



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 25, 2024 – 10:51 AM EDT

PDB ID : 6OHG  
Title : Structure of Plasmodium falciparum vaccine candidate Pfs230D1M in complex with the Fab of a transmission blocking antibody  
Authors : Garboczi, D.N.; Singh, K.; Gittis, A.G.  
Deposited on : 2019-04-05  
Resolution : 2.38 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.37.1  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.37.1

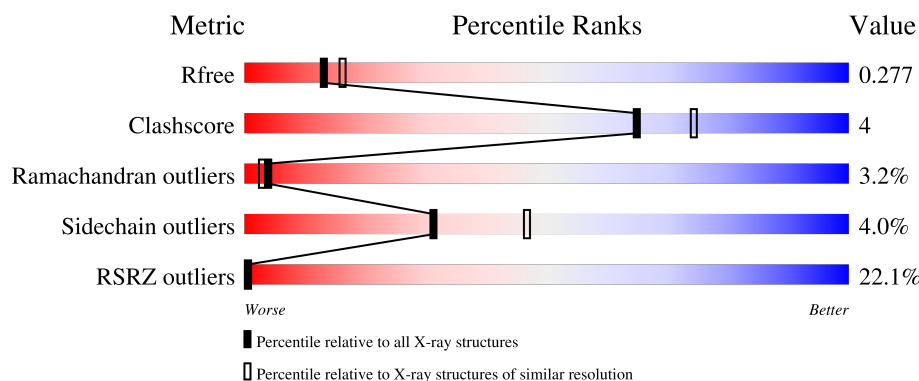
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.38 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))
$R_{free}$	130704	5509 (2.40-2.36)
Clashscore	141614	6082 (2.40-2.36)
Ramachandran outliers	138981	5973 (2.40-2.36)
Sidechain outliers	138945	5975 (2.40-2.36)
RSRZ outliers	127900	5397 (2.40-2.36)

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  $\geq 3$ , 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	195	<div> <div>19%</div> <div>76%</div> <div>10%</div> <div>13%</div> </div>
2	B	215	<div> <div>26%</div> <div>81%</div> <div>16%</div> <div>..</div> </div>
3	C	228	<div> <div>17%</div> <div>87%</div> <div>8%</div> <div>.</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	ACY	A	202	-	-	-	X
5	EDO	C	309	-	-	-	X

## 2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 4362 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 Gametocyte surface protein P230.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	170	Total	C	N	O	S	0	1	0
			1189	758	194	233	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	585	GLN	ASN	conflict	UNP P68874

- Molecule 2 is a protein called 4F12 Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	213	Total	C	N	O	S	0	0	0
			1418	886	240	287	5			

- Molecule 3 is a protein called 4F12 Heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	218	Total	C	N	O	S	0	0	0
			1599	1017	260	315	7			

- Molecule 4 is ACETIC ACID (three-letter code: ACY) (formula: C<sub>2</sub>H<sub>4</sub>O<sub>2</sub>).



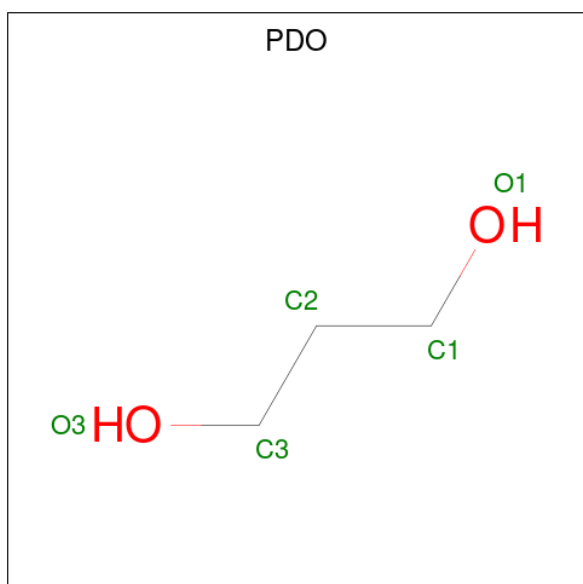
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



