



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:39 PM UTC

PDB ID : 4LGL / pdb_00004lgl
Title : Crystal Structure of Glycine Decarboxylase P-protein from Synechocystis sp. PCC 6803, apo form
Authors : Hasse, D.; Andersson, E.; Carlsson, G.; Masloboy, A.; Hagemann, M.; Bauwe, H.; Andersson, I.
Deposited on : 2013-06-28
Resolution : 2.00 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

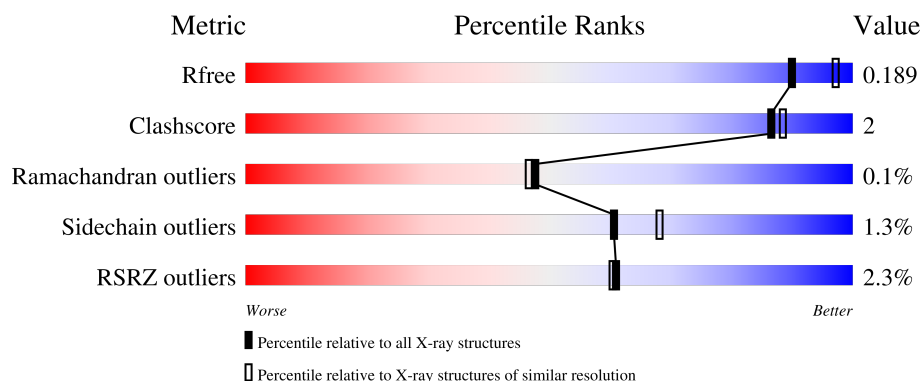
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	983	3% 90% 7%
1	B	983	2% 89% 6% 5%

2 Entry composition [i](#)

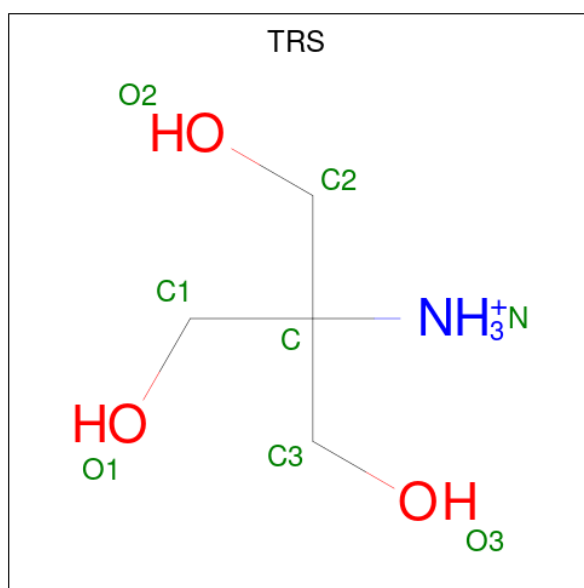
There are 4 unique types of molecules in this entry. The entry contains 15465 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Glycine dehydrogenase [decarboxylating].

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	948	Total	C	N	O	S	0	7	0
			7337	4656	1248	1387	46			
1	B	930	Total	C	N	O	S	0	15	0
			7245	4605	1226	1365	49			

- Molecule 2 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS) (formula: C₄H₁₂NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			8	4	1	3		
2	B	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total 1	Cl 1	0	0
3	B	1	Total 1	Cl 1	0	0

