Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 12:48 pm BST

PDB ID	:	5H61
Title	:	Structure of Transferase mutant-C23S,C199S
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Deposited on	:	2016-11-10
Resolution	:	1.86 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:

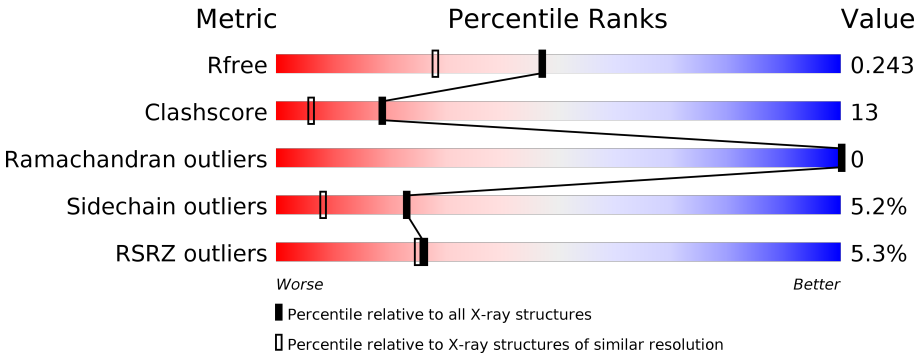
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation 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 1.86 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	2469 (1.86-1.86)
Clashscore	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)
RSRZ outliers	127900	2436 (1.86-1.86)

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 <=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	348	4% 68% 15% • 15%
1	B	348	5% 64% 18% • 15%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5030 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 Transferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	295	Total	C	N	O	S	0	0	0
			2382	1525	406	444	7			
1	B	295	Total	C	N	O	S	0	0	0
			2383	1527	406	443	7			

- Molecule 2 is water.

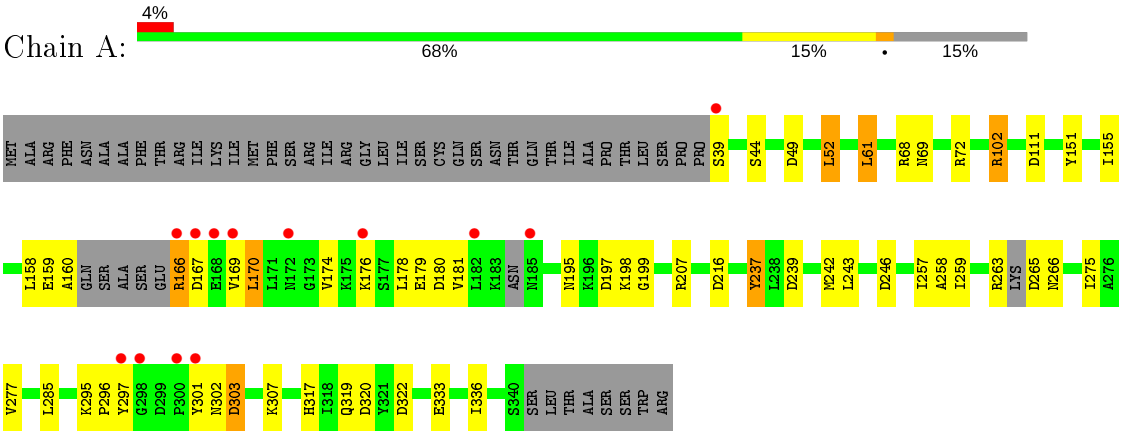
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	141	Total	O	0	0
			141	141		
2	B	124	Total	O	0	0
			124	124		

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.

