



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 01:50 PM UTC

PDB ID : 8TCD / pdb_00008tcd
Title : Structure of Alistipes sp. 3-Keto-beta-glucopyranoside-1,2-Lyase AL1
Authors : Lazarski, A.C.; Worrall, L.J.; Strynadka, N.C.J.
Deposited on : 2023-06-30
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
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

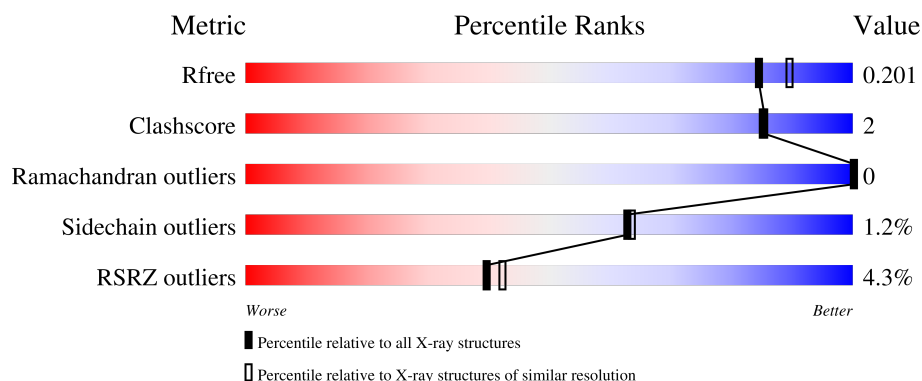
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	286	2% 86% 8% 5%
1	B	286	3% 88% 6% 5%
1	C	286	6% 88% 6% 5%
1	D	286	5% 87% 7% 5%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9186 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 Sugar phosphate isomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	271	Total	C	N	O	S	0	0	0
			2160	1383	351	412	14			
1	C	271	Total	C	N	O	S	0	0	0
			2153	1380	349	410	14			
1	D	272	Total	C	N	O	S	0	0	0
			2174	1390	355	415	14			
1	A	271	Total	C	N	O	S	0	0	0
			2148	1377	347	410	14			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	24	MET	-	expression tag	UNP A0A4Y1X717
B	302	LEU	-	expression tag	UNP A0A4Y1X717
B	303	GLU	-	expression tag	UNP A0A4Y1X717
B	304	HIS	-	expression tag	UNP A0A4Y1X717
B	305	HIS	-	expression tag	UNP A0A4Y1X717
B	306	HIS	-	expression tag	UNP A0A4Y1X717
B	307	HIS	-	expression tag	UNP A0A4Y1X717
B	308	HIS	-	expression tag	UNP A0A4Y1X717
B	309	HIS	-	expression tag	UNP A0A4Y1X717
C	24	MET	-	expression tag	UNP A0A4Y1X717
C	302	LEU	-	expression tag	UNP A0A4Y1X717
C	303	GLU	-	expression tag	UNP A0A4Y1X717
C	304	HIS	-	expression tag	UNP A0A4Y1X717
C	305	HIS	-	expression tag	UNP A0A4Y1X717
C	306	HIS	-	expression tag	UNP A0A4Y1X717
C	307	HIS	-	expression tag	UNP A0A4Y1X717
C	308	HIS	-	expression tag	UNP A0A4Y1X717
C	309	HIS	-	expression tag	UNP A0A4Y1X717
D	24	MET	-	expression tag	UNP A0A4Y1X717
D	302	LEU	-	expression tag	UNP A0A4Y1X717
D	303	GLU	-	expression tag	UNP A0A4Y1X717

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Chain	Residue	Modelled	Actual	Comment	Reference
D	304	HIS	-	expression tag	UNP A0A4Y1X717
D	305	HIS	-	expression tag	UNP A0A4Y1X717
D	306	HIS	-	expression tag	UNP A0A4Y1X717
D	307	HIS	-	expression tag	UNP A0A4Y1X717
D	308	HIS	-	expression tag	UNP A0A4Y1X717
D	309	HIS	-	expression tag	UNP A0A4Y1X717
A	24	MET	-	expression tag	UNP A0A4Y1X717
A	302	LEU	-	expression tag	UNP A0A4Y1X717
A	303	GLU	-	expression tag	UNP A0A4Y1X717
A	304	HIS	-	expression tag	UNP A0A4Y1X717
A	305	HIS	-	expression tag	UNP A0A4Y1X717
A	306	HIS	-	expression tag	UNP A0A4Y1X717
A	307	HIS	-	expression tag	UNP A0A4Y1X717
A	308	HIS	-	expression tag	UNP A0A4Y1X717
A	309	HIS	-	expression tag	UNP A0A4Y1X717

- Molecule 2 is COBALT (II) ION (CCD ID: CO) (formula: Co).