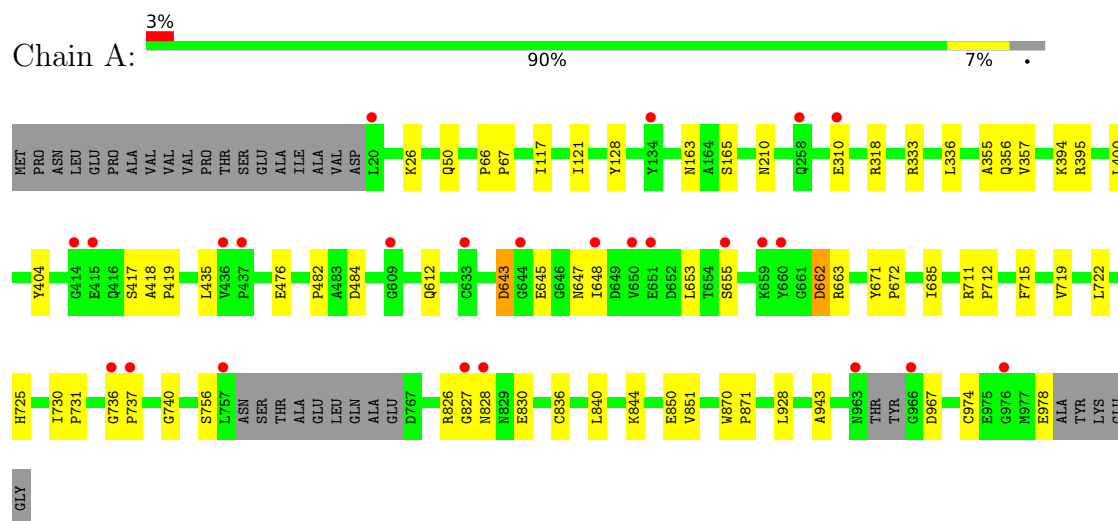
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	405	Total 405	O 405	0	0
4	B	460	Total 460	O 460	0	0

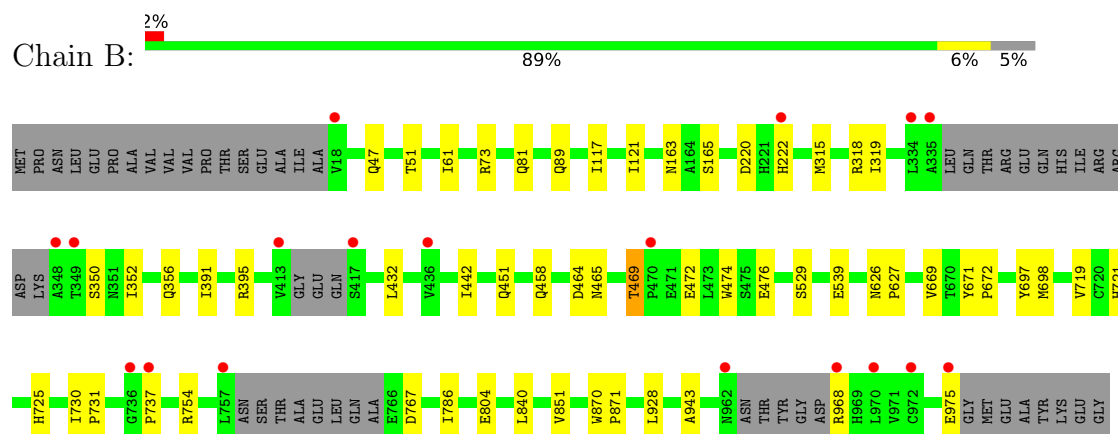
3 Residue-property plots [i](#)

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: Glycine dehydrogenase [decarboxylating]



- Molecule 1: Glycine dehydrogenase [decarboxylating]



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	96.30Å 135.81Å 179.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	54.11 – 2.00 54.11 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (54.11-2.00) 99.8 (54.11-2.00)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.07 (at 2.00Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.161 , 0.192 0.158 , 0.189	Depositor DCC
R_{free} test set	7941 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	32.9	Xtriage
Anisotropy	0.420	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 45.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	15465	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.25% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: TRS, CL, CME

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	0.42	0/7485	0.76	5/10172 (0.0%)
1	B	0.43	0/7397	0.73	0/10052
All	All	0.43	0/14882	0.75	5/20224 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	210	ASN	CA-C-N	-5.59	114.06	119.87
1	A	210	ASN	C-N-CA	-5.59	114.06	119.87
1	A	357	VAL	N-CA-C	5.29	115.92	110.36
1	A	711	ARG	CA-C-N	5.00	124.44	119.24
1	A	711	ARG	C-N-CA	5.00	124.44	119.24

There are no chirality outliers.

