W O R L D W I D E
wwPDB
PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 30, 2017 – 04:08 AM EDT

PDB ID	:	3PGQ
Title	:	Crystal Structure of the Carboxyltransferase Domain of S. cerevisiae Acetyl CoA Carboxylase in Complex with Pinoxaden
Authors	:	Tong, L.; Yu, L.P.C.; Kim, Y.S.
Deposited on	:	unknown
Resolution	:	2.80 Å(reported)

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

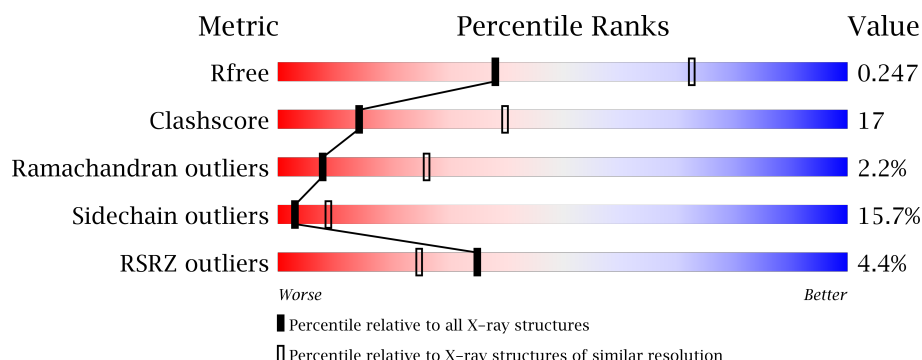|		
MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20030345
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20030345

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	Percentile Ranks	Value
Rfree		0.247
Clashscore		17
Ramachandran outliers		2.2%
Sidechain outliers		15.7%
RSRZ outliers		4.4%

Worse   *Better*

■ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	2583 (2.80-2.80)
Clashscore	112137	3033 (2.80-2.80)
Ramachandran outliers	110173	2983 (2.80-2.80)
Sidechain outliers	110143	2985 (2.80-2.80)
RSRZ outliers	101464	2610 (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. 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	764	3% / 59% / 24% / 6% · 10%
1	B	764	5% / 56% / 25% / 7% · 11%
1	C	764	4% / 58% / 25% / 5% / 12%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

| Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	GY3	B	2240	-	-	X	X
2	GY3	B	3000	-	-	-	X

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 16368 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 Acetyl-CoA carboxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	688	Total 5491	C 3500	N 944	O 1028	S 19	0	0	0
1	B	680	Total 5421	C 3456	N 932	O 1014	S 19	0	0	0
1	C	675	Total 5387	C 3428	N 927	O 1013	S 19	0	0	0

- Molecule 2 is 8-(2-ethenyl-6-ethyl-4-methylphenyl)tetrahydro-7H-pyrazolo[1,2-d][1,4,5]oxadi azepine-7,9(8H)-dione (three-letter code: GY3) (formula: $C_{18}H_{22}N_2O_3$).
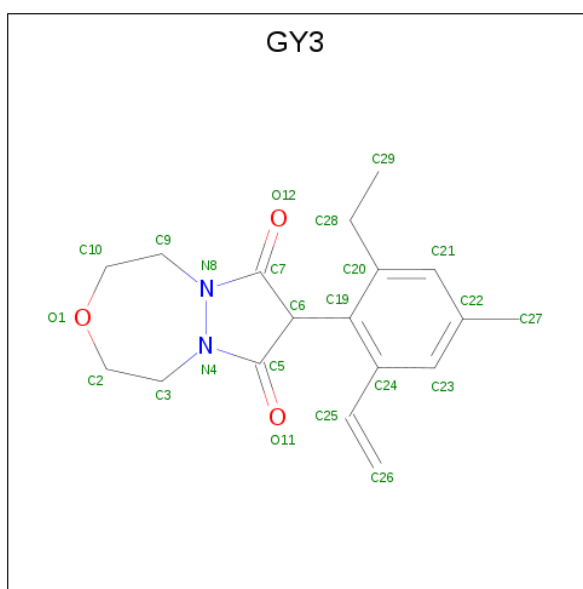
| Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total 23	C 18	N 2	O 3	0	0
2	B	1	Total 23	C 18	N 2	O 3	0	0
2	B	1	Total 23	C 18	N 2	O 3	0	0