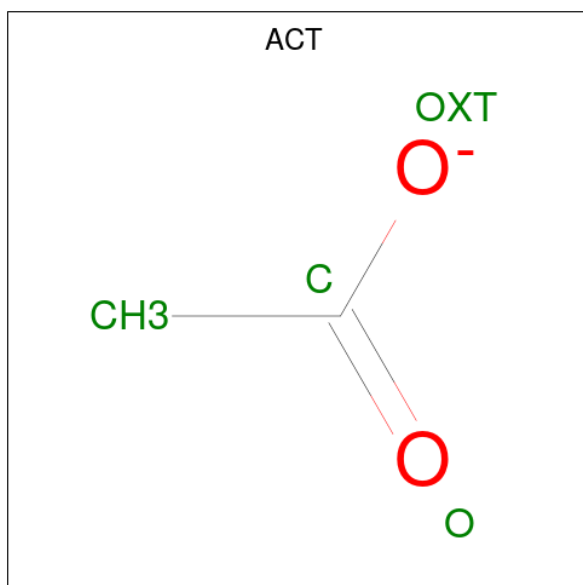
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Co 1 1	0	0
2	C	1	Total Co 1 1	0	0
2	D	1	Total Co 1 1	0	0
2	A	1	Total Co 1 1	0	0

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

- Molecule 4 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



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

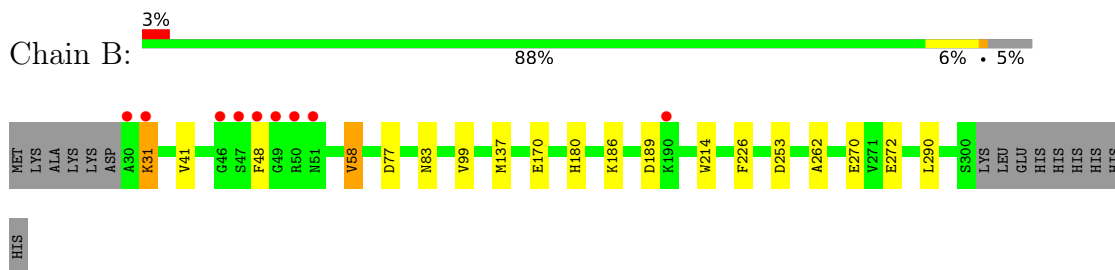
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	125	Total	O	0	0
			125	125		
5	C	144	Total	O	0	0
			144	144		
5	D	122	Total	O	0	0
			122	122		
5	A	124	Total	O	0	0
			124	124		

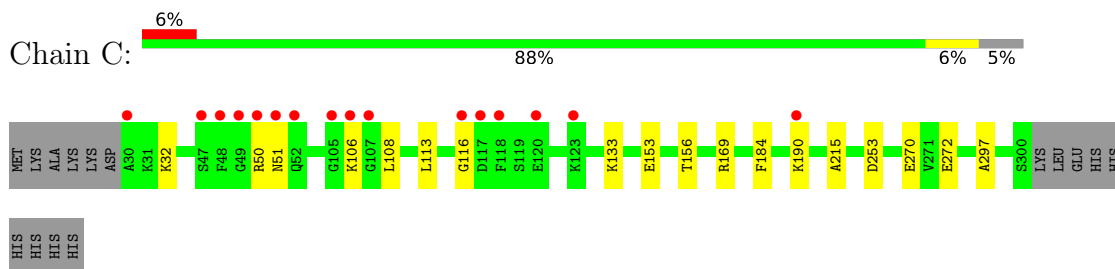
3 Residue-property plots [i](#)

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.

