



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:56 AM UTC

PDB ID : 4N44 / pdb_00004n44
Title : Crystal structure of oxidized form of thiolase from Clostridium acetobutylicum
Authors : Kim, S.; Ha, S.C.; Ahn, J.W.; Kim, E.J.; Lim, J.H.; Kim, K.J.
Deposited on : 2013-10-08
Resolution : 1.77 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
Mogul : 2022.3.0, CSD as543be (2022)
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

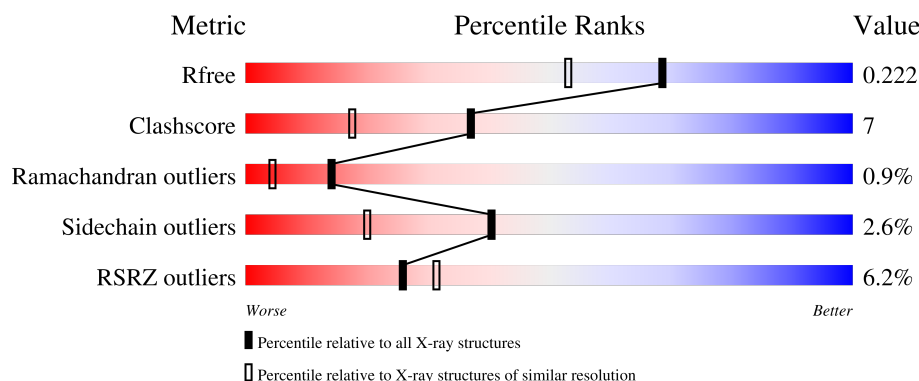
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.77 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	1365 (1.78-1.78)
Clashscore	190562	1395 (1.78-1.78)
Ramachandran outliers	187476	1382 (1.78-1.78)
Sidechain outliers	187428	1382 (1.78-1.78)
RSRZ outliers	180081	1365 (1.78-1.78)

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	400	6% 82% 15% ..
1	B	400	6% 78% 18% ..

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6249 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 acetyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	392	Total	C	N	O	S	0	0	0
			2892	1824	501	552	15			
1	B	392	Total	C	N	O	S	0	0	0
			2892	1824	501	552	15			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	393	LEU	-	expression tag	UNP F0K5D8
A	394	GLU	-	expression tag	UNP F0K5D8
A	395	HIS	-	expression tag	UNP F0K5D8
A	396	HIS	-	expression tag	UNP F0K5D8
A	397	HIS	-	expression tag	UNP F0K5D8
A	398	HIS	-	expression tag	UNP F0K5D8
A	399	HIS	-	expression tag	UNP F0K5D8
A	400	HIS	-	expression tag	UNP F0K5D8
B	393	LEU	-	expression tag	UNP F0K5D8
B	394	GLU	-	expression tag	UNP F0K5D8
B	395	HIS	-	expression tag	UNP F0K5D8
B	396	HIS	-	expression tag	UNP F0K5D8
B	397	HIS	-	expression tag	UNP F0K5D8
B	398	HIS	-	expression tag	UNP F0K5D8
B	399	HIS	-	expression tag	UNP F0K5D8
B	400	HIS	-	expression tag	UNP F0K5D8

