



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 03:19 AM UTC

PDB ID : 1U0V / pdb_00001u0v
Title : An Aldol Switch Discovered in Stilbene Synthases Mediates Cyclization of Specificity of Type III Polyketide Synthases: 18xCHS structure
Authors : Austin, M.B.; Bowman, M.E.; Ferrer, J.-L.; Schroder, J.; Noel, J.P.
Deposited on : 2004-07-14
Resolution : 1.90 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

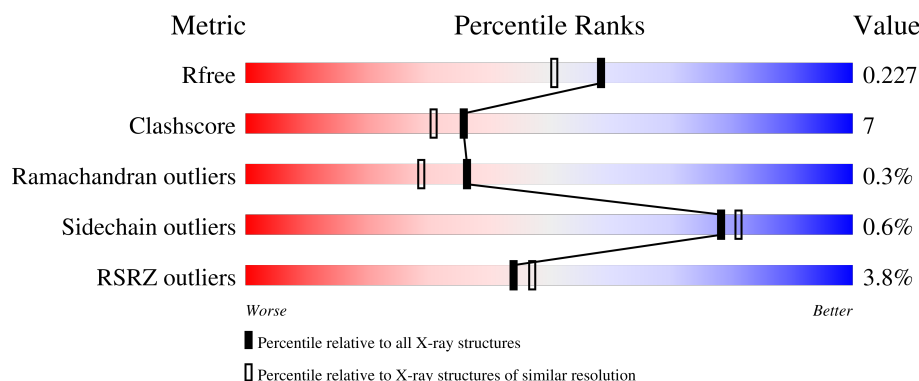
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	393	3% 83% 14% ..
1	B	393	4% 79% 16% ..

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6597 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 Chalcone synthase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	388	Total	C	N	O	S	0	0	0
			2970	1889	504	560	17			
1	B	380	Total	C	N	O	S	0	0	0
			2911	1853	493	548	17			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	cloning artifact	UNP P30074
A	-2	SER	-	cloning artifact	UNP P30074
A	-1	HIS	-	cloning artifact	UNP P30074
A	0	GLY	-	cloning artifact	UNP P30074
A	96	ALA	ASP	engineered mutation	UNP P30074
A	98	LEU	VAL	engineered mutation	UNP P30074
A	99	ALA	VAL	engineered mutation	UNP P30074
A	100	MET	VAL	engineered mutation	UNP P30074
A	131	SER	THR	engineered mutation	UNP P30074
A	133	THR	SER	engineered mutation	UNP P30074
A	134	THR	GLY	engineered mutation	UNP P30074
A	135	PRO	VAL	engineered mutation	UNP P30074
A	137	LEU	MET	engineered mutation	UNP P30074
A	157	VAL	TYR	engineered mutation	UNP P30074
A	158	GLY	MET	engineered mutation	UNP P30074
A	159	VAL	MET	engineered mutation	UNP P30074
A	160	PHE	TYR	engineered mutation	UNP P30074
A	162	HIS	GLN	engineered mutation	UNP P30074
A	268	LYS	LEU	engineered mutation	UNP P30074
A	269	GLY	LYS	engineered mutation	UNP P30074
A	270	ALA	ASP	engineered mutation	UNP P30074
A	273	ASP	GLY	engineered mutation	UNP P30074
B	-3	GLY	-	cloning artifact	UNP P30074
B	-2	SER	-	cloning artifact	UNP P30074
B	-1	HIS	-	cloning artifact	UNP P30074

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	GLY	-	cloning artifact	UNP P30074
B	96	ALA	ASP	engineered mutation	UNP P30074
B	98	LEU	VAL	engineered mutation	UNP P30074
B	99	ALA	VAL	engineered mutation	UNP P30074
B	100	MET	VAL	engineered mutation	UNP P30074
B	131	SER	THR	engineered mutation	UNP P30074
B	133	THR	SER	engineered mutation	UNP P30074
B	134	THR	GLY	engineered mutation	UNP P30074
B	135	PRO	VAL	engineered mutation	UNP P30074
B	137	LEU	MET	engineered mutation	UNP P30074
B	157	VAL	TYR	engineered mutation	UNP P30074
B	158	GLY	MET	engineered mutation	UNP P30074
B	159	VAL	MET	engineered mutation	UNP P30074
B	160	PHE	TYR	engineered mutation	UNP P30074
B	162	HIS	GLN	engineered mutation	UNP P30074
B	268	LYS	LEU	engineered mutation	UNP P30074
B	269	GLY	LYS	engineered mutation	UNP P30074
B	270	ALA	ASP	engineered mutation	UNP P30074
B	273	ASP	GLY	engineered mutation	UNP P30074