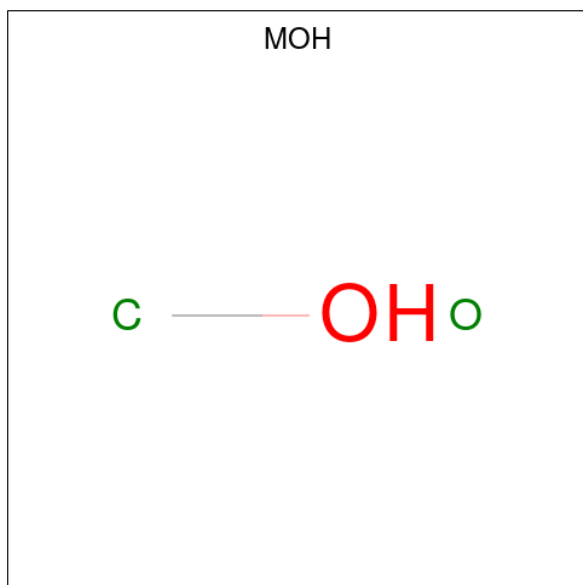
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		
5	C	1	Total	C	O	0	0
			4	2	2		
5	C	1	Total	C	O	0	0
			4	2	2		

- Molecule 6 is 1,3-PROPANDIOL (three-letter code: PDO) (formula:  $C_3H_8O_2$ ).



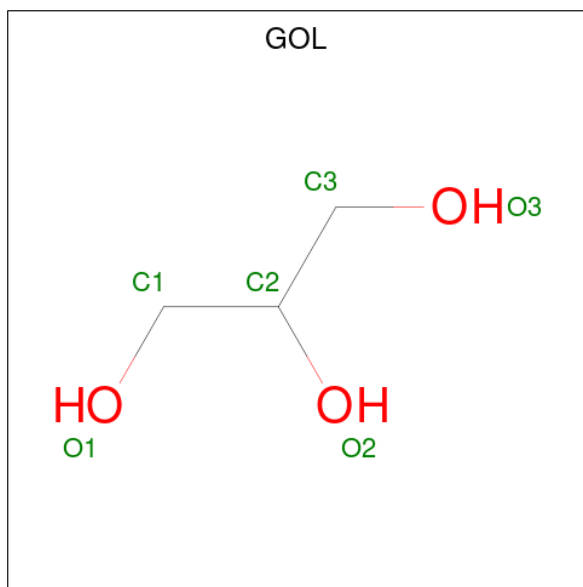
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			5	3	2		
6	C	1	Total	C	O	0	0
			5	3	2		
6	C	1	Total	C	O	0	0
			5	3	2		
6	C	1	Total	C	O	0	0
			5	3	2		

- Molecule 7 is METHANOL (three-letter code: MOH) (formula: CH<sub>4</sub>O).



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

- Molecule 8 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	C	1	Total	C	O	0	1
			12	6	6		
8	C	1	Total	C	O	0	1
			12	6	6		

- Molecule 9 is water.

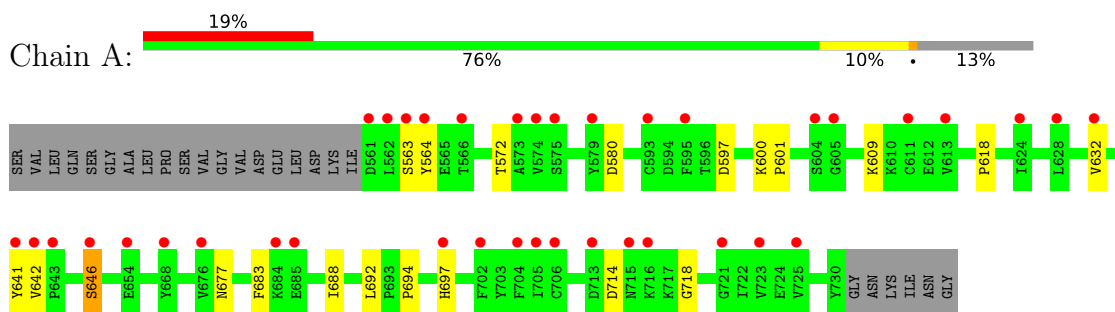
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	19	Total	O	0	0
			19	19		
9	B	14	Total	O	0	0
			14	14		
9	C	27	Total	O	0	0
			27	27		