- Molecule 2 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		

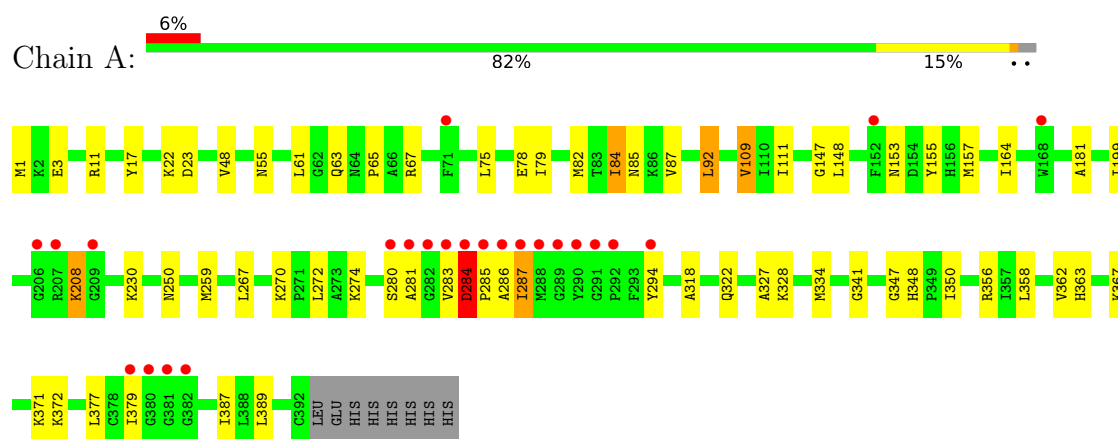
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	225	Total	O	0	0
			225	225		
4	B	212	Total	O	0	0
			212	212		

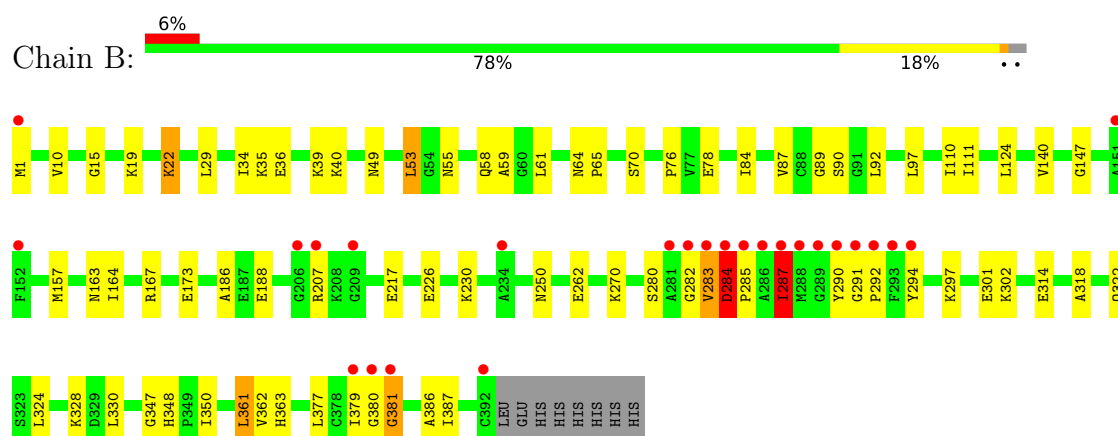
3 Residue-property plots

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: Acetyl-CoA acetyltransferase



• Molecule 1: Acetyl-CoA acetyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	203.23Å 53.99Å 72.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.44 – 1.77 43.44 – 1.77	Depositor EDS
% Data completeness (in resolution range)	98.5 (43.44-1.77) 98.5 (43.44-1.77)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.91 (at 1.77Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.168 , 0.208 0.183 , 0.222	Depositor DCC
R_{free} test set	3911 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	23.8	Xtriage
Anisotropy	0.669	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 31.3	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	0.96	EDS
Total number of atoms	6249	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 4.92% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	1.48	14/2933 (0.5%)	1.29	13/3958 (0.3%)
1	B	1.48	24/2933 (0.8%)	1.30	11/3958 (0.3%)
All	All	1.48	38/5866 (0.6%)	1.29	24/7916 (0.3%)

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	2

All (38) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	70	SER	C-O	7.12	1.32	1.24
1	A	17	TYR	N-CA	6.67	1.54	1.46
1	A	281	ALA	N-CA	6.65	1.54	1.46
1	A	377	LEU	C-O	-6.59	1.15	1.23
1	B	284	ASP	C-N	6.59	1.41	1.33
1	B	186	ALA	N-CA	6.36	1.53	1.46
1	A	48	VAL	N-CA	6.25	1.53	1.46
1	B	15	GLY	N-CA	5.99	1.52	1.44
1	B	318	ALA	N-CA	5.95	1.53	1.46
1	B	53	LEU	C-O	5.91	1.31	1.23
1	A	65	PRO	N-CD	5.79	1.55	1.47
1	B	65	PRO	N-CD	5.71	1.55	1.47
1	A	341	GLY	N-CA	5.60	1.51	1.45
1	B	90	SER	C-O	-5.60	1.17	1.24
1	B	22	LYS	N-CA	5.52	1.53	1.46
1	A	318	ALA	N-CA	5.51	1.52	1.46

