



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:55 AM UTC

PDB ID : 4O99 / pdb_00004o99
Title : Crystal structure of Beta-ketothiolase (PhaA) from Ralstonia eutropha H16
Authors : Kim, E.J.; Kim, J.; Kim, S.; Kim, K.J.
Deposited on : 2014-01-02
Resolution : 1.96 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

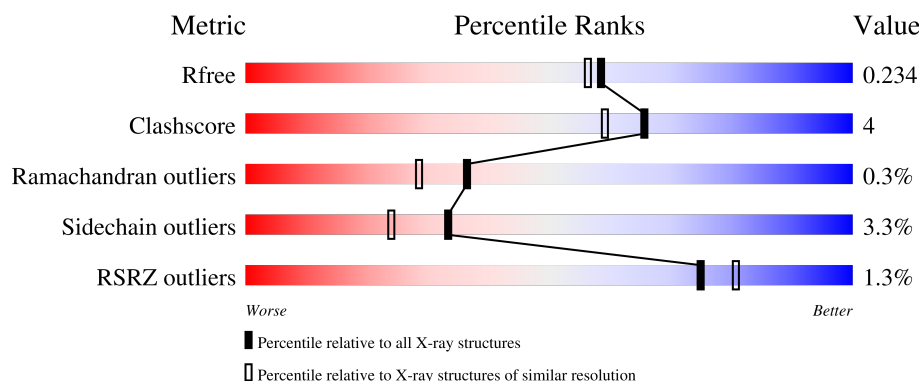
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.96 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	392	3% 91% 8%
1	B	392	% 89% 9%
1	C	392	% 89% 10%
1	D	392	% 88% 11%

2 Entry composition [i](#)

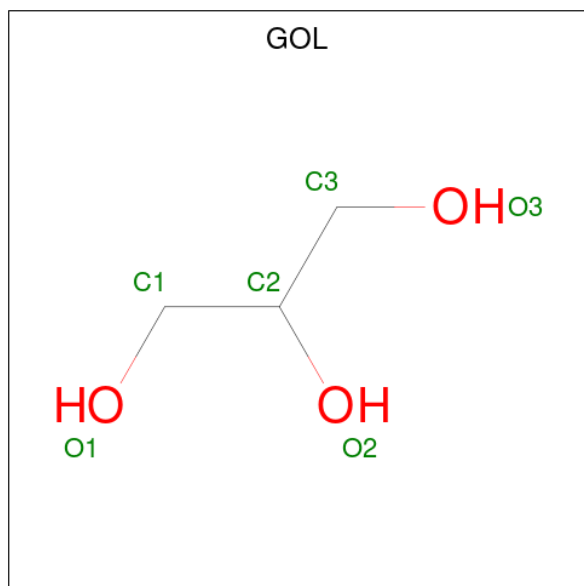
There are 3 unique types of molecules in this entry. The entry contains 12325 atoms, of which 0 are hydrogens and 0 are deuteriums.

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
			2827	1769	501	537	20			
1	B	392	Total	C	N	O	S	0	0	0
			2827	1769	501	537	20			
1	C	392	Total	C	N	O	S	0	0	0
			2826	1769	501	536	20			
1	D	392	Total	C	N	O	S	0	0	0
			2827	1769	501	537	20			

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

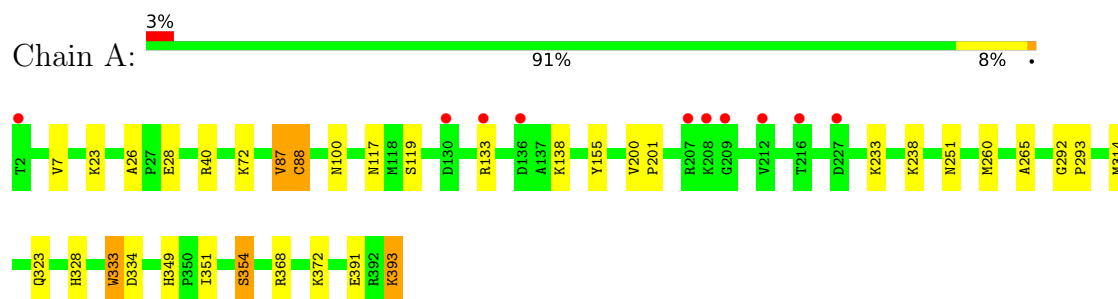
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	254	Total 254	O 254	0	0
3	B	249	Total 249	O 249	0	0
3	C	255	Total 255	O 255	0	0
3	D	248	Total 248	O 248	0	0

