



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:27 AM UTC

PDB ID : 7OI5 / pdb_00007oi5
Title : Crystal structure of AP2 Mu2 - FCHO2 chimera (GST cleaved)
Authors : Zaccai, N.R.; Kelly, B.T.; Evans, P.R.; Owen, D.J.
Deposited on : 2021-05-11
Resolution : 2.61 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

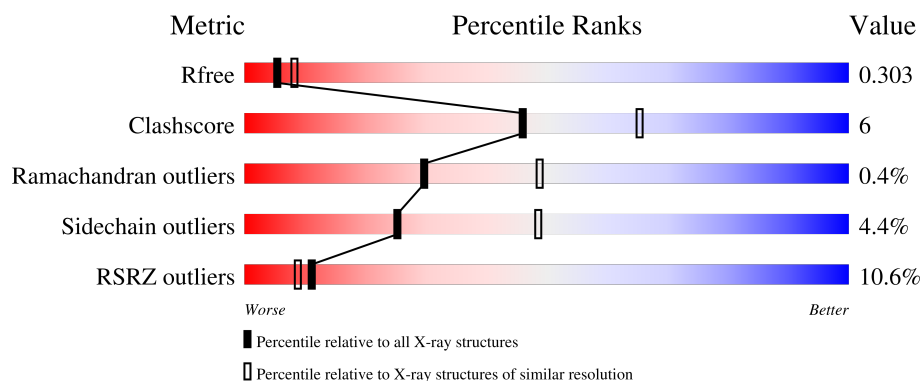
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.61 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	4951 (2.64-2.60)
Clashscore	190562	5303 (2.64-2.60)
Ramachandran outliers	187476	5217 (2.64-2.60)
Sidechain outliers	187428	5217 (2.64-2.60)
RSRZ outliers	180081	4950 (2.64-2.60)

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	B	359	8% 64% 16% • 19%
1	D	359	9% 66% 11% • 22%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4669 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 AP-2 complex subunit mu,F-BAR domain only protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	292	Total	C	N	O	S	0	0	0
			2362	1512	411	424	15			
1	D	281	Total	C	N	O	S	0	0	0
			2273	1459	396	403	15			

There are 90 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	153	PRO	-	expression tag	UNP P84092
B	154	GLY	-	expression tag	UNP P84092
B	155	ILE	-	expression tag	UNP P84092
B	156	HIS	-	expression tag	UNP P84092
B	157	MET	-	expression tag	UNP P84092
B	436	GLY	-	linker	UNP P84092
B	437	ALA	-	linker	UNP P84092
B	438	SER	-	linker	UNP P84092
B	439	GLY	-	linker	UNP P84092
B	440	SER	-	linker	UNP P84092
B	441	ALA	-	linker	UNP P84092
B	442	GLY	-	linker	UNP P84092
B	443	SER	-	linker	UNP P84092
B	444	ALA	-	linker	UNP P84092
B	445	GLY	-	linker	UNP P84092
B	446	PRO	-	linker	UNP P84092
B	447	SER	-	linker	UNP P84092
B	448	GLY	-	linker	UNP P84092
B	449	ALA	-	linker	UNP P84092
B	450	GLY	-	linker	UNP P84092
B	451	SER	-	linker	UNP P84092
B	452	ALA	-	linker	UNP P84092
B	453	GLY	-	linker	UNP P84092
B	454	SER	-	linker	UNP P84092
B	455	ALA	-	linker	UNP P84092

