Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 02:01 AM GMT

PDB ID	:	2FA3
Title	:	HMG-CoA synthase from Brassica juncea in complex with acetyl-CoA and acetyl-cys117.
Authors	:	Pojer, F.; Ferrer, J.L.; Richard, S.B.; Noel, J.P.
Deposited on	:	2005-12-06
Resolution	:	2.52 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

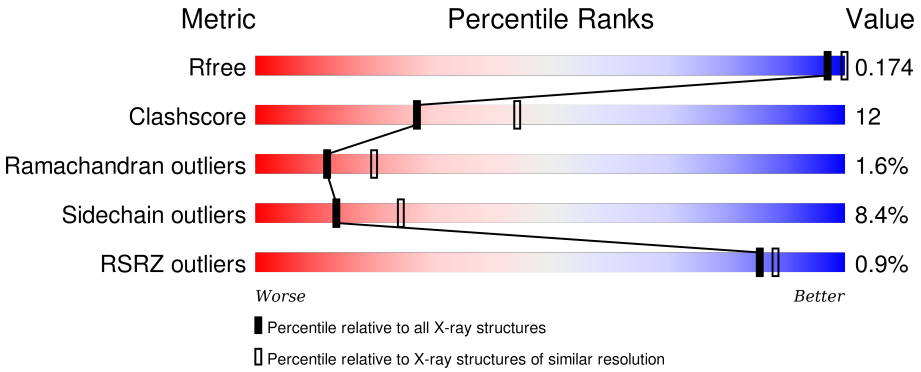
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.52 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}	91344	4241 (2.54-2.50)
Clashscore	102246	4968 (2.54-2.50)
Ramachandran outliers	100387	4873 (2.54-2.50)
Sidechain outliers	100360	4875 (2.54-2.50)
RSRZ outliers	91569	4253 (2.54-2.50)

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. 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	450	% 74% 21% 5%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3697 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 HMG-CoA synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	450	3513	2239	575	676	23	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	117	SCY	CYS	MODIFIED RESIDUE	UNP Q9M6U3

- Molecule 2 is ACETYL COENZYME *A (three-letter code: ACO) (formula: $C_{23}H_{38}N_7O_{17}P_3S$).

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	N	O	P	S		
2	A	1	51	23	7	17	3	1	0	0

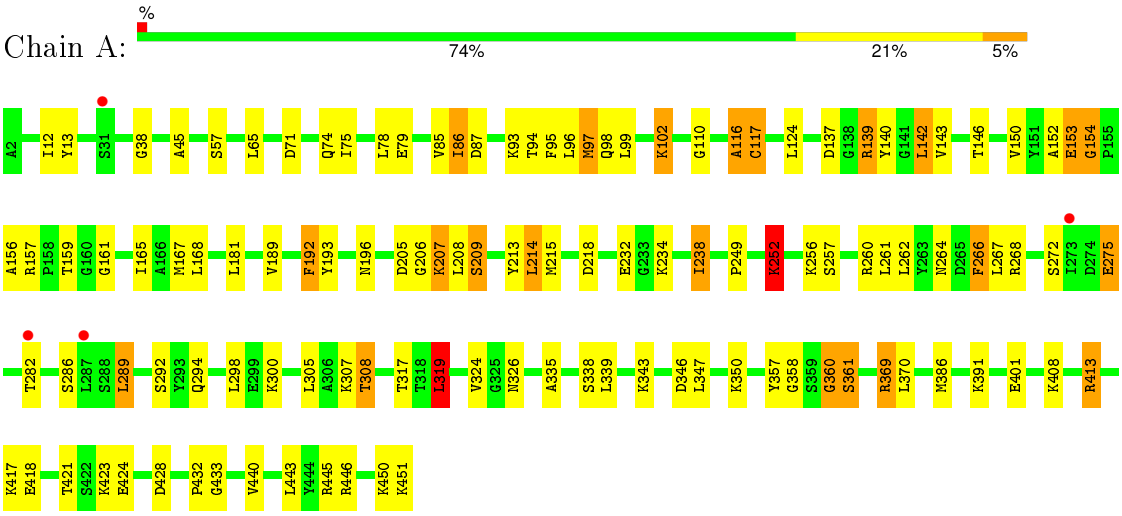
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	133	Total	O	0	0
			133	133		

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 errors 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: HMG-CoA synthase