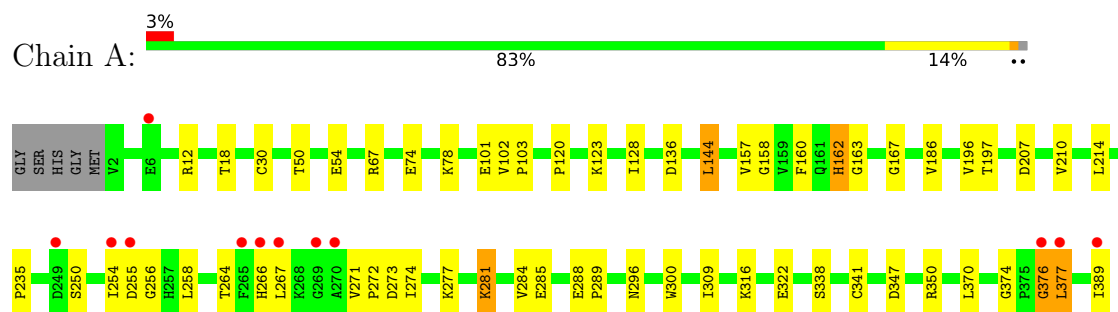
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	360	Total O 360 360	0	0
2	B	356	Total O 356 356	0	0

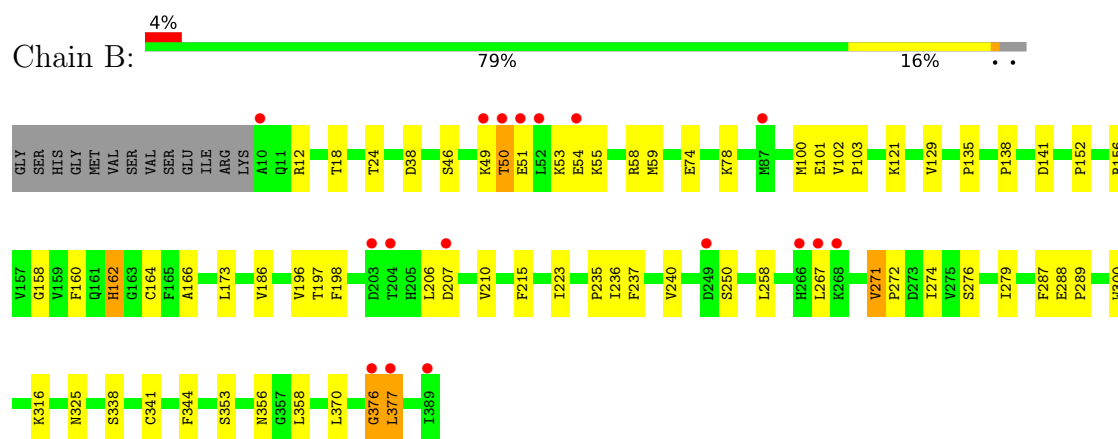
3 Residue-property plots

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: Chalcone synthase 2



• Molecule 1: Chalcone synthase 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	71.64Å 59.75Å 82.54Å 90.00° 108.17° 90.00°	Depositor
Resolution (Å)	24.93 – 1.90 24.93 – 1.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (24.93-1.90) 99.9 (24.93-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.25 (at 1.80Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.192 , 0.227 0.191 , 0.227	Depositor DCC
R_{free} test set	2639 reflections (4.34%)	wwPDB-VP
Wilson B-factor (Å ²)	18.8	Xtriage
Anisotropy	0.331	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 56.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6597	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.37% 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	0.43	0/3028	0.93	15/4102 (0.4%)
1	B	0.42	0/2969	0.94	18/4022 (0.4%)
All	All	0.43	0/5997	0.93	33/8124 (0.4%)

There are no bond length outliers.