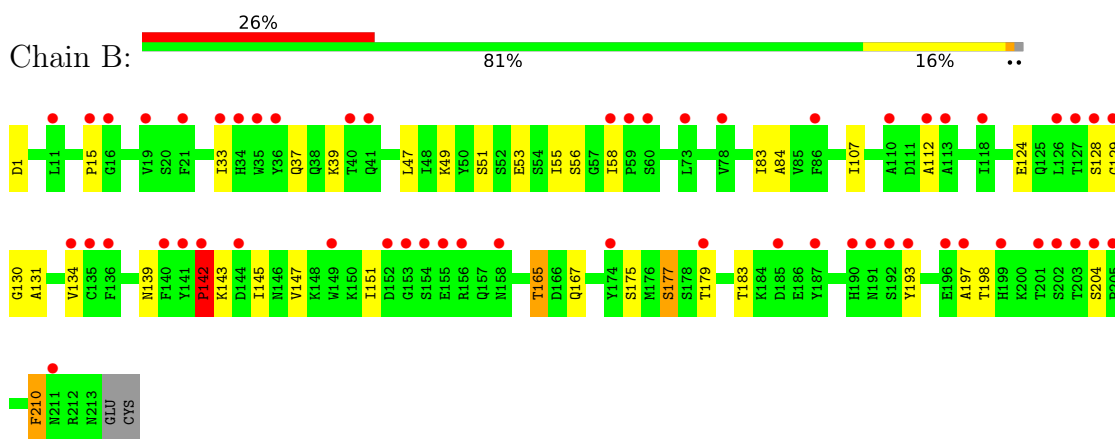
### 3 Residue-property plots [i](#)

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.

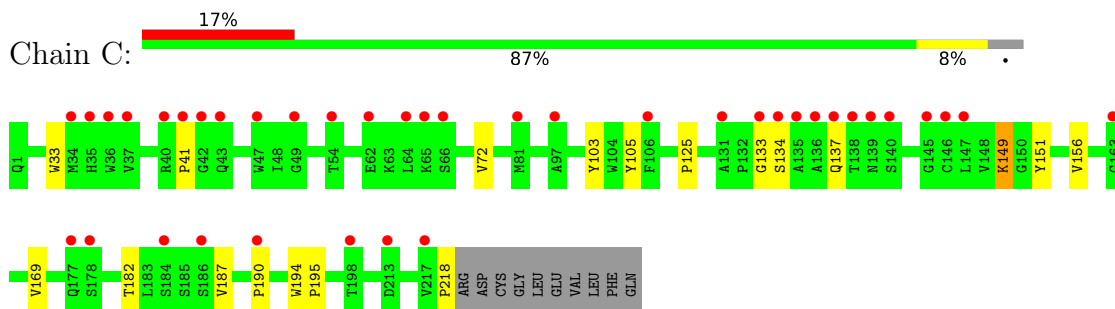
- Molecule 1: Gametocyte surface protein P230



- Molecule 2: 4F12 Light Chain



- Molecule 3: 4F12 Heavy chain



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	79.95Å 191.33Å 41.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.05 – 2.38 24.05 – 2.39	Depositor EDS
% Data completeness (in resolution range)	98.4 (24.05-2.38) 98.5 (24.05-2.39)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.63 (at 2.39Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, $R_{free}$	0.229 , 0.277 0.230 , 0.277	Depositor DCC
$R_{free}$ test set	2000 reflections (7.79%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	52.7	Xtriage
Anisotropy	0.647	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 63.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	4362	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.99% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: EDO, ACY, MOH, PDO, 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	0.26	0/1213	0.46	0/1646
2	B	0.26	0/1452	0.48	0/1973
3	C	0.26	0/1646	0.48	0/2263
All	All	0.26	0/4311	0.47	0/5882

There are no bond length outliers.