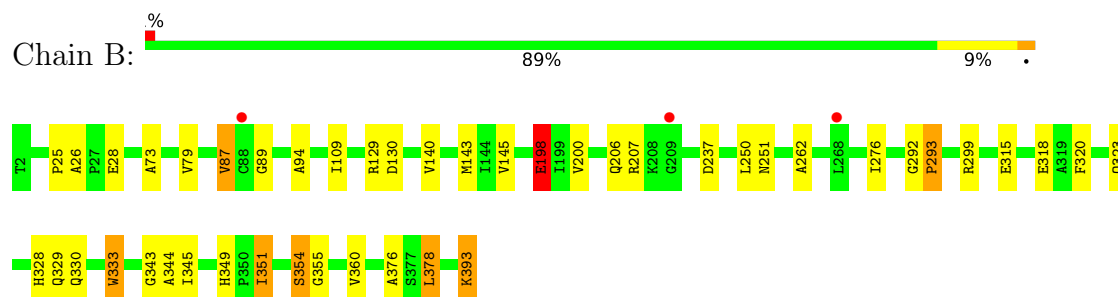
3 Residue-property plots [i](#)

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.

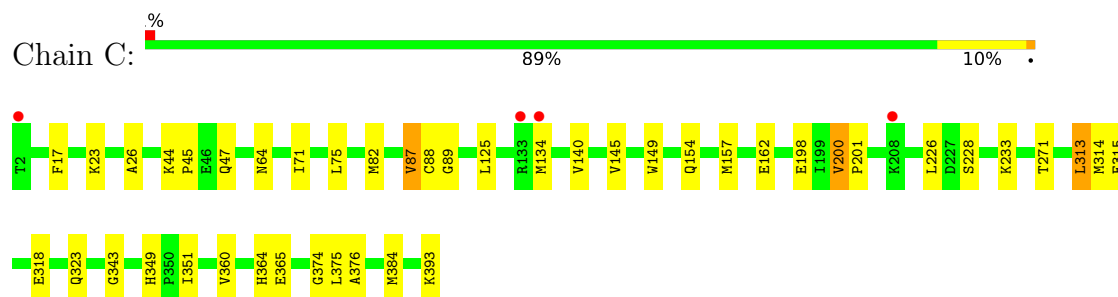
- Molecule 1: Acetyl-CoA acetyltransferase



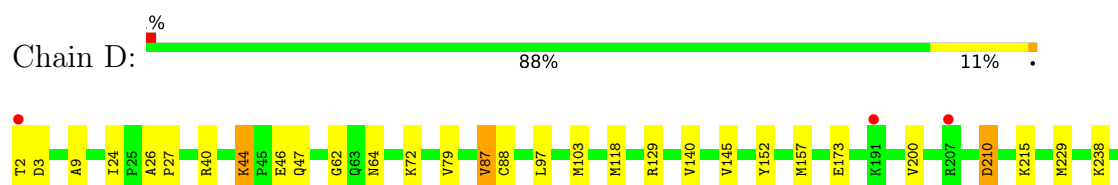
- Molecule 1: Acetyl-CoA acetyltransferase

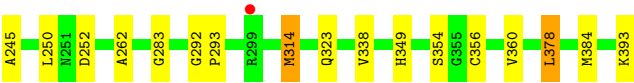


- Molecule 1: Acetyl-CoA acetyltransferase



- Molecule 1: Acetyl-CoA acetyltransferase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	68.38Å 105.47Å 106.91Å 90.00° 106.18° 90.00°	Depositor
Resolution (Å)	30.62 – 1.96 30.62 – 1.96	Depositor EDS
% Data completeness (in resolution range)	94.4 (30.62-1.96) 94.5 (30.62-1.96)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	15.71 (at 1.96Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.171 , 0.230 0.183 , 0.234	Depositor DCC
R_{free} test set	4918 reflections (4.74%)	wwPDB-VP
Wilson B-factor (Å ²)	16.8	Xtriage
Anisotropy	1.094	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 40.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.013 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12325	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.04% 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