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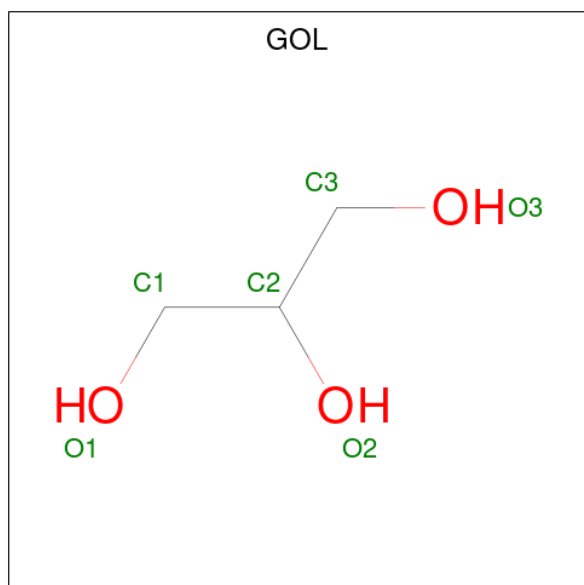
Chain	Residue	Modelled	Actual	Comment	Reference
B	456	GLY	-	linker	UNP P84092
B	457	PRO	-	linker	UNP P84092
B	458	SER	-	linker	UNP P84092
B	459	ALA	-	linker	UNP P84092
B	460	GLY	-	linker	UNP P84092
B	461	SER	-	linker	UNP P84092
B	462	ALA	-	linker	UNP P84092
B	463	GLY	-	linker	UNP P84092
B	464	SER	-	linker	UNP P84092
B	465	ALA	-	linker	UNP P84092
B	466	GLY	-	linker	UNP P84092
B	467	SER	-	linker	UNP P84092
B	468	GLY	-	linker	UNP P84092
B	469	SER	-	linker	UNP P84092
B	470	ALA	-	linker	UNP P84092
B	471	GLY	-	linker	UNP P84092
B	472	SER	-	linker	UNP P84092
B	473	ALA	-	linker	UNP P84092
B	474	PRO	-	linker	UNP P84092
B	475	GLY	-	linker	UNP P84092
D	153	PRO	-	expression tag	UNP P84092
D	154	GLY	-	expression tag	UNP P84092
D	155	ILE	-	expression tag	UNP P84092
D	156	HIS	-	expression tag	UNP P84092
D	157	MET	-	expression tag	UNP P84092
D	436	GLY	-	linker	UNP P84092
D	437	ALA	-	linker	UNP P84092
D	438	SER	-	linker	UNP P84092
D	439	GLY	-	linker	UNP P84092
D	440	SER	-	linker	UNP P84092
D	441	ALA	-	linker	UNP P84092
D	442	GLY	-	linker	UNP P84092
D	443	SER	-	linker	UNP P84092
D	444	ALA	-	linker	UNP P84092
D	445	GLY	-	linker	UNP P84092
D	446	PRO	-	linker	UNP P84092
D	447	SER	-	linker	UNP P84092
D	448	GLY	-	linker	UNP P84092
D	449	ALA	-	linker	UNP P84092
D	450	GLY	-	linker	UNP P84092
D	451	SER	-	linker	UNP P84092
D	452	ALA	-	linker	UNP P84092

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Chain	Residue	Modelled	Actual	Comment	Reference
D	453	GLY	-	linker	UNP P84092
D	454	SER	-	linker	UNP P84092
D	455	ALA	-	linker	UNP P84092
D	456	GLY	-	linker	UNP P84092
D	457	PRO	-	linker	UNP P84092
D	458	SER	-	linker	UNP P84092
D	459	ALA	-	linker	UNP P84092
D	460	GLY	-	linker	UNP P84092
D	461	SER	-	linker	UNP P84092
D	462	ALA	-	linker	UNP P84092
D	463	GLY	-	linker	UNP P84092
D	464	SER	-	linker	UNP P84092
D	465	ALA	-	linker	UNP P84092
D	466	GLY	-	linker	UNP P84092
D	467	SER	-	linker	UNP P84092
D	468	GLY	-	linker	UNP P84092
D	469	SER	-	linker	UNP P84092
D	470	ALA	-	linker	UNP P84092
D	471	GLY	-	linker	UNP P84092
D	472	SER	-	linker	UNP P84092
D	473	ALA	-	linker	UNP P84092
D	474	PRO	-	linker	UNP P84092
D	475	GLY	-	linker	UNP P84092

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	12	Total	O	0	0
			12	12		
3	D	4	Total	O	0	0
			4	4		

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	116.05Å 55.38Å 167.74Å 90.00° 109.05° 90.00°	Depositor
Resolution (Å)	79.27 – 2.61 79.27 – 2.61	Depositor EDS
% Data completeness (in resolution range)	99.5 (79.27-2.61) 99.7 (79.27-2.61)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.63 (at 2.62Å)	Xtriage
Refinement program	REFMAC 5.8.0257, PHENIX 1.19rc1_4016	Depositor
R, R_{free}	0.238 , 0.297 0.240 , 0.303	Depositor DCC
R_{free} test set	1563 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	51.5	Xtriage
Anisotropy	0.914	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 49.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4669	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.48% 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	B	0.13	0/2410	0.38	0/3239
1	D	0.20	0/2321	0.41	0/3119
All	All	0.17	0/4731	0.40	0/6358

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	D	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	253	ARG	Sidechain

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	B	2362	0	2424	36	0
1	D	2273	0	2339	23	0
2	B	12	0	16	0	0
2	D	6	0	8	1	0
3	B	12	0	0	1	0
3	D	4	0	0	0	0
All	All	4669	0	4787	55	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 6.

