



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:07 AM UTC

PDB ID : 1UWT / pdb_00001uwt
Title : Structure of beta-glycosidase from *Sulfolobus solfataricus* in complex with D-galactohydroxymo-1,5-lactam
Authors : Gloster, T.M.; Roberts, S.; Ducros, V.M.-A.; Perugino, G.; Rossi, M.; Hoos, R.; Moracci, M.; Vasella, A.; Davies, G.J.
Deposited on : 2004-02-11
Resolution : 1.95 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

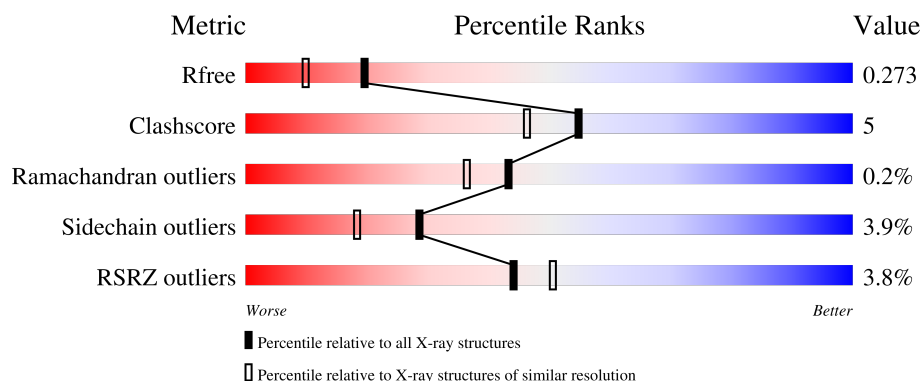
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	489	4% 87% 11% ..
1	B	489	4% 88% 10% ..

2 Entry composition [i](#)

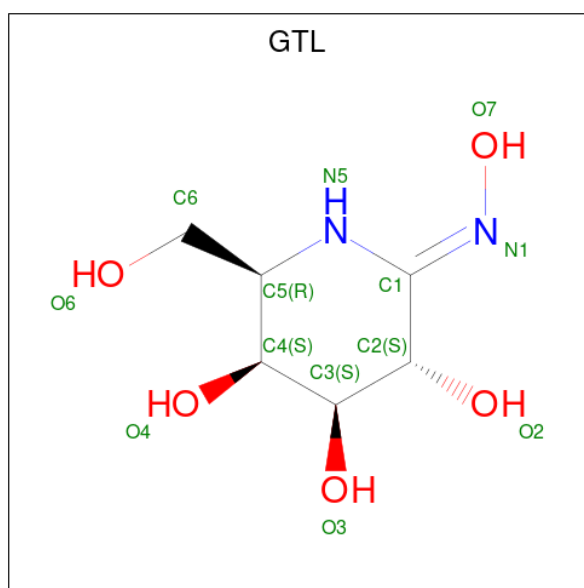
There are 4 unique types of molecules in this entry. The entry contains 8905 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 BETA-GALACTOSIDASE.

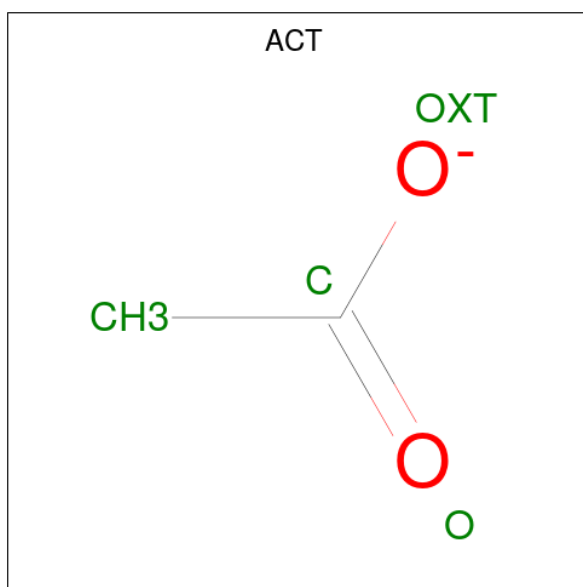
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	485	Total	C	N	O	S	0	10	0
			3983	2561	673	737	12			
1	B	484	Total	C	N	O	S	0	11	0
			3977	2555	681	729	12			

