



Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2020 – 06:30 am BST

PDB ID : 6J6U
Title : Rat PTPRZ D1-D2 domain
Authors : Sugawara, H.
Deposited on : 2019-01-15
Resolution : 3.32 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

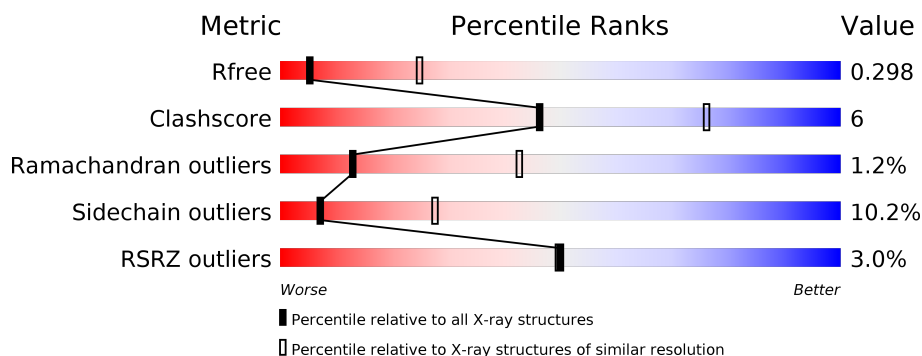
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.32 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}	130704	1089 (3.36-3.28)
Clashscore	141614	1137 (3.36-3.28)
Ramachandran outliers	138981	1115 (3.36-3.28)
Sidechain outliers	138945	1114 (3.36-3.28)
RSRZ outliers	127900	1059 (3.36-3.28)

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 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	618	<div> <div> <div></div> <div>66%</div> <div>18%</div> <div>•</div> <div>14%</div> </div> </div>
1	B	618	<div> <div>4%</div> <div>64%</div> <div>17%</div> <div>•</div> <div>17%</div> </div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 8547 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.

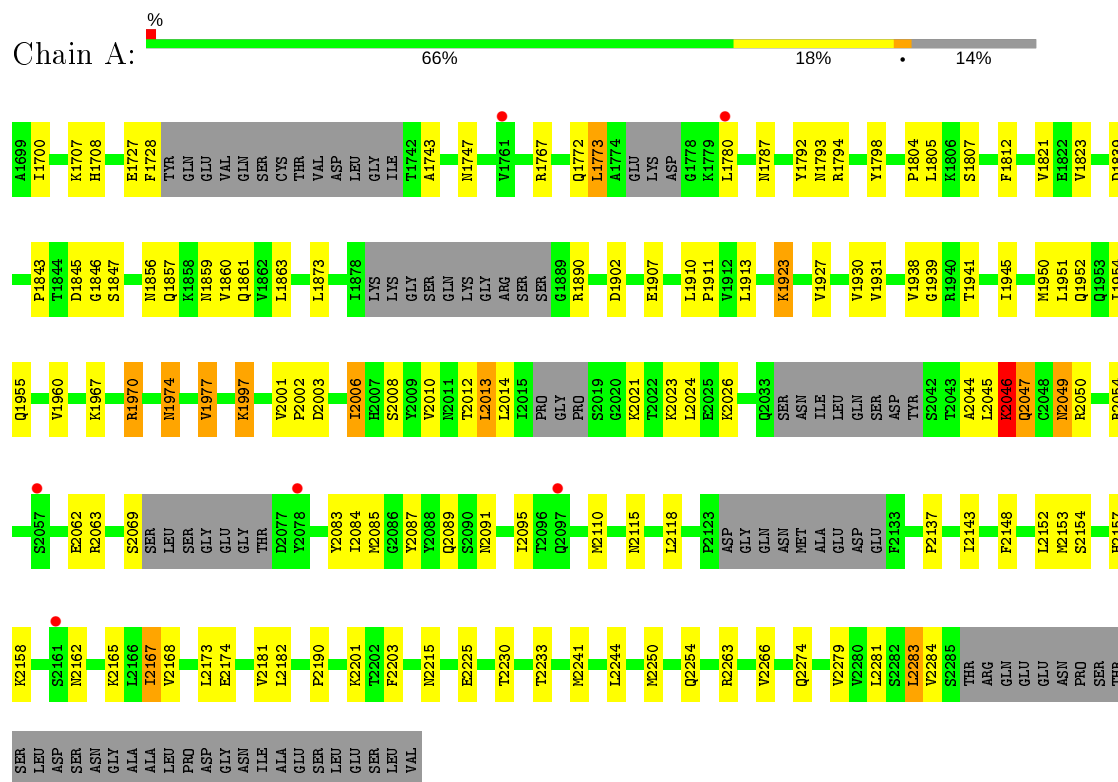
- Molecule 1 is a protein called Receptor-type tyrosine-protein phosphatase zeta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	534	Total	C	N	O	S	0	0	0
			4346	2777	744	805	20			
1	B	514	Total	C	N	O	S	0	0	0
			4201	2682	719	780	20			