All (55) 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:377:ASP:O	1:D:379:LYS:NZ	2.25	0.70
1:B:432:GLU:OE1	1:D:434:ARG:NH2	2.27	0.68
1:B:156:HIS:CD2	1:B:158:GLN:HE21	2.15	0.64
1:B:480:GLU:HG3	1:B:481:GLU:H	1.63	0.63
1:D:157:MET:HE3	1:D:159:ILE:HD13	1.80	0.63
1:D:376:ASN:O	1:D:378:LYS:NZ	2.27	0.60
1:B:250:GLN:H	1:B:250:GLN:CD	2.10	0.59
1:B:306:VAL:HG22	1:B:365:GLN:HG3	1.84	0.59
1:D:480:GLU:OE1	1:D:481:GLU:N	2.36	0.56
1:B:322:VAL:HG22	1:B:388:MET:HG3	1.90	0.54
1:B:312:LYS:HD2	1:B:314:SER:OG	2.07	0.54
1:B:209:MET:N	1:B:408:GLU:OE1	2.38	0.53
1:B:287:PHE:HE1	1:B:358:MET:HE2	1.73	0.53
1:D:172:GLU:OE2	1:D:486:LYS:NZ	2.32	0.53
1:B:345:LYS:HD2	1:B:348:GLU:OE2	2.08	0.52
1:B:247:THR:OG1	1:B:276:ARG:HG3	2.09	0.52
1:B:325:PRO:HB3	1:B:384:PRO:HG2	1.93	0.51
1:B:480:GLU:HG3	1:B:481:GLU:N	2.25	0.50
1:D:218:ASP:OD2	1:D:219:LYS:N	2.45	0.50
1:D:159:ILE:HG22	1:D:162:ARG:H	1.76	0.49
1:B:250:GLN:NE2	3:B:701:HOH:O	2.24	0.49
1:D:174:PHE:HB2	1:D:203:LYS:HB2	1.94	0.49
1:D:196:VAL:HG23	1:D:283:ILE:HD13	1.95	0.48
1:D:183:LEU:HG	1:D:285:LEU:HD22	1.94	0.48
1:B:218:ASP:CG	1:B:219:LYS:H	2.20	0.48
1:B:289:VAL:HG22	1:B:307:ILE:HG22	1.95	0.47
1:B:218:ASP:OD1	1:B:261:ARG:NE	2.42	0.47
1:B:324:ILE:HD12	1:B:351:ILE:HD11	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:253:ARG:HD3	1:D:256:LYS:HG3	1.96	0.46
1:D:328:LEU:H	1:D:328:LEU:HD22	1.79	0.46
1:B:327:PRO:O	1:B:330:THR:OG1	2.31	0.45
1:B:312:LYS:HD3	1:B:313:PRO:HD2	1.98	0.45
1:B:300:LYS:HE3	1:B:369:GLU:HB3	1.98	0.45
1:B:348:GLU:HG2	1:D:381:TRP:CZ2	2.52	0.45
1:B:434:ARG:NH2	1:D:432:GLU:OE1	2.48	0.45
1:B:410:LYS:HA	1:B:410:LYS:HD2	1.77	0.44
1:D:202:MET:HB3	1:D:272:PHE:CE1	2.52	0.44
1:B:335:VAL:HG23	1:B:368:ALA:HB2	2.00	0.44
1:B:348:GLU:HG2	1:D:381:TRP:CH2	2.53	0.44
1:B:481:GLU:O	1:B:481:GLU:HG2	2.18	0.44
1:D:415:ASP:HA	1:D:418:VAL:HG22	1.99	0.44
1:B:174:PHE:HB2	1:B:203:LYS:HB2	1.99	0.44
1:B:239:GLN:HE22	1:B:284:ILE:HD11	1.83	0.43
1:B:281:LYS:HB3	1:B:281:LYS:HE3	1.65	0.43
1:B:353:TRP:CZ2	1:B:355:ILE:HD11	2.54	0.42
1:B:216:MET:HE2	1:B:399:LEU:HD11	2.00	0.42
1:B:293:VAL:O	1:B:293:VAL:HG13	2.19	0.42
1:D:375:THR:OG1	1:D:379:LYS:NZ	2.49	0.42
1:B:296:VAL:HG23	1:B:296:VAL:O	2.20	0.42
1:D:253:ARG:HA	2:D:601:GOL:H2	2.01	0.41
1:B:319:LYS:NZ	1:B:391:GLU:OE1	2.53	0.41
1:D:183:LEU:HD23	1:D:194:ALA:HB2	2.03	0.41
1:B:389:ASN:HA	1:B:428:SER:OG	2.21	0.41
1:D:296:VAL:HB	1:D:300:LYS:HB3	2.03	0.40
1:D:159:ILE:HG23	1:D:161:TRP:CE2	2.56	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	B	284/359 (79%)	263 (93%)	20 (7%)	1 (0%)	30	49
1	D	273/359 (76%)	257 (94%)	15 (6%)	1 (0%)	30	49
All	All	557/718 (78%)	520 (93%)	35 (6%)	2 (0%)	30	49

