Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 02:00 am BST

PDB ID	:	6F93
Title	:	Helicobacter pylori serine hydroxymethyl transferase in apo form
Authors	:	Sodolescu, A.; Dian, C.; Terradot, L.; Bouzhir-Sima, L.; Lestini, R.; Myllykallio, H.; Skouloubris, S.; Liebl, U.
Deposited on	:	2017-12-13
Resolution	:	2.80 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:

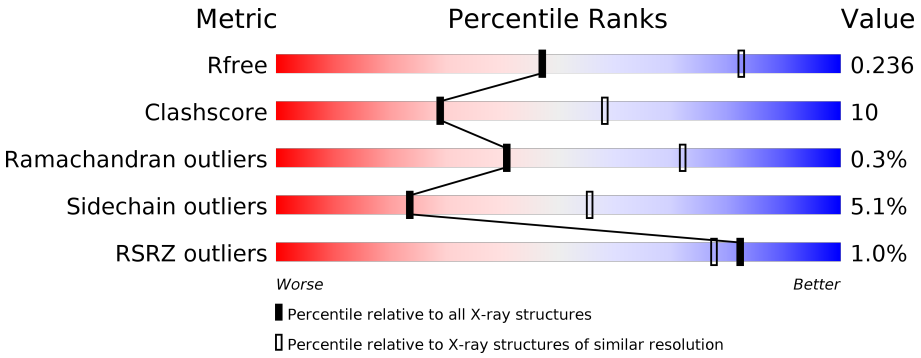
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation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

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

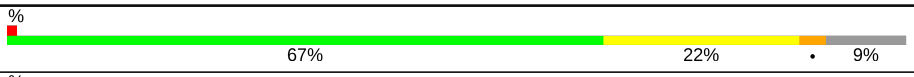
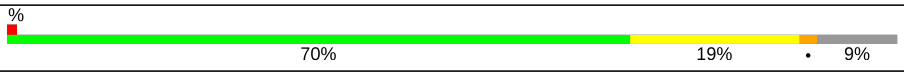
The reported resolution of this entry is 2.80 Å.

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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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	424	
1	B	424	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5909 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 Serine hydroxymethyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	387	Total	C	N	O	S	0	1	0
			2948	1876	503	556	13			
1	B	385	Total	C	N	O	S	0	3	0
			2945	1876	499	558	12			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	417	ARG	-	expression tag	UNP P56089
A	418	SER	-	expression tag	UNP P56089
A	419	HIS	-	expression tag	UNP P56089
A	420	HIS	-	expression tag	UNP P56089
A	421	HIS	-	expression tag	UNP P56089
A	422	HIS	-	expression tag	UNP P56089
A	423	HIS	-	expression tag	UNP P56089
A	424	HIS	-	expression tag	UNP P56089
B	417	ARG	-	expression tag	UNP P56089
B	418	SER	-	expression tag	UNP P56089
B	419	HIS	-	expression tag	UNP P56089
B	420	HIS	-	expression tag	UNP P56089
B	421	HIS	-	expression tag	UNP P56089
B	422	HIS	-	expression tag	UNP P56089
B	423	HIS	-	expression tag	UNP P56089
B	424	HIS	-	expression tag	UNP P56089

- Molecule 2 is water.