- Molecule 2 is (2E,3R,4R,5R,6S)-3,4,5-TRIHYDROXY-6-(HYDROXYMETHYL)-2-PIPERIDINONE (CCD ID: GTL) (formula: $C_6H_{12}N_2O_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			13	6	2	5		
2	B	1	Total	C	N	O	0	0
			13	6	2	5		

- Molecule 3 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



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

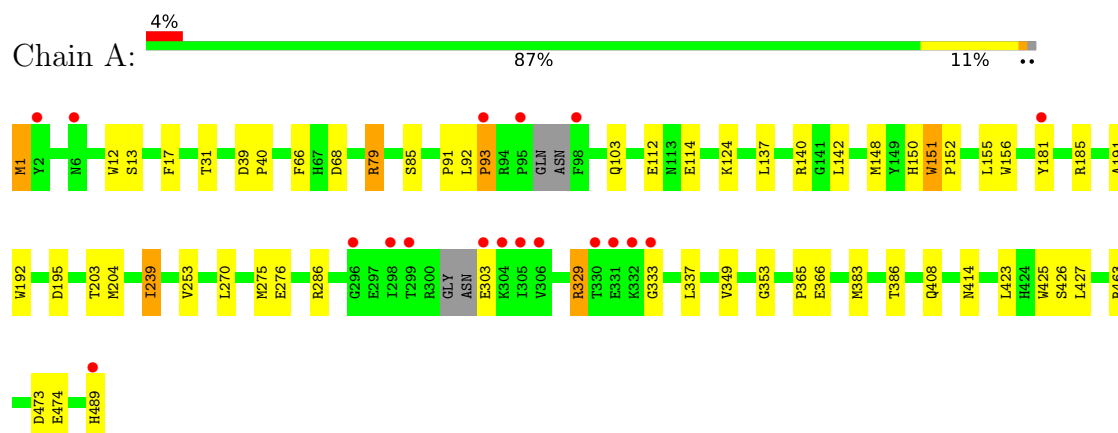
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	432	Total	O	0	0
			432	432		
4	B	483	Total	O	0	0
			483	483		