There are no planarity outliers.

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	7337	0	7213	30	0
1	B	7245	0	7128	32	0
2	A	8	0	12	0	0
2	B	8	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	405	0	0	0	0
4	B	460	0	0	2	0
All	All	15465	0	14365	61	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 (61) 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:B:73[B]:ARG:NH2	4:B:1531:HOH:O	2.21	0.73
1:A:612:GLN:O	1:A:663:ARG:NH1	2.22	0.72
1:B:754:ARG:NH2	1:B:767:ASP:OD1	2.23	0.71
1:A:394:LYS:HE2	1:A:400:LEU:HD12	1.73	0.70
1:A:662:ASP:N	1:A:662:ASP:OD1	2.26	0.68
1:A:643:ASP:HB3	1:A:645:GLU:H	1.60	0.66
1:A:395:ARG:NH2	1:A:476:GLU:OE2	2.30	0.64
1:B:356:GLN:OE1	1:B:737[B]:PRO:HB3	1.99	0.62
1:B:395:ARG:NH1	4:B:1466:HOH:O	2.35	0.59
1:B:870:TRP:CD1	1:B:871:PRO:HA	2.38	0.59
1:B:315:MET:SD	1:B:319[B]:ILE:HD11	2.46	0.56
1:A:840:LEU:HD22	1:A:851:VAL:HG23	1.90	0.53
1:A:870:TRP:CD1	1:A:871:PRO:HA	2.42	0.53
1:B:117:ILE:HG23	1:B:121:ILE:HD12	1.91	0.53
1:B:725:HIS:HA	1:B:730:ILE:HB	1.91	0.52
1:B:163:ASN:HA	1:B:319[B]:ILE:HG12	1.92	0.51
1:B:451:GLN:OE1	1:B:451:GLN:N	2.39	0.51
1:A:643:ASP:HB2	1:A:647:ASN:H	1.75	0.50
1:A:356:GLN:OE1	1:A:737[B]:PRO:HB3	2.11	0.50
1:B:697:TYR:OH	1:B:721:HIS:ND1	2.40	0.50
1:A:404:TYR:CG	1:A:482:PRO:HD3	2.47	0.50
1:B:458:GLN:HG2	1:B:464:ASP:HA	1.95	0.49
1:B:928:LEU:CD1	1:B:943:ALA:HB2	2.43	0.48
1:B:626:ASN:HB2	1:B:627:PRO:HD3	1.94	0.48
1:B:671:TYR:HA	1:B:672:PRO:C	2.38	0.47
1:B:870:TRP:CG	1:B:871:PRO:HA	2.49	0.46
1:B:469:THR:O	1:B:472:GLU:HB3	2.16	0.46
1:B:840:LEU:HD22	1:B:851:VAL:HG23	1.98	0.46
1:A:435:LEU:HA	1:A:435:LEU:HD23	1.73	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:418:ALA:HB3	1:A:419:PRO:HD3	1.98	0.45
1:A:671:TYR:HA	1:A:672:PRO:C	2.41	0.45
1:A:712:PRO:HA	1:A:715:PHE:CE2	2.52	0.45
1:B:220:ASP:OD1	1:B:222:HIS:ND1	2.48	0.45
1:B:163:ASN:HB2	1:B:318:ARG:O	2.17	0.45
1:A:26:LYS:HD3	1:B:474:TRP:CD1	2.53	0.44
1:A:117:ILE:HG23	1:A:121:ILE:HD12	2.00	0.44
1:A:826:ARG:HD3	1:A:830:GLU:HB3	1.98	0.44
1:A:725:HIS:HA	1:A:730:ILE:HB	1.99	0.44
1:A:163:ASN:HB2	1:A:318:ARG:O	2.18	0.43
1:B:81:GLN:NE2	1:B:89:GLN:OE1	2.39	0.43
1:A:355:ALA:O	1:A:736[A]:GLY:HA2	2.18	0.43
1:B:61:ILE:HG13	1:B:804:GLU:HG2	2.01	0.43
1:B:350:SER:OG	1:B:352:ILE:HG22	2.18	0.42
1:A:333:ARG:HH22	1:A:978:GLU:CD	2.27	0.42
1:A:928:LEU:CD1	1:A:943:ALA:HB2	2.49	0.42
1:A:128:TYR:O	1:A:731:PRO:HB2	2.19	0.42
1:A:827:GLY:HA3	1:A:828:ASN:HB2	2.02	0.42
1:B:539:GLU:HB3	1:B:786:ILE:HG23	2.00	0.42
1:A:844:LYS:HE3	1:A:850:GLU:OE2	2.19	0.42
1:B:391:ILE:HD13	1:B:476:GLU:HB2	2.02	0.42
1:B:469:THR:HG23	1:B:472:GLU:HB2	2.00	0.42
1:A:722:LEU:O	1:A:740:GLY:HA2	2.21	0.41
1:B:47:GLN:O	1:B:51:THR:HG23	2.20	0.41
1:B:697:TYR:HH	1:B:721:HIS:HD1	1.61	0.41
1:A:336:LEU:O	1:A:978:GLU:HG2	2.20	0.41
1:A:643:ASP:HB2	1:A:647:ASN:N	2.36	0.41
1:A:66:PRO:HA	1:A:67:PRO:HD3	1.93	0.41
1:B:432:LEU:HD22	1:B:442:ILE:HG12	2.03	0.41
1:B:669:VAL:O	1:B:698:MET:HA	2.21	0.41
1:B:731:PRO:HD2	1:B:786:ILE:HD13	2.02	0.41
1:A:826:ARG:HB3	1:A:830:GLU:HA	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	947/983 (96%)	923 (98%)	23 (2%)	1 (0%)	48	46
1	B	933/983 (95%)	911 (98%)	21 (2%)	1 (0%)	48	46
All	All	1880/1966 (96%)	1834 (98%)	44 (2%)	2 (0%)	48	46