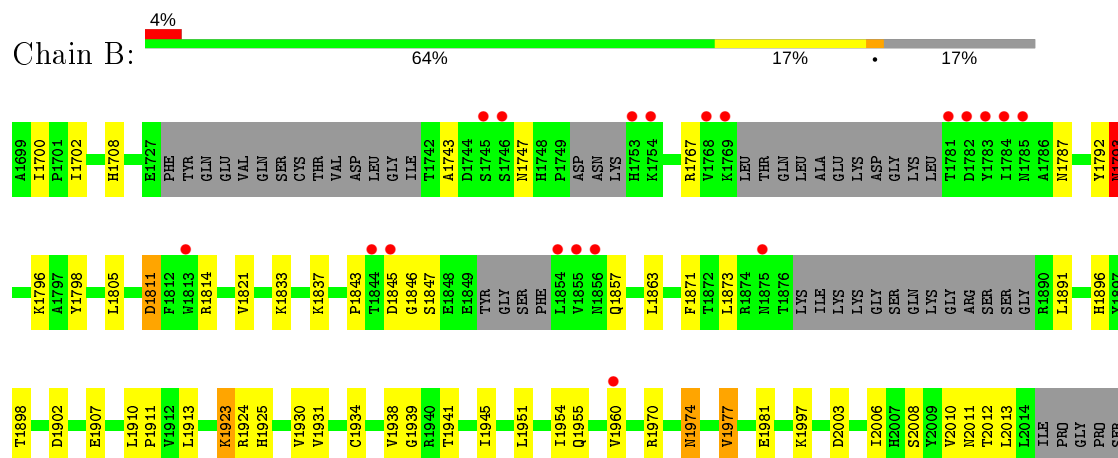
3 Residue-property plots [i](#)

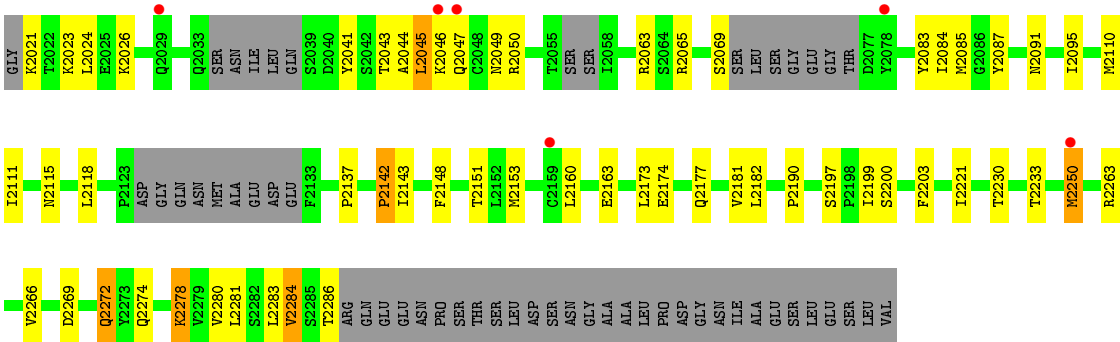
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: Receptor-type tyrosine-protein phosphatase zeta