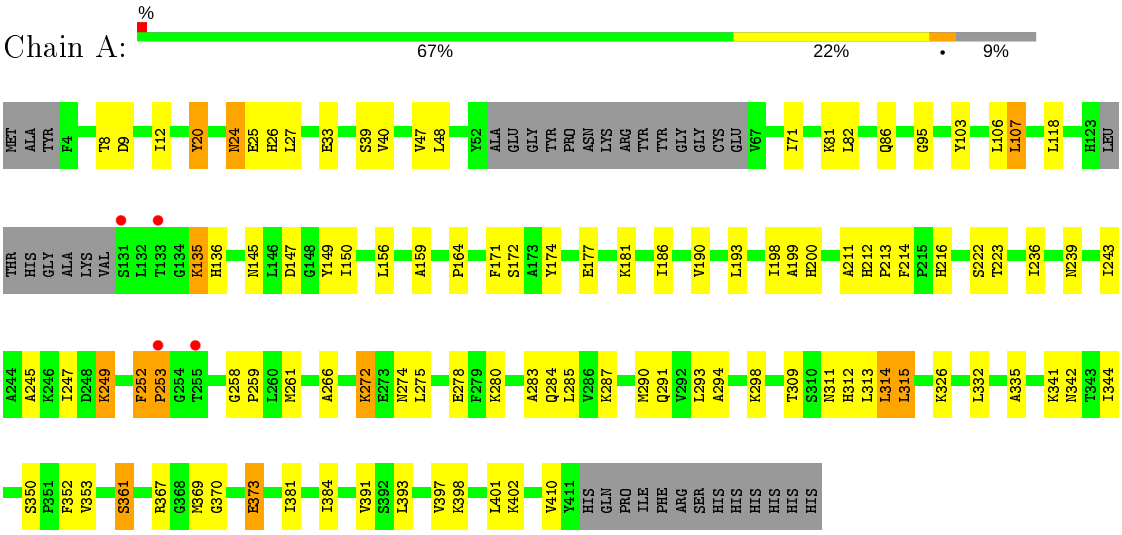
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	5	Total	O	0	0
			5	5		
2	B	11	Total	O	0	0
			11	11		

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.

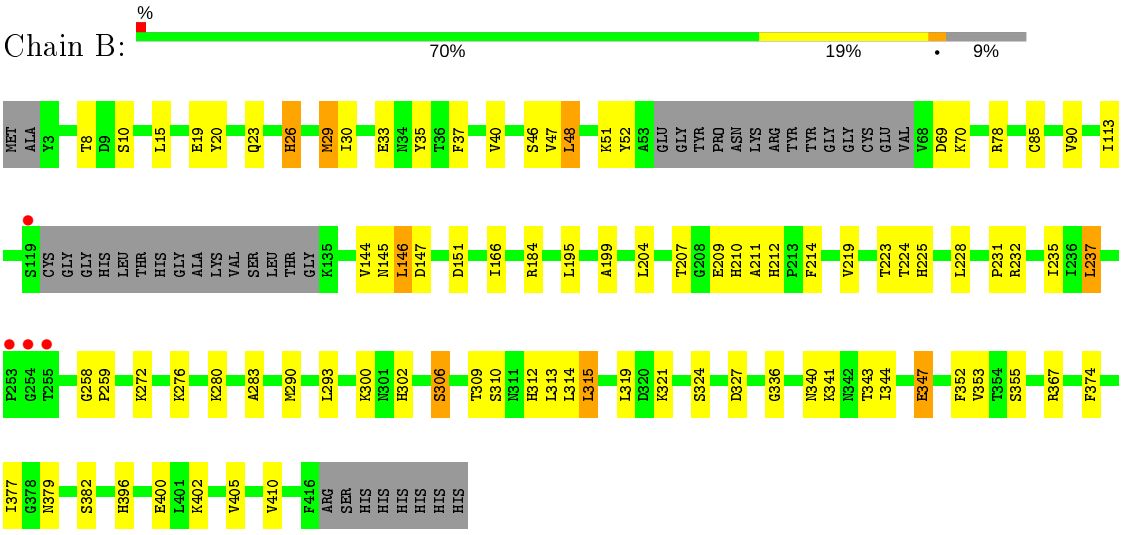
- Molecule 1: Serine hydroxymethyltransferase

Chain A:



- Molecule 1: Serine hydroxymethyltransferase

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	57.35Å 87.55Å 162.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.85 – 2.80 46.85 – 2.60	Depositor EDS
% Data completeness (in resolution range)	98.6 (46.85-2.80) 98.6 (46.85-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$< I/\sigma(I) >$ [1]	1.62 (at 2.61Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.194 , 0.236 0.194 , 0.236	Depositor DCC
R_{free} test set	1287 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	39.9	Xtriage
Anisotropy	0.733	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 39.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	5909	wwPDB-VP
Average B, all atoms (Å^2)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.89% 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	0.31	0/3003	0.50	1/4058 (0.0%)
1	B	0.31	0/3002	0.51	1/4062 (0.0%)
All	All	0.31	0/6005	0.50	2/8120 (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(^{o})	Ideal(^{o})
1	B	315	LEU	CA-CB-CG	6.69	130.69	115.30
1	A	314	LEU	CA-CB-CG	5.14	127.13	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	310	SER	Peptide

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	2948	0	2907	63	0
1	B	2945	0	2853	59	0
2	A	5	0	0	0	0
2	B	11	0	0	1	0
All	All	5909	0	5760	112	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 10.