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	165	SER
1	B	165	SER

5.3.2 Protein sidechains ⓘ

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	773/797 (97%)	759 (98%)	14 (2%)	51	58
1	B	766/797 (96%)	760 (99%)	6 (1%)	73	80
All	All	1539/1594 (96%)	1519 (99%)	20 (1%)	61	68

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	50	GLN
1	A	310	GLU
1	A	417	SER
1	A	484	ASP
1	A	643	ASP
1	A	648	ILE
1	A	653	LEU
1	A	655	SER
1	A	662	ASP
1	A	685	ILE

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Mol	Chain	Res	Type
1	A	719	VAL
1	A	756	SER
1	A	836	CYS
1	A	967	ASP
1	B	465	ASN
1	B	469	THR
1	B	529	SER
1	B	719	VAL
1	B	968	ARG
1	B	975	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	47	GLN
1	A	222	HIS
1	A	416	GLN
1	A	511	HIS
1	A	626	ASN
1	A	951	GLN
1	B	45	GLN
1	B	98	GLN
1	B	431	ASN
1	B	465	ASN
1	B	511	HIS
1	B	559	GLN
1	B	592	GLN
1	B	626	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

4 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	CME	A	642	1	8,9,10	1.04	0	6,9,11	1.37	0
1	CME	A	974	1	8,9,10	1.11	0	6,9,11	1.47	1 (16%)
1	CME	B	974	1	8,9,10	1.01	0	6,9,11	1.25	0
1	CME	B	642	1	8,9,10	1.07	0	6,9,11	1.38	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	CME	A	642	1	-	2/5/8/10	-
1	CME	A	974	1	-	2/5/8/10	-
1	CME	B	974	1	-	2/5/8/10	-
1	CME	B	642	1	-	1/5/8/10	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	974	CME	CB-SG-SD	2.54	110.44	103.86