- Molecule 1: Receptor-type tyrosine-protein phosphatase zeta





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	127.72Å 147.59Å 65.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.97 – 3.32 38.97 – 3.33	Depositor EDS
% Data completeness (in resolution range)	83.3 (38.97-3.32) 83.4 (38.97-3.33)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.47 (at 3.32Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.235 , 0.318 0.218 , 0.298	Depositor DCC
R_{free} test set	859 reflections (5.45%)	wwPDB-VP
Wilson B-factor (Å ²)	66.4	Xtriage
Anisotropy	0.350	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 34.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.21$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	8547	wwPDB-VP
Average B, all atoms (Å ²)	85.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.86% 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	0/4447	0.76	1/6026 (0.0%)
1	B	0.51	0/4297	0.74	1/5823 (0.0%)
All	All	0.52	0/8744	0.75	2/11849 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	1811	ASP	CB-CG-OD1	6.67	124.31	118.30
1	A	1970	ARG	NE-CZ-NH2	5.26	122.93	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	2045	LEU	Peptide

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	4346	0	4274	58	0
1	B	4201	0	4113	48	0
All	All	8547	0	8387	106	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 (106) 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:2203:PHE:CZ	1:A:2279:VAL:HG12	2.22	0.74
1:B:2006:ILE:HD13	1:B:2284:VAL:HG21	1.68	0.74
1:B:1821:VAL:HG11	1:B:1931:VAL:HG23	1.72	0.71
1:B:2269:ASP:H	1:B:2272:GLN:HE22	1.36	0.71
1:A:2002:PRO:O	1:A:2006:ILE:HD13	1.92	0.70
1:B:2269:ASP:O	1:B:2272:GLN:NE2	2.25	0.69
1:A:1821:VAL:HG11	1:A:1931:VAL:HG23	1.76	0.67
1:B:2013:LEU:HA	1:B:2023:LYS:HB2	1.75	0.67
1:A:1767:ARG:HA	1:A:1787:ASN:HD22	1.61	0.66
1:B:2142:PRO:HG3	1:B:2151:THR:HG23	1.78	0.66
1:B:2003:ASP:O	1:B:2006:ILE:HD12	1.96	0.65
1:B:1767:ARG:HA	1:B:1787:ASN:HD22	1.62	0.65
1:A:1941:THR:O	1:A:1945:ILE:HD12	1.97	0.64
1:A:2244:LEU:HB2	1:A:2250:MET:SD	2.38	0.64
1:B:1941:THR:O	1:B:1945:ILE:HD12	1.97	0.64
1:A:2003:ASP:HA	1:A:2006:ILE:HD11	1.80	0.62
1:A:2006:ILE:HG13	1:A:2284:VAL:HG11	1.82	0.61
1:A:2203:PHE:CZ	1:A:2283:LEU:HD12	2.35	0.60
1:B:1934:CYS:HG	1:B:1941:THR:HG1	1.49	0.60
1:A:2044:ALA:HB1	1:A:2046:LYS:CG	2.32	0.60
1:B:2111:ILE:HD13	1:B:2221:ILE:HG13	1.87	0.57
1:B:2174:GLU:HG2	1:B:2181:VAL:HG22	1.86	0.57
1:A:1950:MET:O	1:A:1954:ILE:HD12	2.04	0.57
1:A:2013:LEU:HA	1:A:2023:LYS:HB2	1.86	0.57
1:B:1793:ASN:HD22	1:B:1793:ASN:C	2.08	0.56
1:A:1974:ASN:HD22	1:A:1974:ASN:N	2.04	0.56
1:B:2200:SER:O	1:B:2203:PHE:CZ	2.58	0.56
1:B:2006:ILE:CD1	1:B:2284:VAL:HG21	2.35	0.56
1:A:1847:SER:OG	1:A:1856:ASN:ND2	2.39	0.55
1:B:2045:LEU:HA	1:B:2046:LYS:HB2	1.89	0.55
1:B:2200:SER:O	1:B:2203:PHE:CE2	2.60	0.55
1:A:2049:ASN:C	1:A:2049:ASN:HD22	2.10	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2006:ILE:HG13	1:A:2284:VAL:HG21	1.90	0.54
1:B:1923:LYS:HD2	1:B:1930:VAL:HG21	1.90	0.54
1:A:1923:LYS:HD2	1:A:1930:VAL:HG21	1.90	0.53
1:A:2157:HIS:HB3	1:A:2165:LYS:CE	2.39	0.53
1:B:2008:SER:O	1:B:2011:ASN:OD1	2.25	0.53
1:A:1859:ASN:OD1	1:A:1860:VAL:N	2.42	0.53
1:A:2162:ASN:HD21	1:A:2201:LYS:HD3	1.73	0.53