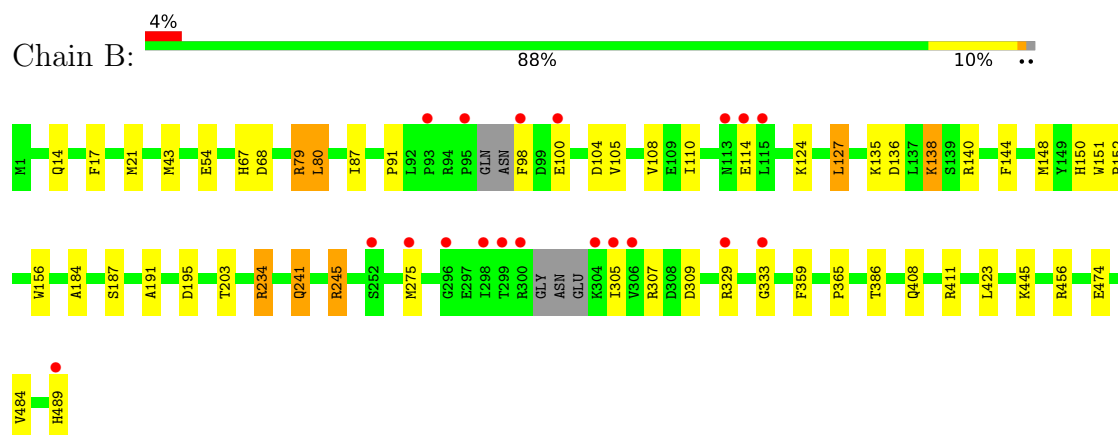
3 Residue-property plots

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: BETA-GALACTOSIDASE



• Molecule 1: BETA-GALACTOSIDASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	168.30Å 168.30Å 95.67Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	141.42 – 1.95 141.42 – 1.95	Depositor EDS
% Data completeness (in resolution range)	96.9 (141.42-1.95) 97.0 (141.42-1.95)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.12 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.201 , 0.239 (Not available) , 0.273	Depositor DCC
R_{free} test set	5527 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	31.5	Xtriage
Anisotropy	0.199	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 56.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.013 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8905	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.61% 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: GTL, 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	0.84	0/4152	0.94	2/5644 (0.0%)
1	B	0.85	2/4150 (0.0%)	0.91	0/5641
All	All	0.85	2/8302 (0.0%)	0.92	2/11285 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	43	MET	SD-CE	-7.34	1.61	1.79
1	B	275	MET	SD-CE	5.42	1.93	1.79

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	93	PRO	CA-C-O	-5.30	115.30	121.34
1	A	66	PHE	N-CA-C	-5.03	105.69	111.07

There are no chirality outliers.

There are no planarity outliers.

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	3983	0	3704	36	0
1	B	3977	0	3722	42	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	13	0	12	0	0
2	B	13	0	12	0	0
3	B	4	0	3	1	0
4	A	432	0	0	3	0
4	B	483	0	0	2	0
All	All	8905	0	7453	74	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 5.