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	1.23	4/2867 (0.1%)	1.14	8/3876 (0.2%)
1	B	1.28	8/2867 (0.3%)	1.14	4/3876 (0.1%)
1	C	1.22	3/2866 (0.1%)	1.12	5/3876 (0.1%)
1	D	1.20	5/2867 (0.2%)	1.11	5/3876 (0.1%)
All	All	1.23	20/11467 (0.2%)	1.13	22/15504 (0.1%)

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	162	GLU	N-CA	6.88	1.54	1.46
1	A	100	ASN	CA-C	6.26	1.60	1.52
1	B	79	VAL	N-CA	6.07	1.51	1.46
1	D	79	VAL	N-CA	5.89	1.50	1.46
1	B	262	ALA	N-CA	5.81	1.53	1.46
1	B	200	VAL	N-CA	5.79	1.51	1.46
1	B	94	ALA	N-CA	5.71	1.53	1.46
1	C	26	ALA	C-O	-5.69	1.19	1.24
1	A	334	ASP	C-O	5.50	1.30	1.24
1	A	26	ALA	CA-C	5.49	1.59	1.52
1	B	293	PRO	C-O	-5.38	1.17	1.24
1	D	283	GLY	N-CA	-5.23	1.40	1.45
1	C	89	GLY	C-O	-5.22	1.17	1.23
1	A	100	ASN	CA-CB	-5.20	1.45	1.53
1	D	24	ILE	N-CA	-5.17	1.42	1.46
1	B	26	ALA	C-O	-5.15	1.19	1.24
1	B	109	ILE	CA-CB	5.13	1.60	1.54
1	B	276	ILE	N-CA	-5.12	1.40	1.46
1	D	62	GLY	N-CA	5.09	1.50	1.45
1	D	79	VAL	CA-C	5.04	1.57	1.53

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	271	THR	CA-C-N	-8.94	111.55	120.31
1	C	271	THR	C-N-CA	-8.94	111.55	120.31
1	A	351	ILE	N-CA-C	7.93	118.69	110.36
1	C	351	ILE	N-CA-C	7.70	118.24	110.23
1	B	198	GLU	CB-CA-C	-7.50	98.09	110.85
1	B	354	SER	N-CA-C	7.19	120.03	111.33
1	B	351	ILE	N-CA-C	6.33	117.00	110.36
1	A	88	CYS	N-CA-C	6.29	120.06	112.38
1	D	79	VAL	N-CA-C	6.23	113.22	107.56
1	A	368	ARG	NE-CZ-NH2	5.72	124.35	119.20
1	D	356	CYS	N-CA-C	-5.57	105.60	112.90
1	A	354	SER	N-CA-C	5.40	118.66	111.75
1	A	233	LYS	CA-C-N	5.29	125.21	119.76
1	A	233	LYS	C-N-CA	5.29	125.21	119.76
1	D	40	ARG	N-CA-C	5.26	117.01	111.28
1	A	265	ALA	CA-C-N	5.21	127.22	120.44
1	A	265	ALA	C-N-CA	5.21	127.22	120.44
1	D	354	SER	N-CA-C	5.13	117.53	111.33
1	D	250	LEU	N-CA-C	-5.11	100.19	108.52
1	C	134	MET	N-CA-C	5.08	116.78	108.55
1	B	89	GLY	N-CA-C	-5.05	108.71	115.32
1	C	198	GLU	N-CA-C	5.04	118.58	112.23

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	2827	0	2895	19	0
1	B	2827	0	2895	26	0
1	C	2826	0	2895	23	0
1	D	2827	0	2895	26	0
2	A	6	0	8	0	0
2	C	6	0	8	0	0
3	A	254	0	0	1	0
3	B	249	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	255	0	0	1	0
3	D	248	0	0	2	0
All	All	12325	0	11596	86	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 4.