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	109	VAL	N-CA	5.46	1.53	1.46
1	B	19	LYS	C-O	-5.46	1.17	1.24
1	B	76	PRO	C-O	5.45	1.30	1.23
1	A	147	GLY	N-CA	5.45	1.53	1.45
1	B	285	PRO	N-CD	5.43	1.55	1.47
1	A	347	GLY	N-CA	5.42	1.50	1.45
1	B	147	GLY	N-CA	5.39	1.53	1.45
1	A	63	GLN	C-O	-5.35	1.17	1.23
1	B	386	ALA	N-CA	5.34	1.52	1.45
1	B	64	ASN	C-O	-5.24	1.17	1.24
1	A	363	HIS	ND1-CE1	5.22	1.37	1.32
1	B	29	LEU	N-CA	-5.21	1.40	1.46
1	B	363	HIS	ND1-CE1	5.14	1.37	1.32
1	A	181	ALA	N-CA	5.14	1.52	1.46
1	B	59	ALA	CA-C	5.14	1.59	1.52
1	A	67	ARG	C-O	5.12	1.30	1.24
1	B	347	GLY	N-CA	5.12	1.51	1.45
1	B	377	LEU	C-O	-5.07	1.17	1.23
1	B	363	HIS	CE1-NE2	5.04	1.37	1.32
1	B	110	ILE	C-O	5.02	1.29	1.24
1	B	59	ALA	N-CA	5.01	1.52	1.46
1	B	361	LEU	C-O	5.00	1.29	1.24

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	283	VAL	N-CA-C	8.09	119.84	107.78
1	B	287	ILE	N-CA-C	7.73	117.80	110.53
1	A	356	ARG	N-CA-C	-7.26	103.30	111.14
1	A	372	LYS	CA-C-N	-7.15	116.10	121.61
1	A	372	LYS	C-N-CA	-7.15	116.10	121.61
1	B	89	GLY	N-CA-C	6.73	122.07	114.67
1	B	291	GLY	CA-C-N	6.60	126.22	119.56
1	B	291	GLY	C-N-CA	6.60	126.22	119.56
1	A	281	ALA	N-CA-C	6.27	119.36	109.96
1	B	111	ILE	N-CA-CB	-6.12	104.05	110.72
1	A	284	ASP	N-CA-C	5.92	122.89	109.81
1	A	208	LYS	N-CA-C	5.78	120.46	113.41
1	B	270	LYS	CA-C-N	-5.72	114.71	120.31
1	B	270	LYS	C-N-CA	-5.72	114.71	120.31
1	A	371	LYS	N-CA-C	5.54	117.13	111.14
1	B	292	PRO	N-CA-C	5.46	120.69	113.86

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	23	ASP	CA-C-N	-5.42	117.29	123.25
1	A	23	ASP	C-N-CA	-5.42	117.29	123.25
1	A	287	ILE	N-CA-C	5.42	116.19	110.72
1	A	111	ILE	N-CA-C	-5.14	100.37	108.23
1	B	285	PRO	CA-N-CD	-5.13	104.82	112.00
1	B	362	VAL	CB-CA-C	-5.06	105.30	112.14
1	A	270	LYS	CA-C-N	-5.03	115.38	120.31
1	A	270	LYS	C-N-CA	-5.03	115.38	120.31

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	207	ARG	Peptide
1	B	284	ASP	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	2892	0	2961	48	0
1	B	2892	0	2961	42	0
2	A	8	0	6	0	0
2	B	8	0	6	0	0
3	B	12	0	16	3	0
4	A	225	0	0	7	0
4	B	212	0	0	8	0
All	All	6249	0	5950	83	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 (83) 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:327:ALA:CB	1:A:334:MET:HE1	1.65	1.25