All (74) 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:489[B]:HIS:ND1	1:B:489[B]:HIS:CD2	2.07	1.23
1:B:234[A]:ARG:HH11	1:B:234[A]:ARG:HB2	1.23	1.01
1:A:489[B]:HIS:CE1	1:B:489[B]:HIS:CD2	2.50	0.99
1:A:13:SER:OG	1:A:79:ARG:HD3	1.77	0.82
1:A:181:TYR:CE1	1:A:185:ARG:HD2	2.16	0.81
1:A:124:LYS:HG3	4:A:2176:HOH:O	1.81	0.80
1:A:270:LEU:HD22	1:A:337:LEU:HD11	1.67	0.76
1:A:489[B]:HIS:CE1	1:B:489[B]:HIS:HD2	2.03	0.73
1:A:192:TRP:HA	1:A:253:VAL:HG11	1.75	0.69
1:B:68[B]:ASP:OD1	1:B:140[B]:ARG:NH1	2.25	0.69
1:B:245:ARG:NH2	1:B:309:ASP:OD2	2.28	0.66
1:B:234[A]:ARG:HB2	1:B:234[A]:ARG:NH1	2.05	0.65
1:A:329:ARG:HD3	1:A:333:GLY:O	1.98	0.64
1:A:68[A]:ASP:OD1	1:A:140:ARG:NH1	2.30	0.64
1:A:286:ARG:HD3	4:A:2291:HOH:O	1.98	0.62
1:A:489[B]:HIS:ND1	1:B:489[B]:HIS:CG	2.69	0.58
1:B:104:ASP:HA	1:B:241:GLN:HE22	1.70	0.57
1:A:270:LEU:HD22	1:A:337:LEU:CD1	2.35	0.56
1:B:241:GLN:NE2	1:B:307:ARG:HH12	2.04	0.56
1:B:110:ILE:HA	1:B:114:GLU:OE1	2.06	0.55
1:A:92:LEU:HB3	1:A:93:PRO:HD2	1.89	0.55
1:B:14:GLN:HG2	1:B:80:LEU:HD23	1.89	0.55
1:A:253:VAL:O	1:A:253:VAL:HG12	2.07	0.54
1:B:148:MET:HG3	1:B:187[A]:SER:HB2	1.88	0.54
1:B:184:ALA:HB2	1:B:245:ARG:HB3	1.93	0.51
1:B:150:HIS:O	1:B:152:PRO:HD3	2.11	0.51
1:B:365:PRO:O	1:B:408:GLN:HG3	2.10	0.51
1:B:411:ARG:HG2	3:B:1490:ACT:H1	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:445[B]:LYS:HG3	1:B:456:ARG:NH2	2.28	0.49
1:A:148:MET:HB2	1:A:203:THR:O	2.12	0.49
1:B:17:PHE:HB2	1:B:152:PRO:HG2	1.94	0.49
1:B:105:VAL:H	1:B:241:GLN:NE2	2.11	0.49
1:B:484:VAL:O	1:B:489[A]:HIS:HE1	1.95	0.48
1:B:108:VAL:HG23	1:B:245:ARG:HG3	1.96	0.47
1:B:241:GLN:HE21	1:B:307:ARG:HH22	1.63	0.47
1:B:245:ARG:CD	4:B:2181:HOH:O	2.63	0.47
1:A:365:PRO:O	1:A:408:GLN:HG3	2.15	0.46
1:B:105:VAL:H	1:B:241:GLN:HE22	1.63	0.46
1:B:241:GLN:HE21	1:B:307:ARG:HH12	1.61	0.46
1:B:245:ARG:HD2	4:B:2181:HOH:O	2.15	0.46
1:A:151:TRP:HB2	1:A:152:PRO:HD3	1.96	0.46
1:B:138:LYS:HA	1:B:138:LYS:HD2	1.70	0.46
1:B:91:PRO:HA	1:B:156:TRP:CD2	2.51	0.45
1:A:1:MET:N	1:A:473:ASP:OD1	2.45	0.45
1:B:79:ARG:HD2	1:B:79:ARG:C	2.41	0.45
1:A:12:TRP:CD1	1:A:427:LEU:HB2	2.53	0.44
1:A:204:MET:HE1	1:A:239:ILE:O	2.17	0.44
1:A:191:ALA:O	1:A:195:ASP:HB2	2.17	0.44
1:B:148:MET:HB2	1:B:203:THR:O	2.18	0.43
1:A:13:SER:OG	1:A:79:ARG:CD	2.56	0.43
1:A:253:VAL:O	1:A:253:VAL:CG1	2.66	0.43
1:A:349:VAL:HG13	1:A:353:GLY:HA2	1.99	0.43
1:A:366:GLU:HB3	4:A:2346:HOH:O	2.18	0.43
1:B:245:ARG:HD3	1:B:245:ARG:HA	1.79	0.43
1:B:87:ILE:HD12	1:B:127:LEU:HD13	2.00	0.43
1:B:21:MET:HB3	1:B:54:GLU:HA	2.01	0.43
1:A:91:PRO:HA	1:A:156:TRP:CD2	2.54	0.43
1:A:425:TRP:HA	1:A:426:SER:HA	1.78	0.43
1:A:31:THR:C	1:A:155:LEU:HG	2.45	0.42
1:A:17:PHE:HB2	1:A:152:PRO:HG2	2.01	0.42
1:A:150:HIS:O	1:A:152:PRO:HD3	2.20	0.42
1:A:137[A]:LEU:HD22	1:A:142:LEU:HD13	2.01	0.42
1:A:79:ARG:HB3	1:A:423:LEU:HD23	2.02	0.41
1:B:98:PHE:HE2	1:B:100:GLU:HG2	1.84	0.41
1:B:136:ASP:O	1:B:140[A]:ARG:HG2	2.19	0.41
1:A:31:THR:HG22	1:A:85:SER:HB3	2.02	0.41
1:A:39:ASP:HA	1:A:40:PRO:HD3	1.94	0.41
1:B:80:LEU:HD12	1:B:144:PHE:CE1	2.56	0.41
1:B:67:HIS:HB3	1:B:140[A]:ARG:HG3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:191:ALA:O	1:B:195:ASP:HB2	2.21	0.41
1:B:329:ARG:HD2	1:B:333:GLY:O	2.21	0.41
1:B:423:LEU:HD12	1:B:423:LEU:N	2.37	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	488/489 (100%)	476 (98%)	11 (2%)	1 (0%)	43	36
1	B	488/489 (100%)	476 (98%)	11 (2%)	1 (0%)	43	36
All	All	976/978 (100%)	952 (98%)	22 (2%)	2 (0%)	43	36

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	151	TRP
1	B	151	TRP

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	329/421 (78%)	312 (95%)	17 (5%)	21	9

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	417/421 (99%)	403 (97%)	14 (3%)	32	23
All	All	746/842 (89%)	715 (96%)	31 (4%)	28	16