All (86) 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:D:103:MET:HG2	3:D:572:HOH:O	1.35	1.22
1:D:140:VAL:HG11	1:D:145:VAL:HG21	1.68	0.75
1:B:328:HIS:HD2	1:B:333:TRP:HE1	1.35	0.73
1:D:140:VAL:CG1	1:D:145:VAL:HG21	2.21	0.70
1:C:45:PRO:HB3	1:C:75:LEU:HD23	1.77	0.66
1:B:328:HIS:CD2	1:B:333:TRP:HE1	2.14	0.64
1:B:393:LYS:HE2	1:B:393:LYS:H	1.62	0.64
1:C:149:TRP:HE1	1:C:154:GLN:NE2	1.97	0.63
1:C:88:CYS:SG	1:C:349:HIS:NE2	2.72	0.63
1:B:393:LYS:H	1:B:393:LYS:CE	2.10	0.62
1:B:329:GLN:HE21	1:B:330:GLN:HE21	1.49	0.60
1:D:88:CYS:SG	1:D:349:HIS:CE1	2.95	0.60
1:A:23:LYS:NZ	1:B:130:ASP:OD2	2.36	0.58
1:B:198:GLU:HG2	1:B:360:VAL:HG12	1.86	0.58
1:C:88:CYS:SG	1:C:349:HIS:CE1	2.96	0.58
1:A:251:ASN:ND2	1:A:349:HIS:H	2.03	0.56
1:D:3:ASP:OD1	1:D:262:ALA:HB2	2.05	0.56
1:B:349:HIS:HD2	1:B:354:SER:OG	1.91	0.54
1:B:251:ASN:ND2	1:B:349:HIS:H	2.06	0.53
1:A:133:ARG:NH1	3:A:559:HOH:O	2.33	0.53
1:C:44:LYS:H	1:C:47:GLN:NE2	2.07	0.53
1:C:313:LEU:HD21	1:C:365:GLU:HG3	1.92	0.52
1:A:251:ASN:HD22	1:A:349:HIS:H	1.58	0.52
1:B:299:ARG:HG3	3:B:508:HOH:O	2.10	0.51
1:A:88:CYS:SG	1:A:349:HIS:NE2	2.81	0.50
1:A:393:LYS:HA	1:A:393:LYS:CE	2.42	0.49
1:B:355:GLY:HA2	1:B:378:LEU:HD11	1.94	0.49
1:C:364:HIS:HE1	3:C:565:HOH:O	1.95	0.49
1:A:40:ARG:NH2	1:A:200:VAL:HG12	2.28	0.49
1:C:64:ASN:ND2	1:D:384:MET:HE1	2.27	0.49
1:B:251:ASN:HD22	1:B:349:HIS:H	1.60	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:73:ALA:O	3:B:538:HOH:O	2.20	0.48
1:C:318:GLU:CD	1:C:343:GLY:HA3	2.39	0.48
1:D:44:LYS:H	1:D:47:GLN:HE21	1.60	0.48
1:A:7:VAL:HG21	1:A:260:MET:HE3	1.96	0.48
1:B:320:PHE:H	1:B:323:GLN:HE21	1.62	0.47
1:C:64:ASN:HD22	1:D:384:MET:HE1	1.79	0.47
1:D:88:CYS:SG	1:D:349:HIS:NE2	2.87	0.47
1:C:88:CYS:HG	1:C:349:HIS:CE1	2.28	0.47
1:A:40:ARG:NH2	1:A:200:VAL:CG1	2.77	0.47
1:D:88:CYS:HG	1:D:349:HIS:CE1	2.33	0.46
1:B:25:PRO:HD2	1:B:28:GLU:CD	2.41	0.46
1:A:372:LYS:O	1:A:391:GLU:HA	2.15	0.46
1:C:140:VAL:CG1	1:C:145:VAL:HG21	2.46	0.46
1:A:349:HIS:HD2	1:A:354:SER:OG	1.99	0.46
1:C:140:VAL:HG11	1:C:145:VAL:HG21	1.97	0.45