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:327:ALA:HB1	1:A:334:MET:CE	1.68	1.21
1:B:36:GLU:OE2	1:B:40:LYS:HE3	1.55	1.06
1:A:230:LYS:HE3	4:A:627:HOH:O	1.58	1.04
1:B:217:GLU:O	3:B:403:GOL:H11	1.63	0.99
1:A:294:TYR:OH	1:B:78:GLU:HB2	1.75	0.86
1:A:274:LYS:HE2	4:A:719:HOH:O	1.75	0.85
1:A:362:VAL:HG12	1:A:389:LEU:CD1	2.13	0.78
3:B:403:GOL:H12	4:B:703:HOH:O	1.86	0.74
1:A:283:VAL:HG22	1:A:284:ASP:H	1.53	0.73
1:A:84:ILE:HD12	1:B:84:ILE:HD12	1.75	0.69
1:B:188:GLU:CG	4:B:628:HOH:O	2.40	0.69
1:B:40:LYS:HD3	4:B:609:HOH:O	1.93	0.67
1:A:287:ILE:HG13	1:A:294:TYR:CD2	2.30	0.67
1:A:367:LYS:HE2	4:A:606:HOH:O	1.95	0.65
1:A:164:ILE:HD11	1:A:379:ILE:CD1	2.28	0.63
1:B:188:GLU:HG2	4:B:628:HOH:O	2.00	0.60
1:A:287:ILE:HG13	1:A:294:TYR:HD2	1.66	0.59
1:B:40:LYS:CD	4:B:609:HOH:O	2.49	0.59
1:A:280:SER:HB3	4:B:517:HOH:O	2.05	0.57
1:B:250:ASN:HD22	1:B:348:HIS:H	1.51	0.57
1:A:82:MET:HE1	1:B:97:LEU:HD21	1.86	0.56
1:A:362:VAL:HG12	1:A:389:LEU:HD13	1.86	0.56
1:B:282:GLY:HA3	1:B:302:LYS:NZ	2.21	0.56
1:B:324:LEU:O	1:B:328:LYS:HG3	2.06	0.56
1:B:188:GLU:CB	4:B:628:HOH:O	2.54	0.56
1:A:84:ILE:HD12	1:B:84:ILE:CD1	2.36	0.55
1:A:92:LEU:HD22	1:A:387:ILE:HD12	1.89	0.54
1:B:282:GLY:HA3	1:B:302:LYS:HZ2	1.71	0.54
1:B:297:LYS:HE2	1:B:330:LEU:CD2	2.38	0.54
1:A:109:VAL:HG22	1:A:259:MET:HE3	1.88	0.53
1:A:250:ASN:HD22	1:A:348:HIS:H	1.56	0.53
1:B:250:ASN:ND2	1:B:348:HIS:H	2.07	0.53
1:A:164:ILE:HD11	1:A:379:ILE:HD11	1.91	0.53
1:B:188:GLU:HB3	4:B:628:HOH:O	2.09	0.53
1:B:163:ASN:O	1:B:167:ARG:HG3	2.09	0.53
1:A:148:LEU:O	1:A:157:MET:HG2	2.09	0.53
1:B:290:TYR:OH	1:B:301:GLU:OE1	2.20	0.52
1:A:283:VAL:HG22	1:A:284:ASP:N	2.25	0.52
1:A:272:LEU:HD12	1:A:272:LEU:N	2.24	0.52
1:A:283:VAL:HG23	1:B:49:ASN:ND2	2.24	0.51
4:A:569:HOH:O	1:B:280:SER:HB3	2.09	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:78:GLU:HB2	1:B:294:TYR:OH	2.11	0.51