There are no bond angle outliers.

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	1189	0	1008	7	0
2	B	1418	0	1137	16	0
3	C	1599	0	1498	10	0
4	A	8	0	6	1	0
4	B	12	0	9	0	0
4	C	8	0	6	0	0
5	A	8	0	11	0	0
5	B	4	0	5	0	0
5	C	8	0	12	0	0
6	B	5	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	C	15	0	24	1	0
7	B	2	0	0	0	0
7	C	2	0	0	0	0
8	C	24	0	32	3	0
9	A	19	0	0	1	0
9	B	14	0	0	0	0
9	C	27	0	0	0	0
All	All	4362	0	3756	33	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 (33) 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)
2:B:83:ILE:HD11	2:B:107:ILE:HG13	1.70	0.73
2:B:147:VAL:HA	2:B:197:ALA:HA	1.84	0.58
2:B:165:THR:HG22	2:B:175:SER:H	1.69	0.57
2:B:124:GLU:HG2	2:B:130:GLY:HA2	1.87	0.57
1:A:597:ASP:HA	1:A:600:LYS:HE2	1.86	0.56
2:B:37:GLN:HB2	2:B:47:LEU:HD11	1.86	0.56
3:C:218:PRO:HD2	8:C:302[B]:GOL:O1	2.05	0.56
2:B:39:LYS:HG2	2:B:84:ALA:HB2	1.90	0.54
2:B:193:TYR:HB2	2:B:210:PHE:HE1	1.73	0.52
1:A:697:HIS:ND1	4:A:201:ACY:H3	2.25	0.51
3:C:190:PRO:HD3	6:C:304:PDO:H21	1.91	0.51
2:B:83:ILE:HG21	2:B:167:GLN:HB2	1.93	0.51
3:C:149:LYS:HB2	3:C:182:THR:HG23	1.93	0.51
1:A:618:PRO:HB3	1:A:694:PRO:HA	1.93	0.51
3:C:125:PRO:HB3	3:C:151:TYR:HB3	1.92	0.50
2:B:55:ILE:HG22	2:B:56:SER:H	1.77	0.49
3:C:33:TRP:HZ2	8:C:301[A]:GOL:H32	1.78	0.49
1:A:601:PRO:HA	1:A:718:GLY:HA2	1.95	0.48
2:B:177:SER:O	2:B:177:SER:OG	2.29	0.48
2:B:134:VAL:HA	2:B:179:THR:HA	1.98	0.45
2:B:142:PRO:HB2	2:B:143:LYS:H	1.53	0.45
3:C:194:TRP:CG	3:C:195:PRO:HA	2.53	0.44
3:C:103:TYR:HB3	3:C:105:TYR:CE2	2.53	0.43
1:A:646:SER:HB3	1:A:688:ILE:HD13	2.00	0.43
3:C:169:VAL:HG22	3:C:187:VAL:HG23	2.00	0.42
2:B:49:LYS:HG3	2:B:53:GLU:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:55:ILE:HB	2:B:58:ILE:HG12	2.02	0.41
1:A:580:ASP:HB2	1:A:609:LYS:HD3	2.03	0.41
1:A:697:HIS:HD2	9:A:318:HOH:O	2.04	0.41
2:B:83:ILE:HG13	2:B:167:GLN:OE1	2.21	0.41
2:B:33:ILE:HG22	2:B:51:SER:HA	2.03	0.40
3:C:33:TRP:CZ2	8:C:301[A]:GOL:H32	2.56	0.40
3:C:149:LYS:HB2	3:C:149:LYS:HE3	1.85	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	169/195 (87%)	147 (87%)	18 (11%)	4 (2%)	6	5
2	B	211/215 (98%)	169 (80%)	31 (15%)	11 (5%)	2	1
3	C	216/228 (95%)	203 (94%)	9 (4%)	4 (2%)	8	9
All	All	596/638 (93%)	519 (87%)	58 (10%)	19 (3%)	4	3