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α, β, γ	61.60Å 61.60Å 411.79Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.52 47.37 – 2.51	Depositor EDS
% Data completeness (in resolution range)	98.3 (50.00-2.52) 98.2 (47.37-2.51)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$< I/\sigma(I) >$ [1]	1.81 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.176 , 0.282 0.182 , 0.174	Depositor DCC
R_{free} test set	842 reflections (5.31%)	DCC
Wilson B-factor (Å^2)	34.2	Xtriage
Anisotropy	0.220	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 48.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.44$, $< L^2 > = 0.27$	Xtriage
Outliers	0 of 16725 reflections	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	3697	wwPDB-VP
Average B, all atoms (Å^2)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.00% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ACO, SCY

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	1.01	0/3579	0.95	10/4833 (0.2%)

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	4

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	413	ARG	NE-CZ-NH1	7.40	124.00	120.30
1	A	139	ARG	NE-CZ-NH1	6.16	123.38	120.30
1	A	142	LEU	CA-CB-CG	5.89	128.86	115.30
1	A	413	ARG	NE-CZ-NH2	-5.46	117.57	120.30
1	A	360	GLY	N-CA-C	-5.44	99.50	113.10
1	A	319	LEU	CB-CG-CD2	5.37	120.12	111.00
1	A	252	LYS	CD-CE-NZ	-5.31	99.48	111.70
1	A	167	MET	CG-SD-CE	5.25	108.59	100.20
1	A	218	ASP	CB-CG-OD2	-5.21	113.61	118.30
1	A	97	MET	CG-SD-CE	5.06	108.30	100.20

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	116	ALA	Mainchain,Peptide
1	A	117	SCY	Mainchain
1	A	360	GLY	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	3513	0	3459	84	0
2	A	51	0	34	4	0
3	A	133	0	0	15	0
All	All	3697	0	3493	84	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 12.