All (112) 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:145:ASN:HB3	1:A:147:ASP:H	1.46	0.78
1:B:312:HIS:CE1	1:B:313:LEU:HD23	2.19	0.78
1:A:272:LYS:NZ	1:B:8:THR:O	2.17	0.76
1:B:207:THR:HG21	1:B:283:ALA:HB3	1.66	0.75
1:A:174:TYR:O	1:A:311:ASN:ND2	2.23	0.71
1:A:47:VAL:HG21	1:B:20:TYR:HB2	1.72	0.70
1:A:199:ALA:HB1	1:A:223:THR:HG23	1.74	0.69
1:B:300:LYS:NZ	1:B:379:ASN:HD22	1.89	0.69
1:B:276:LYS:O	2:B:501:HOH:O	2.10	0.68
1:B:300:LYS:HZ1	1:B:379:ASN:HD22	1.41	0.65
1:A:177:GLU:OE1	1:A:211:ALA:N	2.28	0.65
1:B:347:GLU:OE1	1:B:355:SER:N	2.33	0.62
1:A:315:LEU:HD23	1:A:344:ILE:HG22	1.81	0.62
1:A:236:ILE:HG21	1:A:247:ILE:HD12	1.83	0.61
1:A:95:GLY:HA3	1:A:223:THR:HG22	1.82	0.61
1:A:258:GLY:HA3	1:B:232:ARG:HH22	1.67	0.60
1:A:369:MET:HB3	1:A:373:GLU:HG3	1.83	0.60
1:B:19:GLU:OE1	1:B:23:GLN:NE2	2.33	0.60
1:B:207:THR:HG23	1:B:280:LYS:HG3	1.84	0.59
1:A:8:THR:O	1:B:272:LYS:NZ	2.35	0.59
1:B:30:ILE:HB	1:B:33:GLU:HG2	1.85	0.59
1:B:224:THR:OG1	1:B:231:PRO:O	2.21	0.57
1:B:207:THR:HG22	1:B:209:GLU:HG2	1.87	0.57
1:B:166:ILE:HD11	1:B:195:LEU:HB2	1.85	0.56
1:A:164:PRO:HD2	1:A:190:VAL:HG11	1.86	0.56
1:A:145:ASN:N	1:A:149:TYR:O	2.27	0.56
1:B:199:ALA:HB1	1:B:223:THR:HG23	1.87	0.56
1:A:280:LYS:O	1:A:284:GLN:HG2	2.06	0.56
1:A:290:MET:HG2	1:A:361:SER:HB3	1.89	0.55
1:B:30:ILE:HG23	1:B:340:ASN:HD22	1.71	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:245:ALA:O	1:A:249:LYS:HD2	2.07	0.54
1:B:225:HIS:CD2	1:B:232:ARG:HA	2.43	0.54
1:A:25:GLU:HB3	1:A:402:LYS:HE2	1.90	0.52
1:A:82:LEU:HD13	1:A:275:LEU:HG	1.92	0.52
1:A:106:LEU:HD13	1:A:193:LEU:HD13	1.91	0.52
1:A:24[B]:ASN:HA	1:A:367:ARG:HH12	1.74	0.52
1:B:145:ASN:HB3	1:B:151:ASP:HB2	1.90	0.52
1:A:384:ILE:HD11	1:A:397:VAL:HG21	1.91	0.52
1:A:393:LEU:O	1:A:397:VAL:HG13	2.10	0.52
1:A:9:ASP:OD1	1:B:78:ARG:NH2	2.39	0.52
1:B:402:LYS:HA	1:B:405:VAL:HG12	1.92	0.52
1:B:210:HIS:HD2	1:B:211:ALA:O	1.93	0.52
1:B:324:SER:OG	1:B:353:VAL:HG13	2.10	0.52
1:B:35:TYR:CG	1:B:410:VAL:HG11	2.45	0.52
1:A:326:LYS:HB2	1:A:353:VAL:HA	1.92	0.51
1:B:37:PHE:HB2	1:B:40:VAL:HG23	1.92	0.51
1:A:159:ALA:HB1	1:A:190:VAL:HG21	1.92	0.51
1:A:172:SER:HB3	1:A:200:HIS:CE1	2.45	0.51
1:A:135:LYS:HG3	1:A:136:HIS:CD2	2.45	0.51
1:B:51:LYS:HE3	1:B:69:ASP:OD1	2.10	0.51
1:A:20:TYR:HB2	1:B:47:VAL:HG21	1.92	0.51
1:A:24[A]:ASN:HA	1:A:367:ARG:HH12	1.76	0.50
1:B:85:CYS:SG	1:B:237:LEU:HD22	2.51	0.50
1:B:319:LEU:HG	1:B:344:ILE:HD11	1.94	0.50
1:A:86:GLN:HB2	1:A:239:ASN:HA	1.94	0.49
1:A:212:HIS:HD2	1:A:214:PHE:H	1.61	0.49
1:A:103:TYR:HA	1:A:107:LEU:HD22	1.95	0.48
1:B:29:MET:CE	1:B:377:ILE:HG21	2.43	0.48