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	112	ALA
2	B	128	SER
2	B	198	THR
1	A	564	TYR
1	A	572	THR
1	A	714	ASP
3	C	134	SER
3	C	41	PRO
2	B	142	PRO
2	B	151	ILE

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Mol	Chain	Res	Type
2	B	204	SER
1	A	642	VAL
2	B	129	GLY
2	B	139	ASN
2	B	15	PRO
2	B	131	ALA
3	C	133	GLY
3	C	137	GLN
2	B	145	ILE

### 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	105/180 (58%)	98 (93%)	7 (7%)	16	23
2	B	123/193 (64%)	117 (95%)	6 (5%)	25	38
3	C	174/199 (87%)	171 (98%)	3 (2%)	60	76
All	All	402/572 (70%)	386 (96%)	16 (4%)	31	47

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	563	SER
1	A	632	VAL
1	A	641	TYR
1	A	646	SER
1	A	677	ASN
1	A	683	PHE
1	A	692	LEU
2	B	1	ASP
2	B	142	PRO
2	B	165	THR
2	B	177	SER
2	B	183	THR
2	B	210	PHE

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Mol	Chain	Res	Type
3	C	72	VAL
3	C	149	LYS
3	C	156	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

22 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	$\# Z  > 2$
7	MOH	C	310	-	1,1,1	0.05	0	-		
5	EDO	C	309	-	3,3,3	0.06	0	2,2,2	0.18	0
5	EDO	A	204	-	3,3,3	0.06	0	2,2,2	0.18	0
5	EDO	B	305	-	3,3,3	1.02	0	2,2,2	0.22	0
4	ACY	C	306	-	3,3,3	0.96	0	3,3,3	0.81	0
4	ACY	C	307	-	3,3,3	0.98	0	3,3,3	0.81	0
4	ACY	A	201	-	3,3,3	0.97	0	3,3,3	0.80	0
5	EDO	A	203	-	3,3,3	0.72	0	2,2,2	0.86	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	ACY	B	302	-	3,3,3	0.97	0	3,3,3	0.81	0
8	GOL	C	301[B]	-	5,5,5	0.08	0	5,5,5	0.27	0
8	GOL	C	302[B]	-	5,5,5	0.09	0	5,5,5	0.27	0
6	PDO	C	304	-	4,4,4	0.30	0	3,3,3	0.16	0
7	MOH	B	306	-	1,1,1	0.04	0	-		
6	PDO	C	303	-	4,4,4	0.17	0	3,3,3	0.11	0
6	PDO	C	305	-	4,4,4	0.17	0	3,3,3	0.11	0
6	PDO	B	301	-	4,4,4	0.39	0	3,3,3	0.69	0
4	ACY	B	304	-	3,3,3	0.96	0	3,3,3	0.80	0
8	GOL	C	301[A]	-	5,5,5	0.10	0	5,5,5	0.27	0
8	GOL	C	302[A]	-	5,5,5	0.10	0	5,5,5	0.27	0
5	EDO	C	308	-	3,3,3	0.46	0	2,2,2	0.33	0
4	ACY	B	303	-	3,3,3	0.97	0	3,3,3	0.81	0
4	ACY	A	202	-	3,3,3	0.97	0	3,3,3	0.80	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
5	EDO	A	203	-	-	1/1/1/1	-
6	PDO	C	304	-	-	2/2/2/2	-
8	GOL	C	302[A]	-	-	0/4/4/4	-
5	EDO	C	308	-	-	0/1/1/1	-
5	EDO	C	309	-	-	1/1/1/1	-
5	EDO	A	204	-	-	0/1/1/1	-
5	EDO	B	305	-	-	1/1/1/1	-
8	GOL	C	301[B]	-	-	0/4/4/4	-
6	PDO	C	303	-	-	2/2/2/2	-
6	PDO	C	305	-	-	1/2/2/2	-
6	PDO	B	301	-	-	2/2/2/2	-
8	GOL	C	302[B]	-	-	0/4/4/4	-
8	GOL	C	301[A]	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (10) torsion outliers are listed below:



Mol	Chain	Res	Type	Atoms
6	B	301	PDO	O1-C1-C2-C3
6	B	301	PDO	C1-C2-C3-O3
6	C	303	PDO	O1-C1-C2-C3
6	C	303	PDO	C1-C2-C3-O3
6	C	304	PDO	O1-C1-C2-C3
6	C	304	PDO	C1-C2-C3-O3
6	C	305	PDO	C1-C2-C3-O3
5	A	203	EDO	O1-C1-C2-O2
5	C	309	EDO	O1-C1-C2-O2
5	B	305	EDO	O1-C1-C2-O2

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	201	ACY	1	0
8	C	302[B]	GOL	1	0
6	C	304	PDO	1	0
8	C	301[A]	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	170/195 (87%)	1.20	38 (22%) 0 0	40, 73, 123, 158	0
2	B	213/215 (99%)	1.54	56 (26%) 0 0	40, 93, 155, 273	0
3	C	218/228 (95%)	1.04	39 (17%) 1 1	40, 62, 110, 227	0
All	All	601/638 (94%)	1.26	133 (22%) 0 0	40, 73, 141, 273	0

All (133) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	153	GLY	18.0
2	B	201	THR	16.1
3	C	135	ALA	15.6
2	B	202	SER	13.7
3	C	133	GLY	12.9
3	C	139	ASN	10.9
2	B	110	ALA	10.1
3	C	138	THR	9.8
1	A	562	LEU	8.4
1	A	564	TYR	7.1
2	B	127	THR	6.7
3	C	134	SER	6.3
1	A	561	ASP	6.2
1	A	642	VAL	6.2
1	A	723	VAL	5.7
2	B	149	TRP	5.4
2	B	142	PRO	5.3
1	A	579	TYR	5.1
2	B	187	TYR	5.0
2	B	58	ILE	4.9
2	B	128	SER	4.9
3	C	217	VAL	4.9
1	A	563	SER	4.8