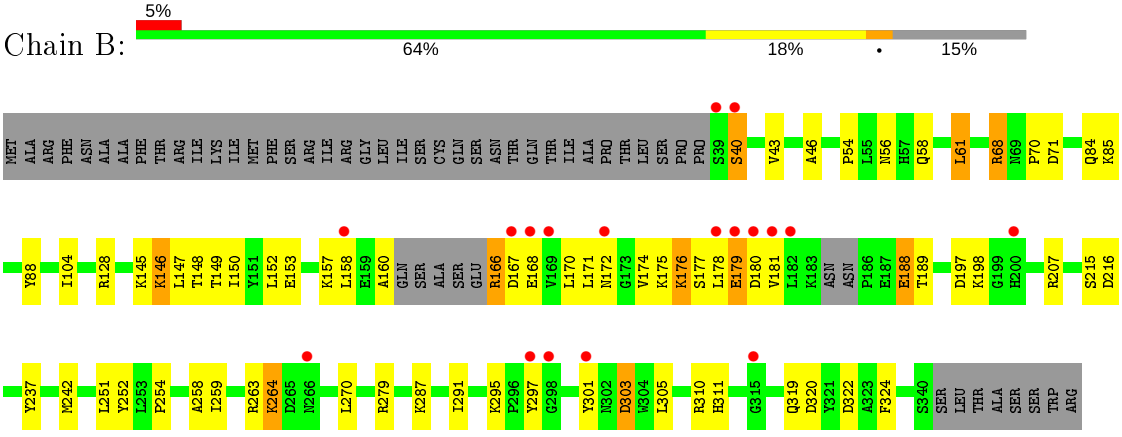
- Molecule 1: Transferase

Chain A:



- Molecule 1: Transferase

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	46.61Å 145.58Å 55.48Å 90.00° 105.12° 90.00°	Depositor
Resolution (Å)	72.79 – 1.86 72.79 – 1.86	Depositor EDS
% Data completeness (in resolution range)	97.8 (72.79-1.86) 97.8 (72.79-1.86)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.12 (at 1.86Å)	Xtriage
Refinement program	REFMAC 5.8.0189	Depositor
R, R_{free}	0.198 , 0.233 0.206 , 0.243	Depositor DCC
R_{free} test set	2856 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å^2)	26.8	Xtriage
Anisotropy	0.047	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 58.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	5030	wwPDB-VP
Average B, all atoms (Å^2)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.56% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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	1.04	2/2438 (0.1%)	0.91	4/3294 (0.1%)
1	B	1.01	1/2440 (0.0%)	0.93	5/3296 (0.2%)
All	All	1.03	3/4878 (0.1%)	0.92	9/6590 (0.1%)

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	A	0	1
1	B	0	1
All	All	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	215	SER	CB-OG	-6.69	1.33	1.42
1	A	102	ARG	CZ-NH1	-5.30	1.26	1.33
1	A	237	TYR	CB-CG	-5.06	1.44	1.51

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	216	ASP	CB-CG-OD1	7.01	124.61	118.30
1	B	128	ARG	NE-CZ-NH2	-5.93	117.33	120.30
1	B	61	LEU	CB-CG-CD1	5.77	120.81	111.00
1	B	310	ARG	NE-CZ-NH2	-5.68	117.46	120.30
1	A	239	ASP	CB-CG-OD1	5.42	123.18	118.30
1	A	52	LEU	CB-CG-CD1	5.28	119.97	111.00
1	A	170	LEU	CB-CG-CD2	-5.22	102.12	111.00
1	A	216	ASP	CB-CG-OD1	5.10	122.89	118.30
1	B	279	ARG	NE-CZ-NH2	-5.02	117.79	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	39	SER	Peptide
1	B	40	SER	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	2382	0	2330	57	2
1	B	2383	0	2339	82	2
2	A	141	0	0	1	0
2	B	124	0	0	2	0
All	All	5030	0	4669	124	2

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 13.