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	376	GLY	N-CA-C	-7.97	102.63	114.90
1	B	135	PRO	N-CA-C	7.29	123.12	113.57
1	A	101	GLU	N-CA-C	7.00	118.99	111.36
1	A	376	GLY	N-CA-C	-6.75	101.61	113.76
1	B	186	VAL	N-CA-C	6.69	117.75	107.99
1	A	300	TRP	N-CA-C	6.53	120.04	109.40
1	B	101	GLU	N-CA-C	6.46	118.41	111.36
1	B	162	HIS	N-CA-C	-6.41	105.10	113.12
1	A	162	HIS	N-CA-C	-6.02	104.67	112.68
1	A	163	GLY	N-CA-C	6.01	120.75	112.52
1	B	240	VAL	N-CA-C	5.88	117.06	112.12
1	B	300	TRP	N-CA-C	5.85	119.00	109.59
1	B	166	ALA	N-CA-C	5.66	119.29	112.38
1	B	156	ARG	N-CA-C	5.66	119.28	110.17
1	B	206	LEU	N-CA-C	5.66	117.53	111.36
1	A	296	ASN	N-CA-C	-5.60	106.45	113.28
1	A	374	GLY	CA-C-N	5.55	126.78	119.84
1	A	374	GLY	C-N-CA	5.55	126.78	119.84
1	A	186	VAL	N-CA-C	5.52	116.04	107.99
1	B	341	CYS	N-CA-C	5.51	117.75	111.02
1	B	287	PHE	N-CA-C	5.42	120.17	113.50
1	B	271	VAL	CB-CA-C	-5.42	108.55	113.70
1	B	223	ILE	N-CA-C	-5.41	99.85	107.75
1	B	338	SER	CB-CA-C	-5.39	110.34	116.54
1	A	136	ASP	N-CA-C	5.35	115.34	108.34

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	214	LEU	N-CA-C	5.27	120.19	113.55
1	A	338	SER	CB-CA-C	-5.18	110.58	116.54
1	B	215	PHE	N-CA-C	5.16	117.69	109.96
1	A	12	ARG	N-CA-C	5.15	118.10	110.48
1	B	325	ASN	N-CA-C	5.14	116.57	110.97
1	A	341	CYS	N-CA-C	5.06	117.20	111.02
1	A	167	GLY	N-CA-C	-5.06	106.59	113.37
1	B	164	CYS	N-CA-C	5.05	118.54	112.38

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	2970	0	3010	43	0
1	B	2911	0	2950	45	0
2	A	360	0	0	2	0
2	B	356	0	0	7	0
All	All	6597	0	5960	86	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 7.