1:D:378:LEU:HD12	1:D:378:LEU:N	2.32	0.45
1:A:28:GLU:HG2	1:A:72:LYS:HD3	1.99	0.45
1:A:88:CYS:SG	1:A:349:HIS:CE1	3.10	0.44
1:D:9:ALA:HB1	1:D:360:VAL:HG22	1.98	0.44
1:D:314:MET:HB2	1:D:338:VAL:HG22	1.98	0.44
1:B:237:ASP:OD1	1:B:237:ASP:C	2.60	0.43
1:D:72:LYS:HG3	3:D:442:HOH:O	2.19	0.43
1:D:118:MET:N	1:D:252:ASP:OD1	2.50	0.43
1:A:119:SER:O	1:B:129:ARG:HD2	2.18	0.43
1:B:315:GLU:O	1:B:376:ALA:HA	2.18	0.43
1:A:328:HIS:HD2	1:A:333:TRP:HE1	1.65	0.42
1:B:140:VAL:CG1	1:B:145:VAL:HG21	2.49	0.42
1:D:26:ALA:HB3	1:D:27:PRO:HD3	2.02	0.42
1:B:344:ALA:O	1:B:345:ILE:C	2.62	0.42
1:D:157:MET:HA	1:D:157:MET:HE2	2.01	0.42
1:D:229:MET:HG2	1:D:245:ALA:HB1	2.01	0.42
1:B:351:ILE:HD13	1:B:351:ILE:HG21	1.82	0.42
1:C:360:VAL:O	1:C:364:HIS:HD2	2.02	0.42
1:A:40:ARG:HH21	1:A:200:VAL:HG12	1.84	0.42
1:C:157:MET:HA	1:C:157:MET:HE2	2.02	0.42
1:C:71:ILE:HD12	1:D:152:TYR:CZ	2.55	0.42
1:C:82:MET:HE1	1:D:97:LEU:HD21	2.01	0.41
1:A:292:GLY:N	1:A:293:PRO:CD	2.83	0.41
1:C:313:LEU:O	1:C:374:GLY:HA2	2.20	0.41
1:B:292:GLY:N	1:B:293:PRO:CD	2.83	0.41
1:D:292:GLY:N	1:D:293:PRO:CD	2.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:17:PHE:CZ	1:D:129:ARG:HD3	2.56	0.41
1:A:117:ASN:OD1	1:A:117:ASN:C	2.64	0.41
1:B:318:GLU:CD	1:B:343:GLY:HA3	2.46	0.41
1:D:238:LYS:N	1:D:238:LYS:HD3	2.36	0.41
1:C:44:LYS:H	1:C:47:GLN:HE21	1.68	0.41
1:B:140:VAL:HG11	1:B:145:VAL:HG21	2.03	0.41
1:C:200:VAL:HG23	1:C:201:PRO:HD2	2.02	0.41
1:C:315:GLU:O	1:C:376:ALA:HA	2.20	0.41
1:D:88:CYS:O	1:D:378:LEU:HD22	2.21	0.41
1:D:210:ASP:OD1	1:D:210:ASP:N	2.53	0.40
1:B:206:GLN:O	1:B:207:ARG:C	2.64	0.40
1:A:200:VAL:HA	1:A:201:PRO:HD3	1.91	0.40
1:B:143:MET:HE1	1:B:250:LEU:HD13	2.02	0.40
1:C:384:MET:HE1	1:D:64:ASN:ND2	2.36	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	390/392 (100%)	378 (97%)	11 (3%)	1 (0%)	36	28
1	B	390/392 (100%)	379 (97%)	10 (3%)	1 (0%)	36	28
1	C	390/392 (100%)	382 (98%)	7 (2%)	1 (0%)	36	28
1	D	390/392 (100%)	381 (98%)	8 (2%)	1 (0%)	36	28
All	All	1560/1568 (100%)	1520 (97%)	36 (2%)	4 (0%)	36	28