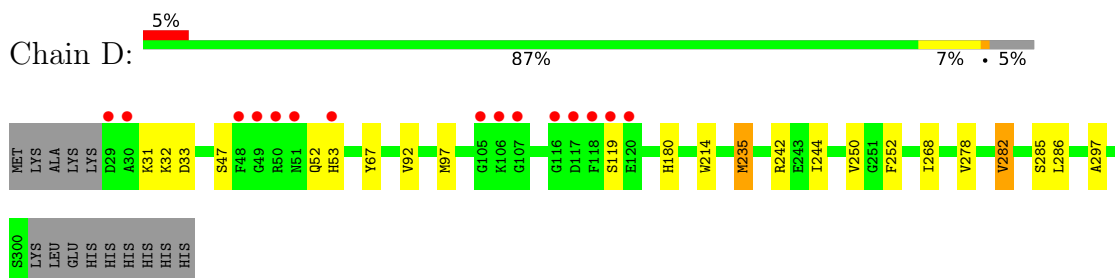
- Molecule 1: Sugar phosphate isomerase



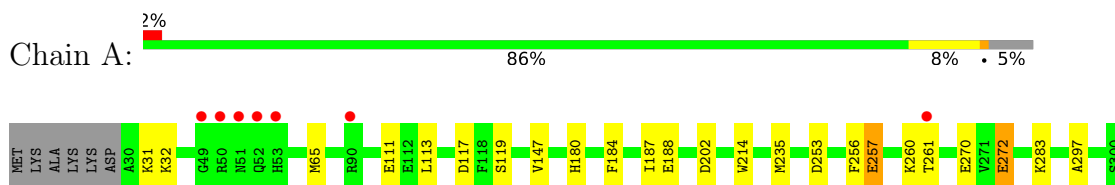
- Molecule 1: Sugar phosphate isomerase



- Molecule 1: Sugar phosphate isomerase



- Molecule 1: Sugar phosphate isomerase



LYS
LEU
GLU
HIS
HIS
HIS
HIS
HIS
HIS

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	47.57Å 112.61Å 209.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.39 – 1.90 46.39 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.9 (46.39-1.90) 99.8 (46.39-1.90)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.92 (at 1.90Å)	Xtriage
Refinement program	REFMAC 5.8.0425	Depositor
R, R_{free}	0.191 , 0.228 0.202 , 0.201	Depositor DCC
R_{free} test set	4421 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	21.0	Xtriage
Anisotropy	0.192	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 32.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9186	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 20.97 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 7.7515e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

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

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	0.60	0/2199	1.08	9/2966 (0.3%)
1	B	0.64	0/2212	1.10	3/2983 (0.1%)
1	C	0.61	0/2205	1.05	7/2974 (0.2%)
1	D	0.61	0/2226	1.04	4/3001 (0.1%)
All	All	0.62	0/8842	1.07	23/11924 (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	C	0	2

There are no bond length outliers.

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	51	ASN	CB-CA-C	-7.38	98.63	110.81
1	B	253	ASP	CA-CB-CG	6.58	119.18	112.60
1	C	253	ASP	CA-CB-CG	6.17	118.77	112.60
1	D	235	MET	CG-SD-CE	-6.15	87.37	100.90
1	A	272	GLU	N-CA-CB	-6.07	102.83	110.90
1	C	51	ASN	N-CA-C	-5.89	98.92	108.41
1	A	256	PHE	CA-CB-CG	-5.87	107.93	113.80
1	D	33	ASP	CA-CB-CG	5.84	118.44	112.60
1	A	184	PHE	CA-CB-CG	-5.75	108.05	113.80
1	A	272	GLU	CB-CG-CD	-5.58	103.11	112.60
1	A	111	GLU	CB-CA-C	-5.45	102.33	110.88
1	A	188	GLU	CB-CA-C	-5.43	103.13	111.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	116	GLY	N-CA-C	-5.42	108.16	115.36
1	B	48	PHE	N-CA-CB	5.40	119.25	110.77
1	A	253	ASP	CA-CB-CG	5.32	117.92	112.60
1	B	58	VAL	N-CA-CB	5.19	117.60	110.54
1	A	235	MET	CG-SD-CE	-5.16	89.55	100.90
1	C	106	LYS	CB-CA-C	5.11	119.11	110.79
1	A	117	ASP	CA-CB-CG	5.11	117.71	112.60
1	C	156	THR	CA-CB-OG1	-5.07	101.99	109.60
1	C	51	ASN	N-CA-CB	5.07	118.27	110.21
1	D	242	ARG	CB-CA-C	5.05	120.46	110.42
1	D	31	LYS	N-CA-CB	-5.01	102.75	110.12

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	169	ARG	Sidechain
1	C	50	ARG	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	2148	0	2076	12	0
1	B	2160	0	2091	7	0
1	C	2153	0	2081	5	0
1	D	2174	0	2106	11	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	6	0	8	2	0
3	B	6	0	8	0	0
3	C	6	0	8	0	0
3	D	6	0	8	0	0
4	A	4	0	3	0	0
4	B	4	0	3	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	124	0	0	8	0
5	B	125	0	0	1	0
5	C	144	0	0	0	0
5	D	122	0	0	1	0
All	All	9186	0	8392	37	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 2.