All (86) 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:250:SER:HB2	1:A:377:LEU:HD12	1.45	0.95
1:A:207:ASP:HB2	1:A:267:LEU:HD13	1.48	0.94
1:A:274:ILE:HG21	1:A:377:LEU:HD13	1.49	0.93
1:B:274:ILE:HG21	1:B:377:LEU:HD13	1.60	0.83
1:B:210:VAL:HG11	1:B:267:LEU:HD11	1.62	0.80
1:A:254:ILE:HD11	1:A:271:VAL:HG21	1.64	0.79
1:A:322:GLU:H	1:A:322:GLU:CD	1.98	0.72
1:B:353:SER:HA	1:B:358:LEU:HD23	1.72	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:267:LEU:O	1:B:267:LEU:HD12	1.91	0.70
1:A:281:LYS:HB2	1:A:281:LYS:NZ	2.06	0.69
1:A:120:PRO:HD2	1:A:123:LYS:HD3	1.74	0.69
1:A:250:SER:HB2	1:A:377:LEU:CD1	2.24	0.67
1:A:207:ASP:O	1:A:210:VAL:HG12	1.96	0.66
1:A:288:GLU:HB3	1:A:289:PRO:HD3	1.77	0.65
1:B:102:VAL:HB	1:B:103:PRO:HD3	1.79	0.63
1:A:102:VAL:HB	1:A:103:PRO:HD3	1.79	0.63
1:A:274:ILE:HG21	1:A:377:LEU:CD1	2.28	0.62
1:B:49:LYS:O	1:B:51:GLU:N	2.33	0.62
1:A:74:GLU:O	1:A:78:LYS:HG3	2.00	0.61
1:B:271:VAL:HB	1:B:272:PRO:HD3	1.83	0.61
1:A:376:GLY:O	1:A:377:LEU:C	2.47	0.58
1:A:281:LYS:HB2	1:A:281:LYS:HZ2	1.67	0.56
1:B:207:ASP:O	1:B:210:VAL:HG12	2.05	0.56
1:A:267:LEU:HD12	1:A:267:LEU:N	2.23	0.54
1:B:18:THR:HG21	1:B:235:PRO:HB3	1.90	0.53
1:B:196:VAL:HG13	1:B:197:THR:HG23	1.89	0.53
1:A:274:ILE:CG2	1:A:377:LEU:HD13	2.32	0.53
1:B:274:ILE:HG21	1:B:377:LEU:CD1	2.37	0.53
1:B:46:SER:HB3	2:B:670:HOH:O	2.10	0.52
1:B:58:ARG:HG3	1:B:58:ARG:HH11	1.74	0.51
1:A:18:THR:HG21	1:A:235:PRO:HB3	1.93	0.51
1:B:49:LYS:HD2	2:B:670:HOH:O	2.11	0.51
1:A:196:VAL:HG13	1:A:197:THR:HG23	1.93	0.50
1:A:281:LYS:HA	1:A:284:VAL:HG22	1.93	0.49
1:A:120:PRO:HD2	1:A:123:LYS:CD	2.43	0.49
1:A:271:VAL:HB	1:A:272:PRO:HD3	1.93	0.49
1:B:288:GLU:N	1:B:289:PRO:CD	2.76	0.49
1:A:128:ILE:HG12	1:A:157:VAL:CG1	2.43	0.48
1:A:273:ASP:O	1:A:277:LYS:HG3	2.13	0.48
1:B:173:LEU:HG	2:B:459:HOH:O	2.12	0.48
2:A:685:HOH:O	1:B:138:PRO:HA	2.14	0.48
1:A:162:HIS:CE1	1:B:158:GLY:H	2.33	0.47
1:A:284:VAL:O	1:A:288:GLU:HB2	2.15	0.47
1:B:356:ASN:HB2	1:B:358:LEU:HD21	1.94	0.47
1:B:54:GLU:HB3	1:B:58:ARG:HH12	1.79	0.47
1:B:356:ASN:HB2	1:B:358:LEU:CD2	2.44	0.47
1:B:358:LEU:HD22	1:B:358:LEU:N	2.29	0.47
1:B:376:GLY:O	1:B:377:LEU:C	2.58	0.46
1:A:389:ILE:HD12	1:A:389:ILE:N	2.31	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:100:MET:HE3	2:B:478:HOH:O	2.15	0.46
1:B:74:GLU:O	1:B:78:LYS:HG2	2.15	0.46
1:B:54:GLU:OE2	1:B:54:GLU:HA	2.15	0.46
1:B:152:PRO:HD3	2:B:453:HOH:O	2.17	0.45
1:B:370:LEU:C	1:B:370:LEU:HD23	2.42	0.45
1:A:158:GLY:H	1:B:162:HIS:CE1	2.36	0.44
1:B:55:LYS:O	1:B:59:MET:HG3	2.17	0.44
1:B:276:SER:O	1:B:279:ILE:HG22	2.18	0.44
1:B:129:VAL:HG21	1:B:141:ASP:HA	2.00	0.44
1:B:276:SER:HB2	1:B:316:LYS:HG3	2.00	0.44
1:A:322:GLU:CD	1:A:322:GLU:N	2.71	0.43
1:A:377:LEU:HD23	1:A:377:LEU:HA	1.64	0.43
1:B:38:ASP:OD1	1:B:53:LYS:NZ	2.46	0.43
1:A:288:GLU:N	1:A:289:PRO:CD	2.81	0.43
1:B:50:THR:O	1:B:54:GLU:HG2	2.18	0.43
1:B:250:SER:HB2	1:B:377:LEU:CD1	2.48	0.43
1:A:160:PHE:O	1:A:162:HIS:HD2	2.01	0.43
1:A:157:VAL:O	1:A:157:VAL:HG13	2.18	0.43
1:A:370:LEU:C	1:A:370:LEU:HD23	2.44	0.43
1:B:160:PHE:O	1:B:162:HIS:HD2	2.02	0.42
1:A:347:ASP:O	1:A:350:ARG:HG3	2.19	0.42
1:B:258:LEU:C	1:B:258:LEU:HD13	2.44	0.42
1:A:50:THR:O	1:A:54:GLU:HG3	2.19	0.42
1:B:24:THR:HB	1:B:344:PHE:CZ	2.55	0.42
1:A:144:LEU:HD23	1:A:144:LEU:HA	1.87	0.42
1:A:309:ILE:HG13	2:A:680:HOH:O	2.20	0.42
1:B:121:LYS:HG3	2:B:651:HOH:O	2.19	0.42
1:A:255:ASP:OD2	1:A:266:HIS:HB2	2.19	0.41
1:B:12:ARG:HD3	2:B:402:HOH:O	2.20	0.41
1:A:30:CYS:SG	1:A:67:ARG:HD2	2.60	0.41
1:A:256:GLY:HA2	1:A:264:THR:O	2.20	0.41
1:A:258:LEU:HD13	1:A:258:LEU:C	2.46	0.40
1:B:58:ARG:HG3	1:B:58:ARG:NH1	2.36	0.40
1:A:284:VAL:HG23	1:A:285:GLU:N	2.35	0.40
1:B:358:LEU:HD22	1:B:358:LEU:H	1.86	0.40
1:B:198:PHE:CD1	1:B:198:PHE:C	2.99	0.40
1:B:236:ILE:HG22	1:B:237:PHE: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	386/393 (98%)	373 (97%)	12 (3%)	1 (0%)	36	29
1	B	378/393 (96%)	363 (96%)	14 (4%)	1 (0%)	36	29
All	All	764/786 (97%)	736 (96%)	26 (3%)	2 (0%)	36	29