All (124) 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:176:LYS:CB	1:B:301:TYR:HD1	1.52	1.22
1:A:301:TYR:HB3	1:B:176:LYS:HD3	1.28	1.15
1:A:176:LYS:HB3	1:B:301:TYR:HD1	1.04	1.15
1:A:167:ASP:N	1:A:170:LEU:HD21	1.63	1.12
1:A:167:ASP:H	1:A:170:LEU:CD2	1.61	1.12
1:B:176:LYS:O	1:B:179:GLU:HG3	1.49	1.10
1:A:176:LYS:HB3	1:B:301:TYR:CD1	1.93	1.04
1:A:176:LYS:CB	1:B:301:TYR:CD1	2.40	1.04
1:A:167:ASP:H	1:A:170:LEU:HD21	0.87	1.02
1:B:167:ASP:OD1	1:B:168:GLU:N	1.97	0.96
1:A:166:ARG:N	1:A:170:LEU:CD2	2.30	0.94
1:A:176:LYS:HB2	1:B:301:TYR:CD1	2.03	0.93
1:A:320:ASP:OD2	1:A:322:ASP:HB2	1.70	0.92
1:A:167:ASP:N	1:A:170:LEU:CD2	2.28	0.92
1:A:158:LEU:HB3	1:A:174:VAL:HG22	1.53	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:166:ARG:N	1:A:170:LEU:HD21	1.89	0.88
1:B:176:LYS:O	1:B:179:GLU:CG	2.23	0.85
1:A:301:TYR:HB3	1:B:176:LYS:CD	2.07	0.85
1:A:68:ARG:HD2	1:A:198:LYS:O	1.78	0.84
1:A:265:ASP:OD1	1:A:266:ASN:N	2.09	0.84
1:B:176:LYS:HA	1:B:179:GLU:HG2	1.59	0.83
1:B:160:ALA:O	1:B:166:ARG:NE	2.10	0.83
1:A:166:ARG:N	1:A:170:LEU:HD22	1.94	0.81
1:A:167:ASP:O	1:A:170:LEU:HG	1.85	0.76
1:B:303:ASP:OD1	1:B:305:LEU:N	2.17	0.76
1:B:148:THR:O	1:B:152:LEU:HD12	1.89	0.73
1:A:170:LEU:O	1:A:174:VAL:HG23	1.88	0.72
1:B:178:LEU:HA	1:B:181:VAL:HG23	1.71	0.72
1:B:179:GLU:HG3	1:B:180:ASP:N	2.05	0.72
1:A:303:ASP:HB2	2:A:451:HOH:O	1.88	0.72
1:A:166:ARG:HD3	1:A:166:ARG:N	2.04	0.71
1:A:302:ASN:O	1:A:307:LYS:HE3	1.92	0.70
1:A:68:ARG:CD	1:A:198:LYS:O	2.42	0.68
1:B:177:SER:O	1:B:181:VAL:HG23	1.96	0.65
1:B:153:GLU:O	1:B:157:LYS:HG2	1.97	0.65
1:B:146:LYS:H	1:B:146:LYS:CD	2.10	0.64
1:B:179:GLU:HG3	1:B:180:ASP:H	1.62	0.64
1:A:301:TYR:CB	1:B:176:LYS:HD3	2.19	0.63
1:B:167:ASP:N	1:B:170:LEU:HD13	2.14	0.63
1:A:180:ASP:OD2	1:B:301:TYR:OH	2.14	0.62
1:B:146:LYS:HE2	1:B:146:LYS:H	1.65	0.61
1:B:168:GLU:O	1:B:172:ASN:CG	2.38	0.61
1:A:301:TYR:HE1	1:B:297:TYR:HH	1.47	0.61
1:B:46:ALA:H	1:B:319:GLN:HE21	1.49	0.60
1:B:197:ASP:O	1:B:198:LYS:HE2	2.02	0.60
1:B:291:ILE:HG23	1:B:295:LYS:HD2	1.84	0.60
1:B:145:LYS:HE2	1:B:150:ILE:HG12	1.85	0.58
1:B:170:LEU:O	1:B:174:VAL:HG23	2.04	0.58
1:B:178:LEU:CA	1:B:181:VAL:HG23	2.34	0.56
1:B:68:ARG:CG	1:B:198:LYS:HB3	2.35	0.55
1:B:146:LYS:CE	1:B:146:LYS:H	2.18	0.55
1:A:258:ALA:O	1:A:259:ILE:HD13	2.07	0.55
1:B:178:LEU:HA	1:B:181:VAL:CG2	2.36	0.54
1:A:158:LEU:HB3	1:A:174:VAL:CG2	2.33	0.54
1:A:167:ASP:N	1:A:170:LEU:HD23	2.18	0.54
1:B:263:ARG:HG2	1:B:263:ARG:HH11	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:158:LEU:O	1:B:160:ALA:N	2.41	0.53
1:A:259:ILE:CD1	1:A:275:ILE:HG23	2.39	0.52
1:B:320:ASP:OD2	1:B:322:ASP:HB3	2.09	0.52
1:B:258:ALA:O	1:B:259:ILE:HD13	2.10	0.52
1:A:195:ASN:O	1:A:198:LYS:NZ	2.42	0.52
