:LYS:CD	2.80	0.44
1:A:2304:PRO:C	1:A:2306:HIS:N	2.75	0.44
1:A:2240:ASN:N	1:A:2241:PRO:CD	2.81	0.43
1:A:2103:ILE:HG12	2:A:2408:HOH:O	2.18	0.43
1:A:2271:VAL:HA	2:A:2367:HOH:O	2.18	0.43
1:A:2095:TYR:CG	2:A:2450:HOH:O	2.66	0.43
1:A:2174:GLN:HG2	2:A:2490:HOH:O	2.18	0.43
1:A:2117:ILE:HA	1:A:2143:GLN:NE2	2.34	0.42
1:A:2296:GLU:O	1:A:2302:HIS:CD2	2.72	0.42
1:A:2296:GLU:O	1:A:2302:HIS:HD2	2.03	0.42
1:A:2191:LYS:HB3	2:A:2491:HOH:O	2.19	0.42
1:A:2086:ASN:HD21	1:A:2251:LYS:NZ	2.17	0.41
1:A:2302:HIS:HE1	2:A:2367:HOH:O	2.03	0.41
1:A:2156:LEU:HD22	1:A:2196:ASN:OD1	2.19	0.41
1:A:2230:TRP:HZ2	1:A:2241:PRO:HB2	1.83	0.41
1:A:2082:HIS:CD2	2:A:2435:HOH:O	2.72	0.41
1:A:2105:LYS:O	1:A:2109:THR:HG23	2.20	0.41
1:A:2213:PRO:HA	2:A:2405:HOH:O	2.19	0.41
1:A:2103:ILE:HD12	1:A:2138:ILE:HG13	2.03	0.41
1:A:2114:ARG:NH1	2:A:2433:HOH:O	2.54	0.41
1:A:2180:GLN:HB2	1:A:2249:TYR:OH	2.21	0.41
1:A:2300:GLU:HA	1:A:2303:LYS:HE2	2.03	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	244/273 (89%)	236 (97%)	8 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	226/245 (92%)	219 (97%)	7 (3%)	35	39

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2086	ASN
1	A	2092	ASP
1	A	2156	LEU
1	A	2235	THR
1	A	2245	MET
1	A	2269	ASN
1	A	2296	GLU

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	2077	HIS

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Mol	Chain	Res	Type
1	A	2086	ASN
1	A	2143	GLN
1	A	2148	GLN
1	A	2151	ASN
1	A	2159	HIS
1	A	2174	GLN
1	A	2239	ASN
1	A	2248	HIS
1	A	2253	GLN
1	A	2269	ASN
1	A	2275	ASN
1	A	2293	ASN
1	A	2299	HIS
1	A	2302	HIS

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	246/273 (90%)	0.52	25 (10%)	12 12	16, 28, 61, 90	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2307	PHE	5.8
1	A	2235	THR	4.3
1	A	2306	HIS	4.1
1	A	2236	ASP	4.0
1	A	2237	LYS	4.0
1	A	2305	VAL	3.6
1	A	2238	GLY	3.6
1	A	2245	MET	3.4
1	A	2239	ASN	3.3
1	A	2243	GLY	3.2
1	A	2093	THR	3.2
1	A	2131	GLN	3.0
1	A	2241	PRO	2.9
1	A	2128	ASP	2.8
1	A	2092	ASP	2.8
1	A	2240	ASN	2.7
1	A	2063	ARG	2.7
1	A	2233	ALA	2.6
1	A	2062	SER	2.5
1	A	2247	THR	2.3
1	A	2180	GLN	2.2
1	A	2091	LYS	2.2
1	A	2229	GLU	2.1
1	A	2129	ASN	2.1
1	A	2293	ASN	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.