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	87	VAL

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Mol	Chain	Res	Type
1	B	87	VAL
1	C	87	VAL
1	D	87	VAL

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	284/284 (100%)	276 (97%)	8 (3%)	38	30
1	B	284/284 (100%)	279 (98%)	5 (2%)	51	47
1	C	284/284 (100%)	272 (96%)	12 (4%)	26	16
1	D	284/284 (100%)	272 (96%)	12 (4%)	26	16
All	All	1136/1136 (100%)	1099 (97%)	37 (3%)	33	24

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	87	VAL
1	A	138	LYS
1	A	155	TYR
1	A	238	LYS
1	A	314	MET
1	A	323	GLN
1	A	333	TRP
1	A	393	LYS
1	B	87	VAL
1	B	198	GLU
1	B	333	TRP
1	B	378	LEU
1	B	393	LYS
1	C	23	LYS
1	C	87	VAL
1	C	125	LEU
1	C	200	VAL
1	C	226	LEU

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Mol	Chain	Res	Type
1	C	228	SER
1	C	233	LYS
1	C	313	LEU
1	C	314	MET
1	C	323	GLN
1	C	375	LEU
1	C	393	LYS
1	D	2	THR
1	D	44	LYS
1	D	46	GLU
1	D	87	VAL
1	D	173	GLU
1	D	200	VAL
1	D	210	ASP
1	D	215	LYS
1	D	314	MET
1	D	323	GLN
1	D	378	LEU
1	D	393	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	184	ASN
1	A	206	GLN
1	A	251	ASN
1	A	323	GLN
1	A	328	HIS
1	A	329	GLN
1	A	330	GLN
1	A	341	ASN
1	B	64	ASN
1	B	154	GLN
1	B	184	ASN
1	B	206	GLN
1	B	251	ASN
1	B	323	GLN
1	B	328	HIS
1	B	329	GLN
1	B	349	HIS
1	C	47	GLN
1	C	115	GLN

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Mol	Chain	Res	Type
1	C	154	GLN
1	C	190	GLN
1	C	329	GLN
1	C	330	GLN
1	C	364	HIS
1	D	47	GLN
1	D	115	GLN
1	D	154	GLN
1	D	364	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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	GOL	C	401	-	5,5,5	0.57	0	5,5,5	0.60	0
2	GOL	A	401	-	5,5,5	0.46	0	5,5,5	1.57	1 (20%)

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	GOL	C	401	-	-	0/4/4/4	-
2	GOL	A	401	-	-	2/4/4/4	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	GOL	O3-C3-C2	-2.91	97.26	110.38

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	GOL	O1-C1-C2-C3
2	A	401	GOL	O1-C1-C2-O2

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	392/392 (100%)	0.27	10 (2%) 57 64	12, 20, 37, 60	0
1	B	392/392 (100%)	0.21	3 (0%) 82 86	12, 19, 34, 63	0
1	C	392/392 (100%)	0.18	4 (1%) 79 84	12, 19, 34, 75	0
1	D	392/392 (100%)	0.23	4 (1%) 79 84	12, 20, 37, 60	0
All	All	1568/1568 (100%)	0.22	21 (1%) 75 81	12, 20, 36, 75	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	88	CYS	3.8
1	C	2	THR	3.5
1	B	209	GLY	3.2
1	A	136	ASP	3.0
1	A	2	THR	3.0
1	D	207	ARG	2.8
1	C	133	ARG	2.8
1	A	207	ARG	2.6
1	A	130	ASP	2.6
1	A	227	ASP	2.6
1	A	133	ARG	2.5
1	A	209	GLY	2.5
1	A	216	THR	2.4
1	C	134	MET	2.4
1	D	191	LYS	2.3
1	D	2	THR	2.2
1	A	212	VAL	2.2
1	B	268	LEU	2.1
1	A	208	LYS	2.0
1	C	208	LYS	2.0
1	D	299	ARG	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
2	GOL	A	401	6/6	0.88	0.11	22,32,34,35	0
2	GOL	C	401	6/6	0.94	0.07	24,26,28,28	0

6.5 Other polymers [i](#)

There are no such residues in this entry.