1:A:283:VAL:CG2	1:A:284:ASP:H	2.23	0.51
1:A:250:ASN:ND2	1:A:348:HIS:H	2.09	0.50
1:B:290:TYR:HB3	1:B:297:LYS:HD2	1.92	0.50
1:A:358:LEU:O	1:A:362:VAL:HG13	2.11	0.50
1:A:272:LEU:N	1:A:272:LEU:CD1	2.75	0.49
1:A:164:ILE:HD13	1:A:322:GLN:HG2	1.95	0.49
1:A:55:ASN:HD21	1:A:61:LEU:HD12	1.78	0.49
1:A:327:ALA:HB1	1:A:334:MET:HE1	0.72	0.48
1:A:85:ASN:HD22	1:B:58:GLN:NE2	2.11	0.48
1:A:367:LYS:CE	4:A:606:HOH:O	2.59	0.47
1:B:217:GLU:O	3:B:403:GOL:C1	2.50	0.47
1:B:10:VAL:CG2	1:B:40:LYS:HD2	2.45	0.46
1:A:327:ALA:CB	1:A:334:MET:CE	2.55	0.45
1:A:164:ILE:CD1	1:A:379:ILE:HD13	2.47	0.45
1:A:78:GLU:HG3	1:B:287:ILE:HG21	1.99	0.45
1:A:153:ASN:HB3	1:A:155:TYR:CE2	2.52	0.45
1:A:92:LEU:HD22	1:A:387:ILE:CD1	2.47	0.44
1:B:226:GLU:O	1:B:230:LYS:HG3	2.18	0.44
1:B:34:ILE:HD11	1:B:53:LEU:HD11	2.00	0.44
1:A:259:MET:HE1	1:A:267:LEU:HD12	1.99	0.43
1:B:35:LYS:NZ	1:B:39:LYS:NZ	2.66	0.43
1:A:230:LYS:CE	4:A:627:HOH:O	2.35	0.43
1:A:285:PRO:HA	1:A:286:ALA:HA	1.80	0.43
1:B:164:ILE:HD13	1:B:322:GLN:HG2	2.01	0.43
1:A:3:GLU:HG3	1:A:274:LYS:NZ	2.35	0.42
1:B:10:VAL:HG22	1:B:40:LYS:HD2	2.01	0.42
1:B:55:ASN:HD22	1:B:58:GLN:HG2	1.84	0.42
1:B:173:GLU:CD	1:B:173:GLU:N	2.78	0.41
1:A:362:VAL:HG12	1:A:389:LEU:HD11	1.98	0.41
1:A:11:ARG:O	1:A:199:ILE:HA	2.20	0.41
1:A:164:ILE:CD1	1:A:379:ILE:CD1	2.97	0.41
1:B:164:ILE:HD11	1:B:379:ILE:CD1	2.49	0.41
1:A:3:GLU:HG3	1:A:274:LYS:HZ2	1.84	0.41
1:B:157:MET:HE2	1:B:157:MET:HA	2.03	0.41
1:B:380:GLY:O	1:B:381:GLY:C	2.63	0.41
1:B:55:ASN:ND2	1:B:58:GLN:HG2	2.36	0.41
1:B:124:LEU:HB2	1:B:140:VAL:HB	2.03	0.40
1:B:55:ASN:HD21	1:B:61:LEU:HD12	1.85	0.40
1:A:157:MET:HE2	4:A:690:HOH:O	2.21	0.40
1:B:314:GLU:HG3	1:B:361:LEU:HB2	2.03	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	390/400 (98%)	374 (96%)	13 (3%)	3 (1%)	16	6
1	B	390/400 (98%)	374 (96%)	12 (3%)	4 (1%)	12	4
All	All	780/800 (98%)	748 (96%)	25 (3%)	7 (1%)	14	4