All (84) 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:116:ALA:HB1	1:A:117:SCY:HE3	1.55	0.87
1:A:238:ILE:HD11	1:A:261:LEU:HB3	1.65	0.78
1:A:401:GLU:HB2	3:A:837:HOH:O	1.83	0.78
1:A:207:LYS:NZ	1:A:207:LYS:HB2	1.98	0.78
1:A:369:ARG:HH11	1:A:369:ARG:HG3	1.49	0.77
1:A:117:SCY:OCD	2:A:796:ACO:HH31	1.88	0.73
1:A:408:LYS:HG2	3:A:909:HOH:O	1.89	0.72
1:A:369:ARG:HH11	1:A:369:ARG:CG	2.03	0.71
1:A:209:SER:HB2	2:A:796:ACO:H31	1.71	0.71
1:A:286:SER:HB2	3:A:925:HOH:O	1.91	0.71
1:A:205:ASP:O	1:A:209:SER:HB3	1.89	0.71
1:A:308:THR:HG23	3:A:928:HOH:O	1.91	0.70
1:A:238:ILE:HD11	1:A:261:LEU:CB	2.23	0.69
1:A:38:GLY:O	1:A:252:LYS:HD3	1.93	0.68
1:A:213:TYR:HE1	1:A:257:SER:HG	1.43	0.67
1:A:98:GLN:O	1:A:102:LYS:HE3	1.94	0.66
1:A:369:ARG:NH1	1:A:369:ARG:CG	2.58	0.65
1:A:300:LYS:HE3	3:A:902:HOH:O	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:137:ASP:OD1	1:A:139:ARG:HD3	1.96	0.65
1:A:266:PHE:O	1:A:268:ARG:N	2.31	0.63
1:A:432:PRO:HB3	1:A:451:LYS:NZ	2.14	0.63
1:A:86:ILE:CD1	1:A:446:ARG:HD2	2.28	0.63
1:A:238:ILE:CD1	1:A:261:LEU:HB3	2.28	0.62
1:A:153:GLU:HG2	1:A:154:GLY:H	1.65	0.61
1:A:196:ASN:HB3	3:A:915:HOH:O	1.99	0.61
1:A:86:ILE:HD13	1:A:446:ARG:HD2	1.83	0.60
1:A:86:ILE:HD13	1:A:446:ARG:CD	2.32	0.59
1:A:157:ARG:HD2	3:A:926:HOH:O	2.02	0.58
1:A:443:LEU:HD12	1:A:445:ARG:NH1	2.18	0.58
1:A:207:LYS:HZ2	1:A:207:LYS:HB2	1.67	0.57
1:A:152:ALA:O	3:A:929:HOH:O	2.17	0.57
1:A:206:GLY:HA2	1:A:209:SER:OG	2.05	0.57
1:A:57:SER:OG	1:A:146:THR:HG21	2.05	0.56
1:A:433:GLY:H	1:A:451:LYS:HA	1.71	0.55
1:A:308:THR:CG2	3:A:928:HOH:O	2.50	0.55
1:A:421:THR:O	1:A:423:LYS:NZ	2.39	0.55
1:A:189:VAL:HG22	1:A:361:SER:HB2	1.87	0.55
1:A:192:PHE:C	1:A:192:PHE:CD2	2.81	0.54
1:A:153:GLU:CG	1:A:154:GLY:N	2.71	0.54
1:A:317:THR:HG22	1:A:339:LEU:HB2	1.90	0.54
1:A:153:GLU:HG2	1:A:154:GLY:N	2.23	0.53
1:A:264:ASN:O	1:A:268:ARG:HG3	2.09	0.53
1:A:232:GLU:O	1:A:234:LYS:HE3	2.09	0.52
1:A:215:MET:HE2	3:A:908:HOH:O	2.08	0.52
1:A:319:LEU:HA	3:A:868:HOH:O	2.09	0.52
1:A:249:PRO:HB3	2:A:796:ACO:HH32	1.91	0.52
1:A:86:ILE:HG13	1:A:87:ASP:N	2.25	0.51
1:A:252:LYS:HE3	2:A:796:ACO:O8A	2.10	0.51
1:A:275:GLU:HG3	3:A:888:HOH:O	2.12	0.50
1:A:38:GLY:O	1:A:252:LYS:CD	2.60	0.49
1:A:432:PRO:HB3	1:A:451:LYS:HZ2	1.77	0.49
1:A:386:MET:O	1:A:391:LYS:HE3	2.13	0.48
1:A:208:LEU:O	1:A:209:SER:C	2.51	0.48
1:A:215:MET:CE	3:A:908:HOH:O	2.61	0.48
1:A:153:GLU:O	1:A:154:GLY:O	2.31	0.48
1:A:418:GLU:HA	1:A:440:VAL:O	2.14	0.48
1:A:417:LYS:NZ	3:A:913:HOH:O	2.47	0.47
1:A:192:PHE:C	1:A:192:PHE:HD2	2.19	0.46
1:A:207:LYS:HZ3	1:A:207:LYS:HB2	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:424:GLU:HA	1:A:424:GLU:OE1	2.16	0.45
1:A:343:LYS:O	1:A:347:LEU:HG	2.15	0.45
1:A:450:LYS:CG	1:A:451:LYS:H	2.30	0.45
1:A:432:PRO:HB3	1:A:451:LYS:HZ3	1.80	0.45
1:A:57:SER:HG	1:A:146:THR:HG21	1.82	0.45
1:A:78:LEU:HD12	1:A:79:GLU:N	2.32	0.44
1:A:161:GLY:HA3	1:A:326:ASN:O	2.17	0.43
1:A:110:GLY:HA2	3:A:857:HOH:O	2.17	0.43
1:A:214:LEU:HG	1:A:260:ARG:HD3	2.00	0.43
1:A:335:ALA:O	1:A:338:SER:HB2	2.19	0.43
1:A:156:ALA:O	1:A:159:THR:OG1	2.36	0.43
1:A:450:LYS:CG	1:A:451:LYS:N	2.82	0.42
1:A:140:TYR:HB3	1:A:168:LEU:HD11	2.01	0.42
1:A:346:ASP:O	1:A:350:LYS:HE2	2.19	0.42
1:A:124:LEU:HA	1:A:143:VAL:HG21	2.02	0.42
1:A:347:LEU:HB3	1:A:370:LEU:HD12	2.03	0.41
1:A:12:ILE:HG12	1:A:13:TYR:N	2.35	0.41
1:A:289:LEU:HD23	1:A:289:LEU:HA	1.69	0.41
1:A:95:PHE:O	1:A:98:GLN:HG3	2.21	0.40
1:A:74:GLN:O	1:A:139:ARG:HB3	2.21	0.40
1:A:94:THR:O	1:A:97:MET:HB2	2.21	0.40
1:A:45:ALA:HB3	1:A:324:VAL:HG13	2.03	0.40
1:A:75:ILE:HD13	1:A:140:TYR:HB2	2.04	0.40
1:A:357:TYR:CG	1:A:358:GLY:N	2.90	0.40
1:A:165:ILE:HG21	1:A:165:ILE:HD13	1.77	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	447/450 (99%)	414 (93%)	26 (6%)	7 (2%)	12 20