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: Acetyl-CoA carboxylase

- Molecule 1: Acetyl-CoA carboxylase

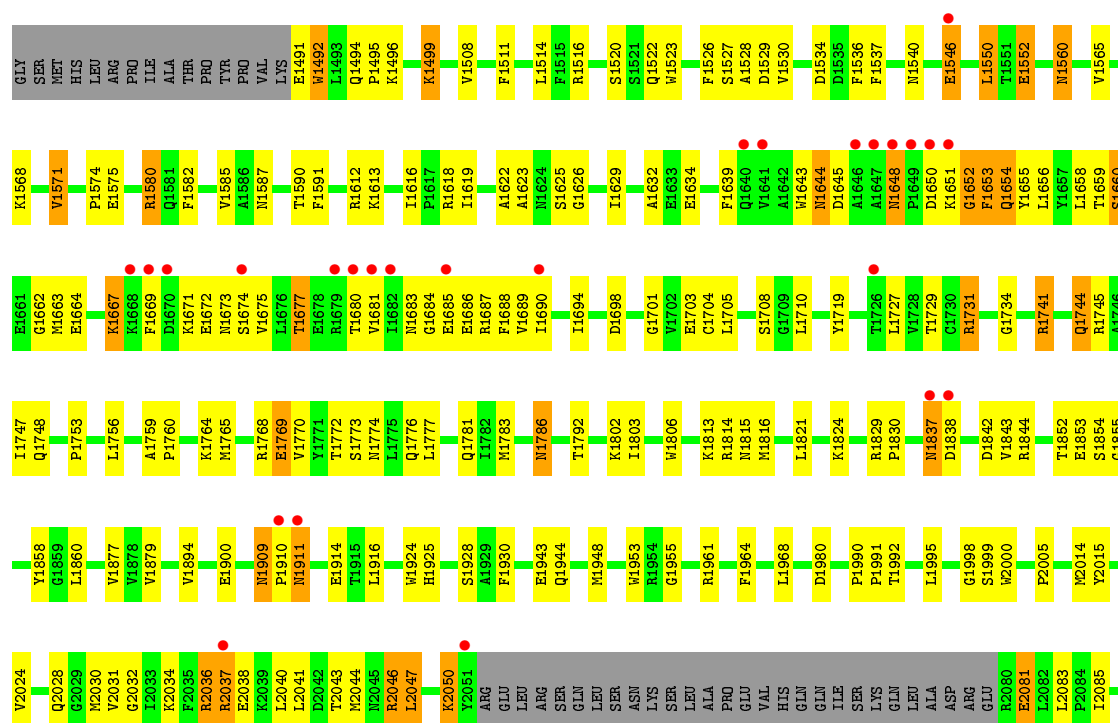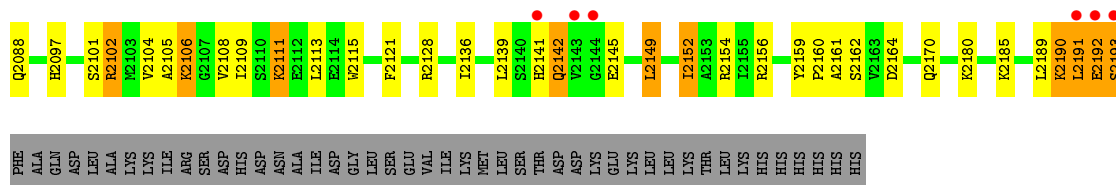● Molecule 1: Acetyl-CoA carboxylase

Chain C:

4%

58% 25% 5% 12%
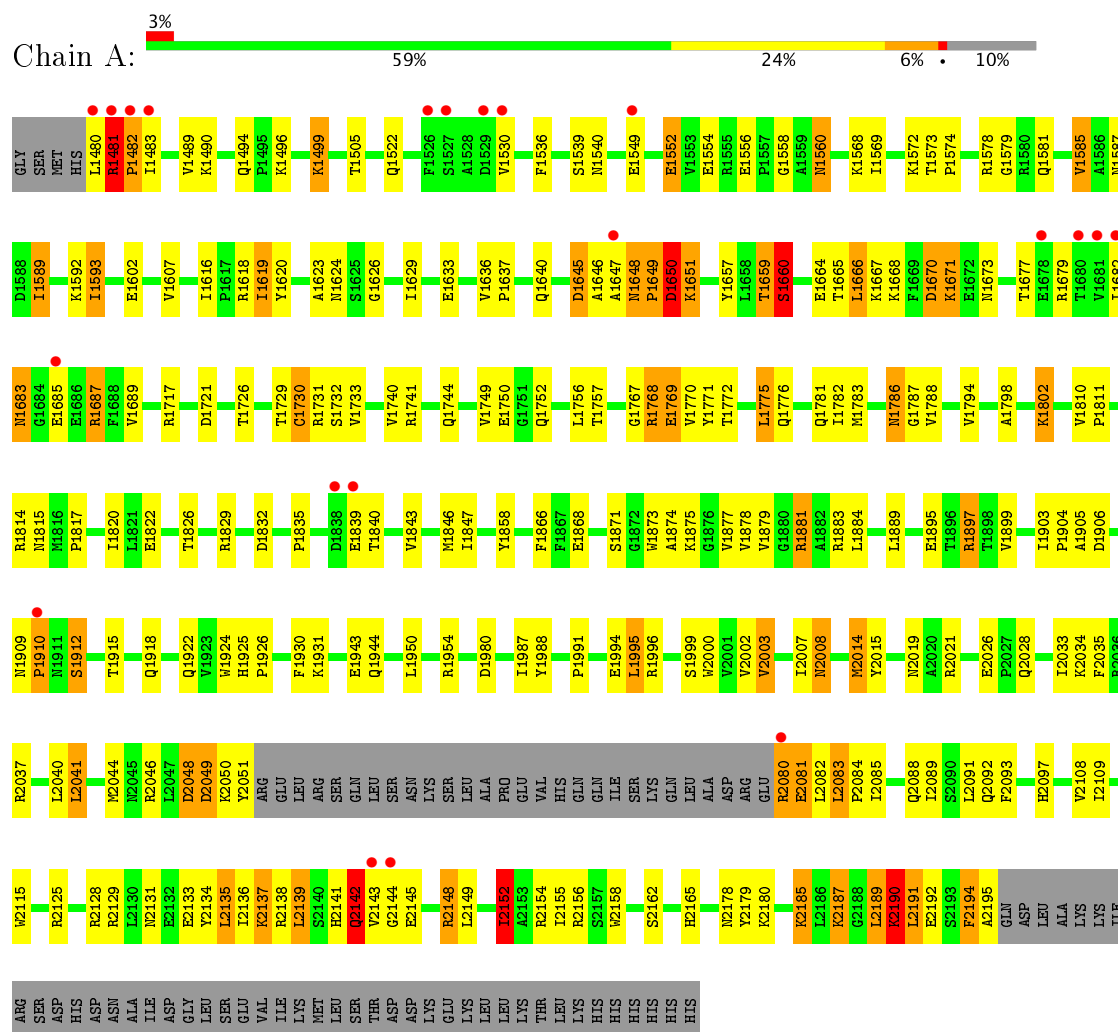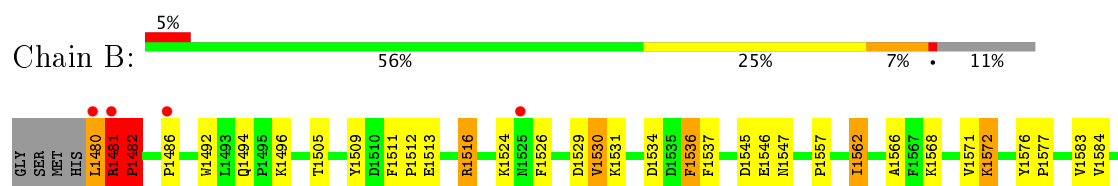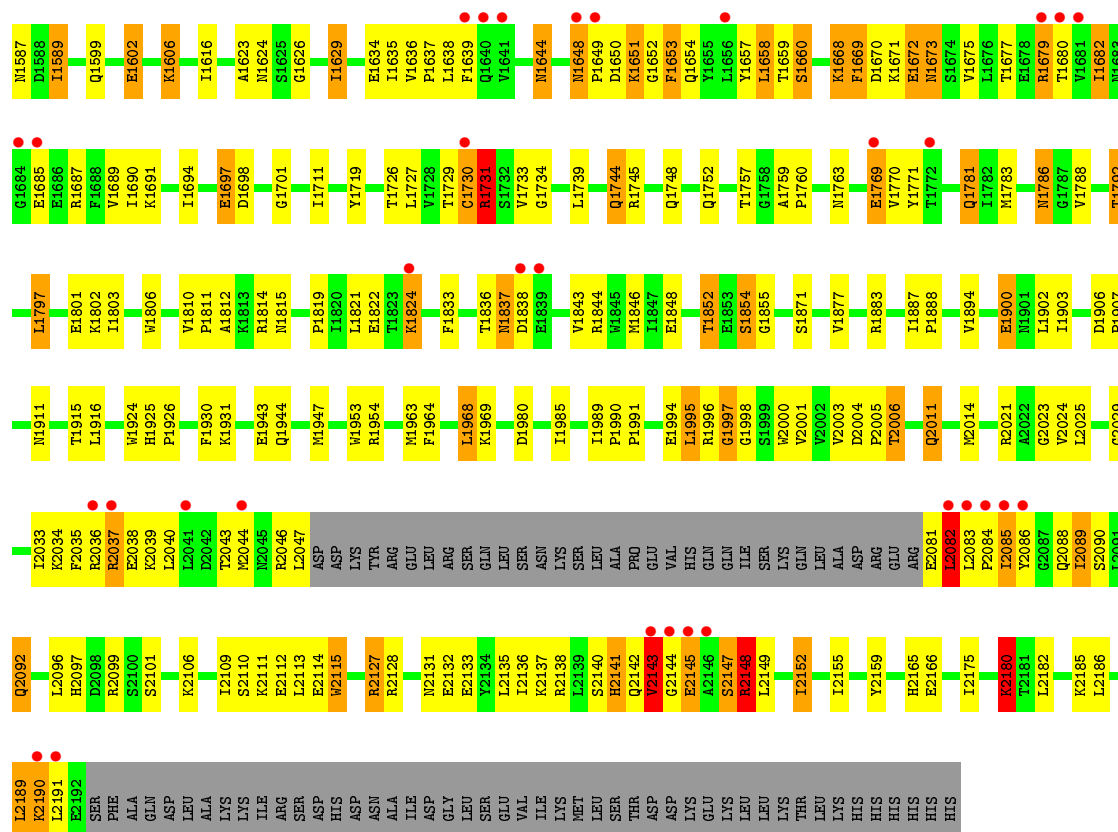
4   Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	247.18Å 123.42Å 145.71Å 90.00° 94.29° 90.00°	Depositor
Resolution (Å)	30.00 – 2.80 29.93 – 2.80	Depositor EDS
% Data completeness (in resolution range)	98.4 (30.00-2.80) 98.4 (29.93-2.80)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	1.68 (at 2.80Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.197 , 0.239 0.215 , 0.247	Depositor DCC
R_{free} test set	5265 reflections (4.98%)	DCC
Wilson B-factor (Å^2)	64.3	Xtriage
Anisotropy	0.081	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 59.2	EDS
L-test for twinning[2]	$<|L|> = 0.50$, $<L^2> = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	16368	wwPDB-VP
Average B, all atoms (Å^2)	107.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.73% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: GY3