1:B:1974:ASN:N	1:B:1974:ASN:HD22	2.05	0.53
1:B:1843:PRO:HB2	1:B:1845:ASP:O	2.10	0.52
1:A:1863:LEU:HD22	1:A:2087:TYR:CE2	2.44	0.51
1:B:1970:ARG:NH1	1:B:1977:VAL:O	2.44	0.51
1:B:1863:LEU:HD22	1:B:2087:TYR:CE2	2.45	0.51
1:A:2045:LEU:HD13	1:A:2047:GLN:HE22	1.76	0.50
1:A:2083:TYR:O	1:A:2084:ILE:HD13	2.11	0.50
1:B:2083:TYR:O	1:B:2084:ILE:HD13	2.10	0.50
1:A:1970:ARG:NH1	1:A:1977:VAL:O	2.44	0.50
1:A:2203:PHE:CE1	1:A:2283:LEU:HD12	2.47	0.50
1:A:2174:GLU:HG2	1:A:2181:VAL:HG22	1.94	0.50
1:B:2024:LEU:HD21	1:B:2274:GLN:HB2	1.94	0.50
1:B:2199:ILE:HD13	1:B:2278:LYS:HD3	1.94	0.50
1:A:2008:SER:O	1:A:2012:THR:HG23	2.13	0.49
1:B:2115:ASN:ND2	1:B:2182:LEU:HD13	2.27	0.49
1:A:1843:PRO:HB2	1:A:1845:ASP:O	2.13	0.49
1:A:2044:ALA:HB1	1:A:2046:LYS:HG3	1.95	0.48
1:B:2008:SER:O	1:B:2012:THR:HG23	2.13	0.48
1:B:2284:VAL:O	1:B:2284:VAL:HG12	2.13	0.48
1:A:2045:LEU:HD23	1:A:2062:GLU:OE2	2.14	0.48
1:A:2006:ILE:O	1:A:2010:VAL:HG23	2.14	0.48
1:B:2200:SER:HA	1:B:2203:PHE:CE1	2.50	0.47
1:A:2044:ALA:HB1	1:A:2046:LYS:HG2	1.96	0.47
1:A:2045:LEU:HD13	1:A:2047:GLN:NE2	2.29	0.47
1:A:2115:ASN:ND2	1:A:2182:LEU:HD13	2.29	0.47
1:B:1871:PHE:O	1:B:1891:LEU:HD12	2.15	0.47
1:B:2250:MET:SD	1:B:2280:VAL:HG13	2.55	0.47
1:B:2084:ILE:HG13	1:B:2095:ILE:HD12	1.97	0.46
1:B:1743:ALA:O	1:B:1747:ASN:ND2	2.44	0.46
1:B:1833:LYS:HG2	1:B:1902:ASP:OD1	2.15	0.46
1:A:1743:ALA:O	1:A:1747:ASN:ND2	2.43	0.46
1:B:2045:LEU:HA	1:B:2046:LYS:CB	2.45	0.46
1:A:2084:ILE:HG13	1:A:2095:ILE:HD12	1.97	0.45
1:A:2167:ILE:HD13	1:A:2167:ILE:N	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2010:VAL:O	1:A:2013:LEU:HD22	2.16	0.45
1:A:2024:LEU:HD21	1:A:2274:GLN:HB2	1.98	0.44
1:B:2044:ALA:O	1:B:2045:LEU:HD23	2.18	0.44
1:A:1794:ARG:NH1	1:A:1952:GLN:OE1	2.51	0.44
1:A:1974:ASN:N	1:A:1974:ASN:ND2	2.66	0.43
1:B:2006:ILE:O	1:B:2010:VAL:HG23	2.18	0.43
1:A:1727:GLU:HA	1:A:1728:PHE:C	2.39	0.43
1:A:1823:VAL:HB	1:A:1930:VAL:HG22	2.01	0.43
1:A:2162:ASN:HD21	1:A:2201:LYS:CD	2.32	0.43
1:A:2137:PRO:HD3	1:A:2143:ILE:HD12	2.01	0.43
1:B:1798:TYR:CE2	1:B:1945:ILE:HG23	2.54	0.43
1:B:1974:ASN:N	1:B:1974:ASN:ND2	2.66	0.43
1:B:1896:HIS:O	1:B:1898:THR:HG23	2.19	0.42
1:A:1700:ILE:HG13	1:A:1708:HIS:CD2	2.54	0.42
1:A:2244:LEU:HD23	1:A:2283:LEU:HD22	2.01	0.42
1:B:1938:VAL:HG23	1:B:1939:GLY:H	1.85	0.42
1:A:1804:PRO:HG3	1:A:1812:PHE:CD2	2.54	0.42
1:B:2137:PRO:HD3	1:B:2143:ILE:HD12	2.01	0.42
1:A:2152:LEU:HD11	1:A:2154:SER:O	2.20	0.42
1:A:2241:MET:HG2	1:A:2283:LEU:HD11	2.01	0.42
1:A:2001:VAL:HG11	1:A:2006:ILE:HA	2.02	0.41
1:A:1773:LEU:N	1:A:1773:LEU:HD13	2.35	0.41
1:B:1910:LEU:N	1:B:1911:PRO:HD2	2.35	0.41
1:B:2263:ARG:O	1:B:2266:VAL:HG23	2.20	0.41
1:A:1798:TYR:CE2	1:A:1945:ILE:HG23	2.54	0.41
1:A:2158:LYS:HE3	1:A:2168:VAL:HG21	2.02	0.41
1:B:2148:PHE:CD1	1:B:2173:LEU:HD23	2.56	0.41
1:A:1910:LEU:HB3	1:A:1911:PRO:HD3	2.02	0.41
1:B:1702:ILE:HG21	1:B:1954:ILE:HG23	2.03	0.40
1:A:1938:VAL:HG23	1:A:1939:GLY:H	1.86	0.40
1:A:2148:PHE:CE1	1:A:2173:LEU:HD23	2.56	0.40
1:A:2263:ARG:O	1:A:2266:VAL:HG23	2.21	0.40
1:B:1700:ILE:HG13	1:B:1708:HIS:CD2	2.57	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	518/618 (84%)	473 (91%)	39 (8%)	6 (1%)	13	43
1	B	492/618 (80%)	455 (92%)	31 (6%)	6 (1%)	13	43
All	All	1010/1236 (82%)	928 (92%)	70 (7%)	12 (1%)	13	43