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	79	ARG
1	A	103	GLN
1	A	112[A]	GLU
1	A	112[B]	GLU
1	A	114[A]	GLU
1	A	114[B]	GLU
1	A	239	ILE
1	A	275	MET
1	A	276	GLU
1	A	303	GLU
1	A	329	ARG
1	A	383	MET
1	A	386	THR
1	A	414	ASN
1	A	463	ARG
1	A	474	GLU
1	B	79	ARG
1	B	80	LEU
1	B	124	LYS
1	B	127	LEU
1	B	135	LYS
1	B	138	LYS
1	B	234[A]	ARG
1	B	234[B]	ARG
1	B	241	GLN
1	B	245	ARG
1	B	305	ILE
1	B	359	PHE
1	B	386	THR
1	B	474	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	6	ASN
1	A	71	GLN
1	B	113	ASN
1	B	241	GLN
1	B	342	HIS
1	B	388	ASN

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](#)

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	GTL	A	1490	-	12,13,13	1.24	2 (16%)	14,18,18	1.37	2 (14%)
3	ACT	B	1490	-	3,3,3	0.86	0	3,3,3	0.73	0
2	GTL	B	1491	-	12,13,13	1.05	1 (8%)	14,18,18	1.64	3 (21%)

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	GTL	A	1490	-	-	2/3/24/24	0/1/1/1
2	GTL	B	1491	-	-	1/3/24/24	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1491	GTL	C1-N5	2.64	1.40	1.35
2	A	1490	GTL	C1-N5	2.60	1.40	1.35
2	A	1490	GTL	C6-C5	2.05	1.56	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1491	GTL	C6-C5-N5	-3.85	102.00	109.56
2	A	1490	GTL	C3-C4-C5	-3.12	106.44	111.02
2	B	1491	GTL	C3-C4-C5	-2.91	106.75	111.02
2	A	1490	GTL	C4-C3-C2	2.51	114.18	110.22
2	B	1491	GTL	C5-N5-C1	-2.09	118.11	124.63

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1490	GTL	N5-C1-N1-O7
2	B	1491	GTL	N5-C1-N1-O7
2	A	1490	GTL	C4-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1490	ACT	1	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	485/489 (99%)	0.48	18 (3%)	45 52	21, 34, 52, 67	10 (2%)
1	B	484/489 (98%)	0.31	19 (3%)	43 50	18, 33, 52, 68	11 (2%)
All	All	969/978 (99%)	0.39	37 (3%)	44 50	18, 33, 52, 68	21 (2%)

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	489[A]	HIS	4.7
1	B	306	VAL	3.8
1	A	98	PHE	3.8
1	B	304	LYS	3.7
1	B	93	PRO	3.6
1	B	275	MET	3.6
1	B	305	ILE	3.5
1	B	95	PRO	3.3
1	A	489[A]	HIS	3.2
1	B	98	PHE	3.2
1	A	305	ILE	3.2
1	A	330	THR	3.1
1	A	333	GLY	2.8
1	A	306	VAL	2.8
1	A	95	PRO	2.7
1	B	333	GLY	2.6
1	B	329	ARG	2.6
1	B	114	GLU	2.5
1	A	298	ILE	2.5
1	B	296	GLY	2.4
1	B	299	THR	2.4
1	A	93	PRO	2.4
1	A	181	TYR	2.4
1	A	331	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	6	ASN	2.3
1	B	300	ARG	2.3
1	A	299	THR	2.2
1	A	296	GLY	2.2
1	B	100	GLU	2.2
1	B	252	SER	2.1
1	B	115	LEU	2.1
1	A	2	TYR	2.1
1	B	298	ILE	2.1
1	A	303	GLU	2.1
1	B	113	ASN	2.1
1	A	304	LYS	2.0
1	A	332	LYS	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](#)

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	ACT	B	1490	4/4	0.77	0.23	60,60,61,61	0
2	GTL	A	1490	13/13	0.95	0.07	22,29,36,43	0
2	GTL	B	1491	13/13	0.96	0.06	21,24,31,41	0

6.5 Other polymers [i](#)

There are no such residues in this entry.