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	153	GLU
1	A	267	LEU
1	A	361	SER
1	A	154	GLY
1	A	209	SER
1	A	266	PHE
1	A	272	SER

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	380/380 (100%)	348 (92%)	32 (8%)	14 25

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

Mol	Chain	Res	Type
1	A	65	LEU
1	A	71	ASP
1	A	85	VAL
1	A	86	ILE
1	A	93	LYS
1	A	96	LEU
1	A	99	LEU
1	A	102	LYS
1	A	142	LEU
1	A	150	VAL
1	A	181	LEU
1	A	192	PHE
1	A	193	TYR
1	A	207	LYS
1	A	214	LEU
1	A	238	ILE
1	A	252	LYS
1	A	256	LYS

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Mol	Chain	Res	Type
1	A	262	LEU
1	A	275	GLU
1	A	282	THR
1	A	289	LEU
1	A	292	SER
1	A	294	GLN
1	A	298	LEU
1	A	305	LEU
1	A	307	LYS
1	A	308	THR
1	A	319	LEU
1	A	369	ARG
1	A	413	ARG
1	A	428	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	GLN
1	A	223	HIS
1	A	304	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)

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	SCY	A	117	1	7,8,9	2.18	1 (14%)	4,9,11	1.09	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	SCY	A	117	1	-	2/5/7/9	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	117	SCY	CB-SG	-5.21	1.74	1.81

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	117	SCY	CE-CD-SG-CB
1	A	117	SCY	OCD-CD-SG-CB

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	117	SCY	2	0

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	ACO	A	796	-	43,53,53	1.09	2 (4%)	55,79,79	2.48	18 (32%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ACO	A	796	-	-	2/47/67/67	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	796	ACO	O4B-C1B	3.32	1.45	1.41
2	A	796	ACO	O-C	4.23	1.43	1.21

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	796	ACO	N3A-C2A-N1A	-11.39	120.17	128.89
2	A	796	ACO	C2P-C3P-N4P	-4.56	103.25	112.36
2	A	796	ACO	C1B-N9A-C4A	-3.88	121.08	126.94
2	A	796	ACO	C6P-C7P-N8P	-3.57	104.05	111.88
2	A	796	ACO	C7P-C6P-C5P	-2.81	107.69	112.31
2	A	796	ACO	O4B-C1B-N9A	-2.69	102.47	108.10
2	A	796	ACO	O3A-P1A-O5B	-2.55	96.17	102.94
2	A	796	ACO	O3B-C3B-C4B	-2.03	102.01	109.99
2	A	796	ACO	N6A-C6A-N1A	2.00	123.50	119.20
2	A	796	ACO	O5A-P2A-O4A	2.07	123.73	112.53
2	A	796	ACO	O2A-P1A-O1A	2.14	124.11	112.53
2	A	796	ACO	C2P-S1P-C	2.22	115.56	101.83
2	A	796	ACO	O6A-CCP-CBP	2.50	114.57	110.55
2	A	796	ACO	C3P-C2P-S1P	2.55	118.18	111.36
2	A	796	ACO	O9A-P3B-O8A	3.04	118.96	107.38
2	A	796	ACO	C7P-N8P-C9P	3.20	128.87	122.53
2	A	796	ACO	CEP-CBP-CCP	3.45	112.97	108.50
2	A	796	ACO	C3P-N4P-C5P	5.31	133.24	122.79

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	796	ACO	O-C-S1P-C2P
2	A	796	ACO	CH3-C-S1P-C2P

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	796	ACO	4	0

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, 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	449/450 (99%)	-0.10	4 (0%) 85 88	14, 29, 53, 63	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	31	SER	2.9
1	A	273	ILE	2.5
1	A	282	THR	2.3
1	A	287	LEU	2.2

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
1	SCY	A	117	9/10	0.95	0.17	-	23,24,36,45	0

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron

density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
2	ACO	A	796	51/51	0.95	0.16	0.02	38,46,62,65	0

6.5 Other polymers (i)

There are no such residues in this entry.