1:A:71:ILE:HG12	1:B:15:LEU:HD13	1.96	0.48
1:A:341:LYS:NZ	1:A:352:PHE:O	2.46	0.48
1:B:90:VAL:HA	1:B:235:ILE:HD13	1.96	0.47
1:A:335:ALA:HA	1:A:398:LYS:HB2	1.95	0.47
1:B:367:ARG:NH2	1:B:405:VAL:HG22	2.29	0.47
1:B:290:MET:HG3	1:B:309:THR:HG21	1.96	0.47
1:A:274:ASN:N	1:A:274:ASN:HD22	2.13	0.47
1:A:156:LEU:HD13	1:A:186:ILE:HG23	1.96	0.46
1:B:85:CYS:SG	1:B:237:LEU:CD2	3.03	0.46
1:A:258:GLY:HA3	1:B:232:ARG:HH12	1.80	0.46
1:B:341:LYS:HE2	1:B:352:PHE:O	2.16	0.46
1:A:259:PRO:HB2	1:A:261:MET:CE	2.46	0.46
1:A:312:HIS:CE1	1:A:313:LEU:HD23	2.51	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:294:ALA:O	1:A:298:LYS:HG3	2.16	0.46
1:A:236:ILE:HG21	1:A:247:ILE:HG21	1.98	0.45
1:B:113:ILE:HG23	1:B:166:ILE:HG23	1.97	0.45
1:B:293:LEU:HB2	1:B:374:PHE:HD1	1.79	0.45
1:A:283:ALA:O	1:A:287:LYS:HG3	2.17	0.45
1:A:290:MET:HE1	1:A:293:LEU:HD23	1.98	0.45
1:A:40:VAL:HG13	1:A:266:ALA:HB1	1.99	0.45
1:B:225:HIS:H	1:B:225:HIS:CD2	2.34	0.45
1:B:26:HIS:HB2	1:B:336:GLY:O	2.16	0.45
1:B:29:MET:HE1	1:B:377:ILE:HG21	1.99	0.45
1:A:106:LEU:HD21	1:A:243:ILE:HG23	1.98	0.45
1:A:367:ARG:HG2	1:A:410:VAL:HG13	1.98	0.45
1:B:324:SER:H	1:B:327:ASP:HB2	1.82	0.45
1:A:252:PHE:CB	1:A:253:PRO:HD3	2.48	0.44
1:B:46:SER:OG	1:B:48:LEU:HB2	2.18	0.44
1:A:332:LEU:HD21	1:A:381:ILE:HG23	1.99	0.43
1:A:48:LEU:HD23	1:B:19:GLU:HG2	2.00	0.43
1:A:12:ILE:HA	1:A:12:ILE:HD13	1.87	0.43
1:B:144:VAL:HG12	1:B:145:ASN:O	2.18	0.43
1:B:90:VAL:HG12	1:B:235:ILE:HD11	1.99	0.43
1:A:198:ILE:HG13	1:A:222:SER:HB2	2.00	0.43
1:B:258:GLY:HA3	1:B:259:PRO:HA	1.81	0.43
1:B:343:THR:HG23	1:B:347:GLU:HG3	2.00	0.43
1:B:396[B]:HIS:O	1:B:400:GLU:HG3	2.18	0.43
1:A:118:LEU:HG	1:A:171:PHE:CE2	2.54	0.43
1:A:181:LYS:HG3	1:A:216:HIS:CE1	2.54	0.42
1:A:278:GLU:N	1:A:278:GLU:OE1	2.51	0.42
1:B:204:LEU:HD23	1:B:283:ALA:HB1	2.02	0.42
1:B:212:HIS:CE1	1:B:214:PHE:HB2	2.54	0.42
1:B:302:HIS:CD2	1:B:382:SER:HG	2.37	0.42
1:A:291:GLN:NE2	1:A:309:THR:O	2.53	0.42
1:A:370:GLY:O	1:A:373:GLU:HG2	2.20	0.41
1:A:212:HIS:CD2	1:A:213:PRO:HD2	2.55	0.41
1:A:290:MET:HG2	1:A:361:SER:CB	2.50	0.41
1:B:195:LEU:HD13	1:B:219:VAL:HG13	2.03	0.41
1:A:33:GLU:OE1	1:B:52:TYR:HB2	2.20	0.41
1:A:27:LEU:HD11	1:A:401:LEU:HB3	2.02	0.41
1:B:147:ASP:O	1:B:306:SER:HA	2.20	0.41
1:B:367:ARG:HG2	1:B:410:VAL:HG22	2.01	0.41
1:A:150:ILE:HG13	1:A:174:TYR:CZ	2.55	0.41
1:B:146:LEU:HD12	1:B:147:ASP:N	2.36	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	382/424 (90%)	364 (95%)	16 (4%)	2 (0%)	29 61
1	B	382/424 (90%)	365 (96%)	17 (4%)	0	100 100
All	All	764/848 (90%)	729 (95%)	33 (4%)	2 (0%)	41 72