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	0.62	0/5614	0.66	0/7605
1	B	0.61	0/5542	0.70	7/7509 (0.1%)
1	C	0.60	0/5505	0.65	1/7454 (0.0%)
All	All	0.61	0/16661	0.67	8/22568 (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	A	0	3
1	B	0	3
1	C	0	1
All	All	0	7

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	1481	ARG	O-C-N	-13.54	95.38	121.10
1	B	1481	ARG	CB-CA-C	10.40	131.20	110.40
1	B	1481	ARG	C-N-CD	-9.78	99.09	120.60
1	B	1481	ARG	CA-C-N	9.54	143.81	117.10
1	B	1482	PRO	C-N-CA	8.72	143.50	121.70

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1481	ARG	Peptide
1	A	1482	PRO	Peptide
1	A	1786	ASN	Mainchain
1	B	1481	ARG	Peptide
1	B	1482	PRO	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	5491	0	5431	156	1
1	B	5421	0	5369	234	0
1	C	5387	0	5318	205	0
2	A	23	0	21	1	0
2	B	46	0	42	24	0
All	All	16368	0	16181	567	1

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 17.

The worst 5 of 567 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:1730:CYS:HA	1:A:1752:GLN:HE21	1.04	1.19
1:B:2004:ASP:OD2	1:B:2006:THR:HB	1.50	1.09
1:B:2148:ARG:HH11	1:B:2148:ARG:CG	1.70	1.05
1:C:1772:THR:H	1:C:1776:GLN:NE2	1.54	1.05
1:B:2006:THR:HG23	1:C:1710:LEU:HA	1.42	1.01

All (1) 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:1717:ARG:NH2	1:A:2007:ILE:O[2_555]	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	684/764 (90%)	621 (91%)	48 (7%)	15 (2%)	8	26
1	B	676/764 (88%)	601 (89%)	55 (8%)	20 (3%)	5	17
1	C	671/764 (88%)	615 (92%)	46 (7%)	10 (2%)	12	37
All	All	2031/2292 (89%)	1837 (90%)	149 (7%)	45 (2%)	8	26

5 of 45 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1650	ASP
1	A	2190	LYS
1	B	1481	ARG
1	B	1651	LYS
1	B	1730	CYS

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	584/654 (89%)	484 (83%)	100 (17%)	2	7
1	B	577/654 (88%)	490 (85%)	87 (15%)	3	10
1	C	573/654 (88%)	488 (85%)	85 (15%)	3	10
All	All	1734/1962 (88%)	1462 (84%)	272 (16%)	3	9

5 of 272 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	1668	LYS
1	B	1924	TRP
1	C	2036	ARG
1	B	1673	ASN
1	B	1781	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 62 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1624	ASN
1	B	1815	ASN
1	C	1922	GLN
1	B	1752	GLN
1	B	1925	HIS

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)

3 ligands are 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	GY3	A	3000	-	23,25,25	3.18	9 (39%)	24,36,36	2.69	10 (41%)
2	GY3	B	2240	-	23,25,25	3.44	10 (43%)	24,36,36	2.25	7 (29%)
2	GY3	B	3000	-	23,25,25	3.08	8 (34%)	24,36,36	2.88	9 (37%)

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	GY3	A	3000	-	-	0/8/36/36	0/2/3/3
2	GY3	B	2240	-	-	0/8/36/36	0/2/3/3
2	GY3	B	3000	-	-	0/8/36/36	0/2/3/3

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2240	GY3	N8-N4	-8.02	1.25	1.40
2	A	3000	GY3	N8-N4	-7.83	1.26	1.40
2	B	3000	GY3	N8-N4	-7.68	1.26	1.40
2	B	2240	GY3	C19-C6	-5.52	1.39	1.52
2	B	3000	GY3	C19-C6	-5.20	1.40	1.52

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	3000	GY3	C24-C25-C26	-6.96	112.59	126.24
2	B	3000	GY3	C24-C25-C26	-6.19	114.09	126.24
2	B	3000	GY3	O1-C10-C9	-5.87	104.34	112.93
2	B	2240	GY3	C24-C25-C26	-5.67	115.13	126.24
2	A	3000	GY3	O1-C10-C9	-5.11	105.45	112.93

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 25 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	3000	GY3	1	0
2	B	2240	GY3	20	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	3000	GY3	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 (i)

6.1 Protein, DNA and RNA chains (i)

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(Å²)	Q<0.9
1	A	688/764 (90%)	-0.09	21 (3%)	49	38	50, 85, 192, 257	0
1	B	680/764 (89%)	0.05	36 (5%)	27	18	49, 95, 221, 292	0
1	C	675/764 (88%)	0.02	32 (4%)	32	22	49, 96, 227, 314	0
All	All	2043/2292 (89%)	-0.01	89 (4%)	35	25	49, 92, 216, 314	0

The worst 5 of 89 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	2143	VAL	8.8
1	B	1685	GLU	7.4
1	B	2191	LEU	7.4
1	A	1685	GLU	5.3
1	B	2143	VAL	5.1

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)

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, 95th 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(Å²)	Q<0.9
2	GY3	B	2240	23/23	0.84	0.31	3.76	139,156,186,191	0
2	GY3	B	3000	23/23	0.94	0.26	2.71	104,116,138,147	0
2	GY3	A	3000	23/23	0.95	0.16	-0.24	59,66,79,86	0

6.5   Other polymers (i)

There are no such residues in this entry.