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	50	THR
1	A	377	LEU

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	320/324 (99%)	317 (99%)	3 (1%)	70	73
1	B	313/324 (97%)	312 (100%)	1 (0%)	86	88
All	All	633/648 (98%)	629 (99%)	4 (1%)	78	81

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	144	LEU
1	A	281	LYS
1	A	316	LYS
1	B	377	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	82	ASN
1	A	119	GLN
1	A	162	HIS
1	A	212	GLN
1	A	312	GLN
1	B	11	GLN
1	B	82	ASN
1	B	119	GLN
1	B	162	HIS
1	B	312	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 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

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	388/393 (98%)	0.04	12 (3%) 51 55	8, 16, 29, 40	0
1	B	380/393 (96%)	0.04	17 (4%) 38 40	8, 17, 34, 44	0
All	All	768/786 (97%)	0.04	29 (3%) 44 47	8, 17, 31, 44	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	376	GLY	6.9
1	B	10	ALA	6.9
1	B	376	GLY	5.3
1	A	389	ILE	4.9
1	A	269	GLY	4.8
1	B	389	ILE	4.4
1	A	377	LEU	4.2
1	B	377	LEU	4.2
1	B	267	LEU	4.1
1	B	204	THR	3.8
1	B	203	ASP	3.7
1	A	267	LEU	3.7
1	A	266	HIS	3.5
1	B	50	THR	3.4
1	A	265	PHE	3.0
1	A	6	GLU	3.0
1	B	52	LEU	2.8
1	B	87	MET	2.8
1	B	54	GLU	2.8
1	B	268	LYS	2.7
1	B	266	HIS	2.4
1	A	255	ASP	2.3
1	A	270	ALA	2.3
1	B	49	LYS	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	207	ASP	2.2
1	A	254	ILE	2.2
1	B	249	ASP	2.2
1	A	249	ASP	2.1
1	B	51	GLU	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.