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	642	CME	CA-CB-SG-SD
1	B	642	CME	CA-CB-SG-SD
1	A	642	CME	CZ-CE-SD-SG
1	A	974	CME	CZ-CE-SD-SG
1	A	974	CME	CA-CB-SG-SD
1	B	974	CME	SD-CE-CZ-OH
1	B	974	CME	CA-CB-SG-SD

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	$\# Z > 2$
2	TRS	B	1001	-	7,7,7	0.31	0	9,9,9	0.30	0
2	TRS	A	1001	-	7,7,7	0.30	0	9,9,9	0.49	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
2	TRS	B	1001	-	-	3/9/9/9	-
2	TRS	A	1001	-	-	2/9/9/9	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1001	TRS	C3-C-C2-O2
2	B	1001	TRS	N-C-C2-O2
2	B	1001	TRS	C1-C-C2-O2
2	A	1001	TRS	C1-C-C3-O3
2	A	1001	TRS	C2-C-C3-O3

There are no ring outliers.

No monomer is involved in short contacts.

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	946/983 (96%)	-0.12	25 (2%) 57 56	12, 39, 72, 111	9 (0%)
1	B	928/983 (94%)	-0.27	18 (1%) 66 66	14, 35, 65, 102	15 (1%)
All	All	1874/1966 (95%)	-0.19	43 (2%) 61 60	12, 37, 69, 111	24 (1%)

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	413	VAL	5.6
1	B	335	ALA	5.4
1	B	18	VAL	5.3
1	A	963	ASN	4.6
1	B	737[A]	PRO	4.4
1	A	414	GLY	3.9
1	A	827	GLY	3.9
1	B	348	ALA	3.8
1	A	737[A]	PRO	3.7
1	B	349	THR	3.7
1	A	651	GLU	3.4
1	A	648	ILE	3.4
1	B	736[A]	GLY	3.3
1	A	966	GLY	3.1
1	A	644	GLY	3.0
1	B	417	SER	2.9
1	A	20	LEU	2.9
1	A	660	TYR	2.8
1	A	757	LEU	2.8
1	B	436	VAL	2.8
1	B	968	ARG	2.6
1	A	310	GLU	2.6
1	B	975	GLU	2.6
1	A	659	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	655	SER	2.5
1	B	970	LEU	2.4
1	B	222	HIS	2.4
1	A	828	ASN	2.4
1	A	437	PRO	2.4
1	A	415	GLU	2.4
1	B	470	PRO	2.3
1	A	633	CYS	2.3
1	B	962	ASN	2.2
1	A	736[A]	GLY	2.2
1	B	972	CYS	2.2
1	B	757	LEU	2.2
1	A	436	VAL	2.2
1	B	334	LEU	2.1
1	A	258	GLN	2.1
1	A	650	VAL	2.1
1	A	134	TYR	2.1
1	A	609	GLY	2.1
1	A	976	GLY	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
1	CME	A	642	10/11	0.88	0.12	50,62,67,71	2
1	CME	B	974	10/11	0.92	0.15	43,53,70,71	2
1	CME	A	974	10/11	0.94	0.11	45,48,69,73	0
1	CME	B	642	10/11	0.95	0.10	39,54,60,65	0

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
2	TRS	B	1001	8/8	0.92	0.09	31,39,43,49	0
2	TRS	A	1001	8/8	0.93	0.10	48,54,57,60	0
3	CL	A	1002	1/1	0.96	0.06	48,48,48,48	0
3	CL	B	1002	1/1	0.98	0.05	33,33,33,33	1

6.5 Other polymers ⓘ

There are no such residues in this entry.