1:A:257:ILE:HD12	1:A:277:VAL:HG12	1.93	0.51
1:A:302:ASN:O	1:A:307:LYS:CE	2.58	0.51
1:A:301:TYR:CE2	1:B:172:ASN:HB2	2.45	0.51
1:B:168:GLU:O	1:B:172:ASN:OD1	2.29	0.51
1:A:167:ASP:O	1:A:170:LEU:CG	2.57	0.50
1:B:147:LEU:CD1	1:B:188:GLU:HG2	2.41	0.50
1:B:146:LYS:HD3	1:B:146:LYS:H	1.75	0.50
1:B:146:LYS:HE3	1:B:149:THR:OG1	2.11	0.49
1:B:167:ASP:H	1:B:170:LEU:HD13	1.76	0.49
1:A:69:ASN:O	1:A:72:ARG:HG2	2.11	0.49
1:B:166:ARG:HA	1:B:170:LEU:HD13	1.93	0.49
1:B:54:PRO:HA	1:B:251:LEU:O	2.12	0.49
1:A:296:PRO:HG2	1:A:297:TYR:CD2	2.48	0.49
1:B:158:LEU:HD23	1:B:170:LEU:HD23	1.95	0.49
1:A:180:ASP:OD2	1:B:301:TYR:CE1	2.68	0.47
1:A:158:LEU:CB	1:A:174:VAL:HG22	2.33	0.47
1:A:303:ASP:N	1:A:303:ASP:OD1	2.37	0.47
1:B:167:ASP:N	1:B:170:LEU:CD1	2.78	0.47
1:A:197:ASP:OD1	1:A:199:GLY:N	2.37	0.47
1:B:177:SER:O	1:B:181:VAL:N	2.38	0.47
1:B:54:PRO:HB3	1:B:252:TYR:CE1	2.51	0.46
1:A:151:TYR:HB3	1:A:181:VAL:HG22	1.97	0.46
1:A:176:LYS:HE2	1:B:301:TYR:HA	1.97	0.46
1:B:167:ASP:H	1:B:170:LEU:CD1	2.29	0.46
1:B:179:GLU:CG	1:B:180:ASP:N	2.77	0.46
1:A:176:LYS:HG3	1:B:301:TYR:HB3	1.97	0.46
1:B:158:LEU:O	1:B:166:ARG:HD2	2.16	0.46
1:B:291:ILE:CG2	1:B:295:LYS:HD2	2.45	0.45
1:A:61:LEU:HD13	1:A:102:ARG:CD	2.46	0.45
1:B:157:LYS:HD3	1:B:157:LYS:N	2.32	0.45
1:B:175:LYS:HA	1:B:175:LYS:HD2	1.73	0.45
1:B:270:LEU:HD11	1:B:324:PHE:HE2	1.81	0.45
1:A:44:SER:HB3	1:A:49:ASP:OD1	2.17	0.45
1:B:147:LEU:HD11	1:B:188:GLU:HG2	1.98	0.44
1:A:301:TYR:HE1	1:B:297:TYR:OH	2.00	0.44
1:A:243:LEU:HD23	1:A:336:ILE:HD12	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:158:LEU:CD2	1:B:170:LEU:HD23	2.48	0.44
1:B:287:LYS:HE2	2:B:438:HOH:O	2.18	0.43
1:B:56:ASN:OD1	1:B:58:GLN:HB2	2.18	0.43
1:A:167:ASP:OD2	1:A:169:VAL:HG23	2.18	0.43
1:A:68:ARG:CG	1:A:198:LYS:O	2.67	0.43
1:B:68:ARG:HG3	1:B:198:LYS:HB3	2.00	0.43
1:B:166:ARG:CA	1:B:170:LEU:HD13	2.49	0.42
1:B:168:GLU:O	1:B:172:ASN:ND2	2.52	0.42
1:A:61:LEU:HD13	1:A:102:ARG:HD3	2.02	0.42
1:B:148:THR:HG23	2:B:425:HOH:O	2.19	0.42
1:A:207:ARG:HG3	1:A:237:TYR:CZ	2.55	0.42
1:B:146:LYS:N	1:B:146:LYS:CD	2.79	0.42
1:B:207:ARG:HG3	1:B:237:TYR:CE2	2.55	0.41
1:B:263:ARG:HG2	1:B:263:ARG:NH1	2.35	0.41
1:B:287:LYS:HE3	1:B:311:HIS:ND1	2.36	0.41
1:B:176:LYS:HE3	1:B:176:LYS:HB3	1.64	0.41
1:B:188:GLU:HG3	1:B:189:THR:N	2.35	0.41
1:B:146:LYS:HD3	1:B:146:LYS:N	2.36	0.41
1:B:43:VAL:HG21	1:B:254:PRO:HB3	2.02	0.41
1:B:88:TYR:N	1:B:88:TYR:CD1	2.88	0.40
1:A:159:GLU:O	1:A:160:ALA:HB2	2.22	0.40
1:A:166:ARG:CA	1:A:170:LEU:HD21	2.50	0.40
1:A:155:ILE:CD1	1:A:178:LEU:HD23	2.51	0.40
1:B:68:ARG:C	1:B:70:PRO:HD3	2.42	0.40
1:B:263:ARG:O	1:B:264:LYS:HG3	2.21	0.40
1:B:68:ARG:HG3	1:B:198:LYS:O	2.20	0.40
1:A:295:LYS:HA	1:A:296:PRO:HD3	2.01	0.40