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1793	ASN
1	B	1793	ASN
1	A	2046	LYS
1	B	1846	GLY
1	A	1846	GLY
1	A	1997	LYS
1	B	1997	LYS
1	A	1977	VAL
1	A	2190	PRO
1	B	1977	VAL
1	B	2190	PRO
1	B	2284	VAL

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	484/555 (87%)	435 (90%)	49 (10%)	7	28

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	469/555 (84%)	421 (90%)	48 (10%)	7	27
All	All	953/1110 (86%)	856 (90%)	97 (10%)	7	27

All (97) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1707	LYS
1	A	1772	GLN
1	A	1773	LEU
1	A	1780	LEU
1	A	1792	TYR
1	A	1805	LEU
1	A	1807	SER
1	A	1839	ASP
1	A	1857	GLN
1	A	1861	GLN
1	A	1873	LEU
1	A	1890	ARG
1	A	1902	ASP
1	A	1907	GLU
1	A	1913	LEU
1	A	1923	LYS
1	A	1927	VAL
1	A	1951	LEU
1	A	1955	GLN
1	A	1960	VAL
1	A	1967	LYS
1	A	1974	ASN
1	A	1997	LYS
1	A	2006	ILE
1	A	2013	LEU
1	A	2014	LEU
1	A	2021	LYS
1	A	2026	LYS
1	A	2046	LYS
1	A	2047	GLN
1	A	2049	ASN
1	A	2050	ARG
1	A	2054	ARG
1	A	2063	ARG
1	A	2069	SER
1	A	2085	MET