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	480	GLU
1	D	291	PRO

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	B	266/304 (88%)	254 (96%)	12 (4%)	24	48
1	D	255/304 (84%)	244 (96%)	11 (4%)	26	49
All	All	521/608 (86%)	498 (96%)	23 (4%)	25	48

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	219	LYS
1	B	247	THR
1	B	255	SER
1	B	299	THR
1	B	333	VAL
1	B	347	SER
1	B	351	ILE
1	B	366	ILE
1	B	367	SER
1	B	376	ASN
1	B	392	VAL
1	B	435	CYS
1	D	183	LEU
1	D	259	SER

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Mol	Chain	Res	Type
1	D	279	THR
1	D	288	ARG
1	D	333	VAL
1	D	347	SER
1	D	392	VAL
1	D	399	LEU
1	D	408	GLU
1	D	435	CYS
1	D	480	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	156	HIS
1	B	158	GLN
1	B	188	GLN
1	B	239	GLN
1	B	318	GLN
1	B	349	ASN
1	B	365	GLN
1	B	389	ASN
1	D	195	HIS
1	D	365	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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 ⓘ

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	GOL	B	601	-	5,5,5	0.96	0	5,5,5	1.04	0
2	GOL	D	601	-	5,5,5	1.04	0	5,5,5	1.04	0
2	GOL	B	602	-	5,5,5	0.97	0	5,5,5	0.99	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	GOL	B	601	-	-	0/4/4/4	-
2	GOL	D	601	-	-	4/4/4/4	-
2	GOL	B	602	-	-	2/4/4/4	-

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
2	B	602	GOL	C1-C2-C3-O3
2	B	602	GOL	O2-C2-C3-O3
2	D	601	GOL	O1-C1-C2-C3
2	D	601	GOL	C1-C2-C3-O3
2	D	601	GOL	O1-C1-C2-O2
2	D	601	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	601	GOL	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	B	292/359 (81%)	0.80	29 (9%) 13 10	36, 63, 120, 165	0
1	D	281/359 (78%)	0.96	32 (11%) 10 7	46, 70, 121, 164	0
All	All	573/718 (79%)	0.88	61 (10%) 11 9	36, 68, 122, 165	0

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	153	PRO	5.0
1	B	153	PRO	4.9
1	D	478	VAL	4.9
1	B	494	THR	4.7
1	D	241	ILE	4.7
1	B	479	ASP	4.1
1	B	246	CYS	4.1
1	B	478	VAL	4.1
1	B	381	TRP	3.7
1	B	222	ILE	3.7
1	D	158	GLN	3.6
1	D	246	CYS	3.6
1	D	407	PHE	3.5
1	D	373	LEU	3.5
1	D	500	TYR	3.4
1	D	381	TRP	3.3
1	B	351	ILE	3.2
1	B	328	LEU	3.2
1	D	336	ILE	3.2
1	D	219	LYS	3.1
1	D	338	MET	3.1
1	B	245	ASP	3.0
1	D	376	ASN	3.0
1	D	298	ARG	2.9

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Mol	Chain	Res	Type	RSRZ
1	D	489	THR	2.9
1	D	292	LEU	2.9
1	D	328	LEU	2.9
1	D	378	LYS	2.8
1	B	373	LEU	2.8
1	D	410	LYS	2.8
1	B	435	CYS	2.8
1	B	338	MET	2.8
1	B	374	PRO	2.7
1	B	372	LEU	2.7
1	D	421	TRP	2.7
1	B	299	THR	2.6
1	B	376	ASN	2.6
1	D	479	ASP	2.5
1	D	156	HIS	2.4
1	B	377	ASP	2.4
1	B	218	ASP	2.3
1	B	292	LEU	2.3
1	D	419	ILE	2.3
1	D	302	GLU	2.3
1	B	190	GLN	2.3
1	D	498	HIS	2.2
1	B	375	THR	2.2
1	B	501	SER	2.2
1	B	480	GLU	2.2
1	B	188	GLN	2.2
1	B	363	GLU	2.2
1	D	375	THR	2.2
1	D	382	ALA	2.1
1	B	362	LYS	2.1
1	D	420	LYS	2.1
1	D	487	PRO	2.1
1	D	312	LYS	2.1
1	D	253	ARG	2.0
1	B	224	LYS	2.0
1	B	477	ASP	2.0
1	D	482	GLY	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 [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	B	601	6/6	0.77	0.14	67,74,82,84	0
2	GOL	B	602	6/6	0.85	0.16	62,78,84,101	0
2	GOL	D	601	6/6	0.90	0.14	60,65,78,84	0

6.5 Other polymers [i](#)

There are no such residues in this entry.