All (2) 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:333:GLU:OE2	1:B:40:SER:OG[2_545]	2.09	0.11
1:A:333:GLU:OE2	1:B:40:SER:CB[2_545]	2.18	0.02

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	287/348 (82%)	284 (99%)	3 (1%)	0	100	100
1	B	289/348 (83%)	285 (99%)	4 (1%)	0	100	100
All	All	576/696 (83%)	569 (99%)	7 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	261/307 (85%)	249 (95%)	12 (5%)	27	11
1	B	261/307 (85%)	246 (94%)	15 (6%)	20	6
All	All	522/614 (85%)	495 (95%)	27 (5%)	23	8

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	52	LEU
1	A	61	LEU
1	A	111	ASP
1	A	166	ARG
1	A	179	GLU
1	A	242	MET
1	A	246	ASP
1	A	263	ARG

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Mol	Chain	Res	Type
1	A	285	LEU
1	A	303	ASP
1	A	317	HIS
1	A	319	GLN
1	B	61	LEU
1	B	68	ARG
1	B	71	ASP
1	B	84	GLN
1	B	85	LYS
1	B	104	ILE
1	B	146	LYS
1	B	166	ARG
1	B	171	LEU
1	B	176	LYS
1	B	179	GLU
1	B	188	GLU
1	B	242	MET
1	B	264	LYS
1	B	303	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	319	GLN

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

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 95^{th} 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	295/348 (84%)	0.08	13 (4%)	34	33	15, 31, 66, 88	0
1	B	295/348 (84%)	0.24	18 (6%)	21	20	14, 33, 71, 94	0
All	All	590/696 (84%)	0.16	31 (5%)	26	25	14, 32, 69, 94	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	169	VAL	6.5
1	B	301	TYR	6.2
1	B	167	ASP	4.5
1	B	178	LEU	4.4
1	A	301	TYR	4.2
1	B	182	LEU	3.8
1	B	297	TYR	3.5
1	B	200	HIS	3.5
1	B	298	GLY	3.4
1	B	158	LEU	3.3
1	A	297	TYR	3.2
1	B	181	VAL	3.2
1	A	167	ASP	3.0
1	A	172	ASN	2.9
1	A	300	PRO	2.8
1	B	315	GLY	2.6
1	A	168	GLU	2.5
1	A	166	ARG	2.5
1	B	172	ASN	2.5
1	B	39	SER	2.5
1	A	298	GLY	2.4
1	B	266	ASN	2.4
1	B	40	SER	2.3
1	A	169	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	179	GLU	2.3
1	A	182	LEU	2.2
1	B	168	GLU	2.2
1	B	180	ASP	2.2
1	A	39	SER	2.1
1	A	176	LYS	2.1
1	A	185	ASN	2.1

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.