All (37) 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:202:ASP:HB2	5:A:605:HOH:O	1.71	0.89
3:A:402:GOL:H32	5:A:611:HOH:O	1.77	0.85
1:B:170:GLU:OE1	5:B:501:HOH:O	2.12	0.66
1:C:32:LYS:HG2	1:C:297:ALA:HA	1.78	0.65
1:D:235:MET:HE1	1:D:268:ILE:HD11	1.82	0.61
1:A:257:GLU:HG3	5:A:542:HOH:O	2.01	0.61
3:A:402:GOL:O2	5:A:501:HOH:O	2.12	0.61
1:A:119:SER:O	5:A:502:HOH:O	2.17	0.57
1:A:31:LYS:HG2	1:A:32:LYS:HG3	1.90	0.53
1:B:180:HIS:C	1:B:214:TRP:HB3	2.33	0.53
1:D:235:MET:CE	1:D:268:ILE:HD11	2.39	0.53
1:D:52:GLN:HG3	1:D:53:HIS:CD2	2.44	0.52
1:B:99:VAL:CG1	1:B:137:MET:HE2	2.41	0.50
1:A:180:HIS:C	1:A:214:TRP:HB3	2.37	0.50
1:A:261:THR:HG23	5:A:612:HOH:O	2.12	0.50
1:B:41:VAL:HB	1:B:58:VAL:HG21	1.94	0.49
1:D:278:VAL:O	1:D:282:VAL:HG13	2.14	0.46
1:A:260:LYS:HB3	5:A:585:HOH:O	2.17	0.46
1:D:92:VAL:HG12	1:D:97:MET:O	2.16	0.45
1:D:67:TYR:CZ	1:D:286:LEU:HB2	2.52	0.45
1:C:270:GLU:OE2	1:C:272:GLU:OE2	2.34	0.45
1:A:260:LYS:HA	5:A:616:HOH:O	2.16	0.45
1:C:184:PHE:CE2	1:C:215:ALA:HA	2.54	0.43
1:D:244:ILE:HG12	1:D:285:SER:HB3	2.00	0.43
1:D:180:HIS:C	1:D:214:TRP:HB3	2.44	0.43
1:B:31:LYS:HD3	1:B:290:LEU:HB3	2.01	0.42
1:C:113:LEU:HG	1:C:153:GLU:HG2	2.02	0.42
1:D:250:VAL:HG11	1:D:252:PHE:CE1	2.55	0.41
1:D:32:LYS:HG2	1:D:297:ALA:HA	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:119:SER:HB2	5:D:596:HOH:O	2.21	0.41
1:C:108:LEU:HD23	1:C:108:LEU:HA	1.88	0.41
1:A:65:MET:HG2	1:A:283:LYS:HD3	2.02	0.41
1:A:270:GLU:OE2	1:A:272:GLU:OE2	2.39	0.41
1:A:147:VAL:HG13	1:A:187:ILE:CD1	2.50	0.40
1:B:270:GLU:OE1	1:B:272:GLU:HG3	2.21	0.40
1:B:226:PHE:CG	1:B:262:ALA:HB2	2.56	0.40
1:A:32:LYS:HG2	1:A:297:ALA:HA	2.04	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	269/286 (94%)	260 (97%)	9 (3%)	0	100	100
1	B	269/286 (94%)	259 (96%)	10 (4%)	0	100	100
1	C	269/286 (94%)	262 (97%)	7 (3%)	0	100	100
1	D	270/286 (94%)	262 (97%)	8 (3%)	0	100	100
All	All	1077/1144 (94%)	1043 (97%)	34 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	225/243 (93%)	223 (99%)	2 (1%)	70	73
1	B	228/243 (94%)	223 (98%)	5 (2%)	45	42
1	C	226/243 (93%)	224 (99%)	2 (1%)	70	73
1	D	230/243 (95%)	228 (99%)	2 (1%)	70	73
All	All	909/972 (94%)	898 (99%)	11 (1%)	63	63

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	31	LYS
1	B	77	ASP
1	B	83	ASN
1	B	186	LYS
1	B	189	ASP
1	C	133	LYS
1	C	190	LYS
1	D	47	SER
1	D	282	VAL
1	A	113	LEU
1	A	257	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	127	GLN
1	C	53	HIS
1	C	76	ASN
1	C	155	GLN
1	C	178	HIS
1	C	185	GLN
1	C	273	GLN
1	D	51	ASN
1	D	53	HIS

5.3.3 RNA ⓘ

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](#)

Of 10 ligands modelled in this entry, 4 are monoatomic - leaving 6 for Mogul analysis.