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Mol	Chain	Res	Type
1	A	2089	GLN
1	A	2091	ASN
1	A	2110	MET
1	A	2118	LEU
1	A	2153	MET
1	A	2167	ILE
1	A	2215	ASN
1	A	2225	GLU
1	A	2230	THR
1	A	2233	THR
1	A	2254	GLN
1	A	2281	LEU
1	A	2283	LEU
1	B	1792	TYR
1	B	1793	ASN
1	B	1796	LYS
1	B	1805	LEU
1	B	1811	ASP
1	B	1814	ARG
1	B	1837	LYS
1	B	1847	SER
1	B	1857	GLN
1	B	1873	LEU
1	B	1907	GLU
1	B	1913	LEU
1	B	1923	LYS
1	B	1924	ARG
1	B	1925	HIS
1	B	1951	LEU
1	B	1955	GLN
1	B	1960	VAL
1	B	1974	ASN
1	B	1981	GLU
1	B	2021	LYS
1	B	2026	LYS
1	B	2041	TYR
1	B	2043	THR
1	B	2047	GLN
1	B	2049	ASN
1	B	2050	ARG
1	B	2063	ARG
1	B	2065	ARG

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Mol	Chain	Res	Type
1	B	2069	SER
1	B	2085	MET
1	B	2091	ASN
1	B	2110	MET
1	B	2118	LEU
1	B	2142	PRO
1	B	2153	MET
1	B	2160	LEU
1	B	2163	GLU
1	B	2177	GLN
1	B	2197	SER
1	B	2230	THR
1	B	2233	THR
1	B	2250	MET
1	B	2272	GLN
1	B	2278	LYS
1	B	2281	LEU
1	B	2283	LEU
1	B	2286	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1708	HIS
1	A	1716	ASN
1	A	1856	ASN
1	A	1953	GLN
1	A	1974	ASN
1	A	2047	GLN
1	A	2049	ASN
1	A	2115	ASN
1	A	2169	GLN
1	A	2254	GLN
1	B	1708	HIS
1	B	1716	ASN
1	B	1753	HIS
1	B	1793	ASN
1	B	1953	GLN
1	B	1974	ASN
1	B	2115	ASN
1	B	2169	GLN
1	B	2272	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 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	534/618 (86%)	-0.12	6 (1%) 80 81	43, 75, 112, 173	5 (0%)
1	B	514/618 (83%)	0.24	25 (4%) 29 29	50, 87, 131, 179	5 (0%)
All	All	1048/1236 (84%)	0.06	31 (2%) 50 49	43, 81, 125, 179	10 (0%)

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1875	ASN	5.3
1	B	1753	HIS	5.2
1	B	2250	MET	4.4
1	B	1854	LEU	4.0
1	A	1761	VAL	3.2
1	A	2161	SER	3.2
1	B	1754	LYS	3.0
1	A	2097	GLN	2.9
1	B	1855	VAL	2.8
1	B	1768	VAL	2.7
1	B	1785	ASN	2.7
1	B	1769	LYS	2.6
1	B	1844	THR	2.6
1	B	1746	SER	2.6
1	A	2057	SER	2.5
1	B	1845	ASP	2.5
1	B	2159	CYS	2.5
1	B	1813	TRP	2.4
1	B	1960	VAL	2.4
1	B	1783	TYR	2.3
1	B	1781	THR	2.2
1	B	1856	ASN	2.2
1	B	2047	GLN	2.2
1	B	1784	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	2078	TYR	2.2
1	A	2078	TYR	2.2
1	B	2029	GLN	2.1
1	B	2046	LYS	2.1
1	A	1780	LEU	2.1
1	B	1745	SER	2.1
1	B	1782	ASP	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.