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	252	PHE
1	A	253	PRO

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	308/350 (88%)	290 (94%)	18 (6%)	20 50
1	B	303/350 (87%)	289 (95%)	14 (5%)	27 60
All	All	611/700 (87%)	579 (95%)	32 (5%)	24 55

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	TYR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	24[A]	ASN
1	A	24[B]	ASN
1	A	26	HIS
1	A	39	SER
1	A	81	LYS
1	A	107	LEU
1	A	135	LYS
1	A	249	LYS
1	A	272	LYS
1	A	285	LEU
1	A	314	LEU
1	A	315	LEU
1	A	342	ASN
1	A	350	SER
1	A	361	SER
1	A	373	GLU
1	A	391	VAL
1	B	10	SER
1	B	26	HIS
1	B	29	MET
1	B	48	LEU
1	B	70	LYS
1	B	146	LEU
1	B	184	ARG
1	B	228	LEU
1	B	237	LEU
1	B	306	SER
1	B	314	LEU
1	B	315	LEU
1	B	321	LYS
1	B	347	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	311	ASN
1	B	24	ASN
1	B	210	HIS
1	B	225	HIS
1	B	311	ASN
1	B	340	ASN
1	B	342	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	379	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

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	387/424 (91%)	-0.48	4 (1%)	82	77	24, 39, 65, 102	0
1	B	385/424 (90%)	-0.44	4 (1%)	82	77	24, 42, 68, 108	0
All	All	772/848 (91%)	-0.46	8 (1%)	82	77	24, 40, 68, 108	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	131	SER	4.6
1	B	255	THR	3.8
1	B	254	GLY	3.2
1	B	253	PRO	3.0
1	A	253	PRO	2.5
1	A	255	THR	2.2
1	B	119	SER	2.1
1	A	133	THR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.