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	A	402	-	5,5,5	0.04	0	5,5,5	0.19	0
3	GOL	B	402	-	5,5,5	0.15	0	5,5,5	0.31	0
4	ACT	B	403	-	3,3,3	1.43	0	3,3,3	0.84	0
3	GOL	D	402	-	5,5,5	0.08	0	5,5,5	0.22	0
3	GOL	C	402	-	5,5,5	0.13	0	5,5,5	0.55	0
4	ACT	A	403	-	3,3,3	1.01	0	3,3,3	0.65	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	D	402	-	-	0/4/4/4	-
3	GOL	A	402	-	-	0/4/4/4	-
3	GOL	B	402	-	-	0/4/4/4	-
3	GOL	C	402	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	402	GOL	O1-C1-C2-C3
3	C	402	GOL	C1-C2-C3-O3
3	C	402	GOL	O1-C1-C2-O2
3	C	402	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	402	GOL	2	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	271/286 (94%)	-0.02	7 (2%) 57 61	14, 21, 43, 65	0
1	B	271/286 (94%)	0.01	9 (3%) 49 52	14, 22, 42, 61	0
1	C	271/286 (94%)	0.05	16 (5%) 28 30	14, 22, 43, 85	0
1	D	272/286 (95%)	0.08	15 (5%) 30 32	14, 21, 43, 74	0
All	All	1085/1144 (94%)	0.03	47 (4%) 40 42	14, 21, 43, 85	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	51	ASN	5.3
1	C	30	ALA	5.0
1	B	30	ALA	4.8
1	A	53	HIS	4.6
1	C	48	PHE	4.6
1	C	50	ARG	4.3
1	B	48	PHE	4.1
1	D	48	PHE	4.1
1	A	52	GLN	4.1
1	C	116	GLY	3.9
1	D	120	GLU	3.8
1	D	49	GLY	3.8
1	D	51	ASN	3.8
1	A	51	ASN	3.7
1	C	120	GLU	3.6
1	C	47	SER	3.4
1	C	117	ASP	3.3
1	B	47	SER	3.3
1	C	49	GLY	3.3
1	D	29	ASP	3.2
1	C	105	GLY	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	46	GLY	3.1
1	B	190	LYS	2.9
1	D	119	SER	2.9
1	C	190	LYS	2.8
1	D	117	ASP	2.8
1	A	261	THR	2.8
1	B	49	GLY	2.7
1	D	105	GLY	2.6
1	C	106	LYS	2.6
1	D	118	PHE	2.6
1	B	50	ARG	2.6
1	C	118	PHE	2.6
1	A	50	ARG	2.6
1	A	49	GLY	2.5
1	B	51	ASN	2.5
1	D	30	ALA	2.5
1	D	116	GLY	2.5
1	C	52	GLN	2.4
1	C	107	GLY	2.4
1	D	106	LYS	2.4
1	B	31	LYS	2.3
1	C	123	LYS	2.2
1	D	50	ARG	2.2
1	A	90	ARG	2.1
1	D	53	HIS	2.1
1	D	107	GLY	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	GOL	A	402	6/6	0.85	0.14	35,43,46,49	0
4	ACT	B	403	4/4	0.87	0.12	23,26,27,29	0
4	ACT	A	403	4/4	0.88	0.15	28,29,30,35	0
3	GOL	B	402	6/6	0.89	0.11	27,36,38,42	0
2	CO	A	401	1/1	0.91	0.16	62,62,62,62	1
3	GOL	C	402	6/6	0.93	0.08	21,25,27,27	0
3	GOL	D	402	6/6	0.94	0.07	21,27,27,30	0
2	CO	B	401	1/1	0.94	0.14	57,57,57,57	1
2	CO	D	401	1/1	0.97	0.15	52,52,52,52	1
2	CO	C	401	1/1	0.97	0.12	51,51,51,51	1

6.5 Other polymers [i](#)

There are no such residues in this entry.