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Mol	Chain	Res	Type	RSRZ
2	B	141	TYR	4.8
1	A	605	GLY	4.6
3	C	136	ALA	4.6
1	A	676	VAL	4.6
2	B	205	PRO	4.5
2	B	15	PRO	4.5
2	B	185	ASP	4.4
1	A	715	ASN	4.4
2	B	191	ASN	4.4
2	B	35	TRP	4.4
2	B	193	TYR	4.3
1	A	706	CYS	4.2
1	A	704	PHE	4.2
3	C	198	THR	4.2
3	C	36	TRP	4.1
2	B	152	ASP	4.0
2	B	59	PRO	3.9
1	A	604	SER	3.9
2	B	113	ALA	3.8
2	B	135	CYS	3.8
2	B	112	ALA	3.7
3	C	34	MET	3.7
3	C	41	PRO	3.6
2	B	211	ASN	3.6
3	C	140	SER	3.6
3	C	49	GLY	3.5
1	A	713	ASP	3.5
1	A	654	GLU	3.5
2	B	73	LEU	3.4
2	B	156	ARG	3.4
2	B	126	LEU	3.4
2	B	197	ALA	3.4
3	C	184	SER	3.4
1	A	716	LYS	3.4
2	B	129	GLY	3.3
3	C	163	GLY	3.3
3	C	64	LEU	3.2
3	C	65	LYS	3.2
3	C	137	GLN	3.2
3	C	66	SER	3.2
1	A	646	SER	3.1
2	B	19	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
2	B	196	GLU	3.1
3	C	37	VAL	3.1
3	C	35	HIS	3.1
2	B	203	THR	3.1
2	B	134	VAL	3.0
3	C	43	GLN	3.0
3	C	146	CYS	3.0
2	B	154	SER	2.9
2	B	40	THR	2.9
2	B	34	HIS	2.9
2	B	36	TYR	2.9
1	A	643	PRO	2.9
3	C	213	ASP	2.9
3	C	62	GLU	2.9
2	B	86	PHE	2.9
3	C	147	LEU	2.9
3	C	42	GLY	2.8
3	C	145	GLY	2.8
2	B	174	TYR	2.8
1	A	574	VAL	2.8
2	B	179	THR	2.8
1	A	684	LYS	2.7
3	C	40	ARG	2.7
2	B	190	HIS	2.7
1	A	725	VAL	2.7
1	A	624	ILE	2.7
1	A	641	TYR	2.7
1	A	566	THR	2.7
1	A	611	CYS	2.7
1	A	573	ALA	2.6
2	B	199	HIS	2.6
3	C	131	ALA	2.6
1	A	705	ILE	2.6
2	B	140	PHE	2.6
2	B	16	GLY	2.6
2	B	155	GLU	2.6
3	C	190	PRO	2.5
3	C	177	GLN	2.5
1	A	595	PHE	2.5
1	A	613	VAL	2.5
3	C	106	PHE	2.5
3	C	54	THR	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	697	HIS	2.4
2	B	21	PHE	2.4
1	A	628	LEU	2.4
1	A	593	CYS	2.4
2	B	158	ASN	2.4
2	B	192	SER	2.4
3	C	97	ALA	2.3
3	C	186	SER	2.3
3	C	47	TRP	2.3
2	B	136	PHE	2.3
1	A	685	GLU	2.3
2	B	78	VAL	2.3
1	A	575	SER	2.2
2	B	41	GLN	2.2
1	A	668	TYR	2.2
1	A	702	PHE	2.2
1	A	721	GLY	2.2
2	B	118	ILE	2.2
3	C	178	SER	2.1
1	A	632	VAL	2.1
2	B	33	ILE	2.1
2	B	11	LEU	2.1
3	C	81	MET	2.1
2	B	204	SER	2.0
2	B	60	SER	2.0
2	B	144	ASP	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 monosaccharides 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, 95<sup>th</sup> 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
6	PDO	C	304	5/5	0.51	0.26	68,69,71,72	5
5	EDO	A	204	4/4	0.60	0.22	65,66,67,67	4
5	EDO	C	309	4/4	0.66	0.68	58,62,67,69	4
7	MOH	B	306	2/2	0.68	0.24	63,63,63,67	2
5	EDO	B	305	4/4	0.69	0.33	65,69,70,72	4
6	PDO	C	305	5/5	0.70	0.28	52,52,54,60	5
5	EDO	A	203	4/4	0.73	0.23	71,72,73,76	4
4	ACY	A	202	4/4	0.77	0.41	53,59,60,63	4
4	ACY	A	201	4/4	0.78	0.21	40,61,64,75	4
6	PDO	C	303	5/5	0.81	0.25	61,66,74,76	5
5	EDO	C	308	4/4	0.81	0.24	63,66,75,79	4
6	PDO	B	301	5/5	0.84	0.37	61,62,67,74	5
8	GOL	C	302[A]	6/6	0.84	0.25	36,38,46,47	6
8	GOL	C	302[B]	6/6	0.84	0.25	35,37,44,48	6
4	ACY	B	304	4/4	0.85	0.20	56,62,65,65	4
8	GOL	C	301[B]	6/6	0.87	0.21	57,58,60,63	6
4	ACY	C	307	4/4	0.87	0.26	53,54,57,59	4
8	GOL	C	301[A]	6/6	0.87	0.21	53,58,60,61	6
4	ACY	B	302	4/4	0.88	0.14	49,58,59,59	4
7	MOH	C	310	2/2	0.89	0.12	63,63,63,65	2
4	ACY	B	303	4/4	0.92	0.19	58,60,62,62	4
4	ACY	C	306	4/4	0.94	0.17	45,53,54,60	4

## 6.5 Other polymers ⓘ

There are no such residues in this entry.