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	284	ASP
1	A	87	VAL
1	A	350	ILE
1	B	87	VAL
1	A	284	ASP
1	B	350	ILE
1	B	381	GLY

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	294/302 (97%)	286 (97%)	8 (3%)	39	19
1	B	294/302 (97%)	287 (98%)	7 (2%)	43	24
All	All	588/604 (97%)	573 (97%)	15 (3%)	40	20

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	22	LYS
1	A	75	LEU
1	A	79	ILE
1	A	84	ILE
1	A	92	LEU
1	A	208	LYS
1	A	328	LYS
1	B	1	MET
1	B	22	LYS
1	B	92	LEU
1	B	262	GLU
1	B	283	VAL
1	B	287	ILE
1	B	387	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	ASN
1	A	153	ASN
1	A	250	ASN
1	A	322	GLN
1	A	366	GLN
1	B	55	ASN
1	B	58	GLN
1	B	153	ASN
1	B	250	ASN
1	B	316	ASN
1	B	322	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

There are no oligosaccharides in this entry.

5.6 Ligand geometry

6 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	$\# Z > 2$
3	GOL	B	404	-	5,5,5	0.80	0	5,5,5	0.77	0
2	ACT	A	402	-	3,3,3	0.83	0	3,3,3	1.00	0
2	ACT	A	401	-	3,3,3	0.74	0	3,3,3	0.68	0
2	ACT	B	402	-	3,3,3	0.85	0	3,3,3	0.81	0
3	GOL	B	403	-	5,5,5	0.44	0	5,5,5	0.66	0
2	ACT	B	401	-	3,3,3	0.91	0	3,3,3	1.29	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
3	GOL	B	404	-	-	2/4/4/4	-
3	GOL	B	403	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	403	GOL	O1-C1-C2-O2
3	B	403	GOL	O1-C1-C2-C3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
3	B	403	GOL	C1-C2-C3-O3
3	B	404	GOL	O1-C1-C2-C3
3	B	403	GOL	O2-C2-C3-O3
3	B	404	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	403	GOL	3	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, 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	392/400 (98%)	0.16	24 (6%) 27 33	15, 25, 55, 119	0
1	B	392/400 (98%)	0.21	25 (6%) 25 30	16, 26, 59, 134	0
All	All	784/800 (98%)	0.18	49 (6%) 26 31	15, 25, 58, 134	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	287	ILE	7.8
1	A	287	ILE	7.7
1	A	283	VAL	6.7
1	B	282	GLY	6.4
1	B	283	VAL	6.2
1	B	285	PRO	6.1
1	A	285	PRO	5.5
1	A	290	TYR	5.3
1	B	286	ALA	5.2
1	B	290	TYR	5.2
1	A	282	GLY	5.0
1	A	286	ALA	4.8
1	B	288	MET	4.5
1	B	289	GLY	4.4
1	B	152	PHE	4.3
1	A	281	ALA	4.2
1	B	281	ALA	4.1
1	A	152	PHE	4.0
1	A	289	GLY	3.9
1	A	294	TYR	3.8
1	B	381	GLY	3.7
1	B	292	PRO	3.7
1	A	206	GLY	3.7
1	B	206	GLY	3.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	288	MET	3.5
1	B	379	ILE	3.4
1	A	168	TRP	3.3
1	A	292	PRO	3.2
1	B	294	TYR	3.1
1	A	379	ILE	3.1
1	B	1	MET	3.0
1	B	291	GLY	2.9
1	A	381	GLY	2.8
1	B	151	ALA	2.8
1	A	284	ASP	2.8
1	B	284	ASP	2.7
1	A	207	ARG	2.7
1	B	380	GLY	2.7
1	A	71	PHE	2.7
1	A	209	GLY	2.5
1	B	207	ARG	2.4
1	B	392	CYS	2.4
1	B	293	PHE	2.4
1	A	280	SER	2.3
1	A	382	GLY	2.2
1	B	209	GLY	2.2
1	A	380	GLY	2.2
1	A	291	GLY	2.1
1	B	234	ALA	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 oligosaccharides 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. 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	B-factors($\text{\AA}^2$)	Q<0.9
3	GOL	B	403	6/6	0.81	0.15	42,53,56,56	0
2	ACT	A	402	4/4	0.82	0.16	39,47,51,53	0
3	GOL	B	404	6/6	0.82	0.16	46,54,55,56	0
2	ACT	B	402	4/4	0.84	0.16	34,38,48,55	0
2	ACT	A	401	4/4	0.96	0.08	23,25,27,27	1
2	ACT	B	401	4/4	0.97	0.07	19,23,24,27	1

6.5 Other polymers [i](#)

There are no such residues in this entry.