



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 8, 2022 – 04:21 pm BST

PDB ID : 7ZY4  
Title : Crystal structure of human CstF77 in complex with hFip1  
Authors : Muckenfuss, L.M.; Jinek, M.  
Deposited on : 2022-05-23  
Resolution : 2.55 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 : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.30  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0267  
CCP4 : 7.1.010 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.30

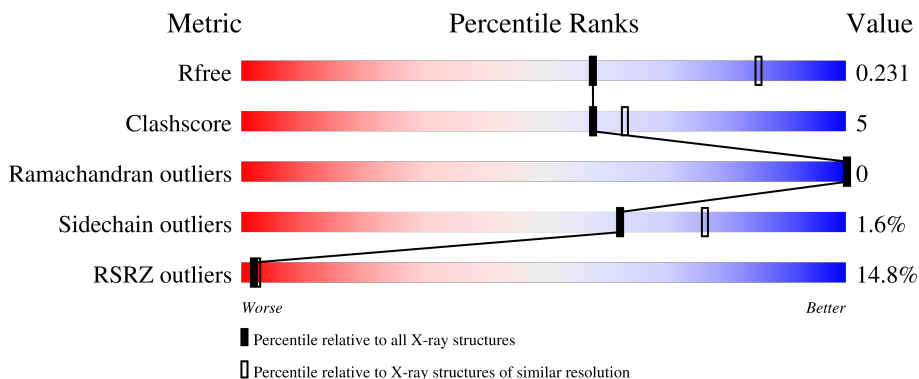
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.55 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	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

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	312	
1	B	312	
2	C	38	
2	D	38	

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
3	GOL	A	602	-	-	-	X
3	GOL	B	601	-	-	-	X
3	GOL	B	603	-	-	-	X

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 10507 atoms, of which 5210 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 Cleavage stimulation factor subunit 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	305	Total	C	H	N	O	S	0	0	0
			5042	1628	2514	419	469	12			
1	B	306	Total	C	H	N	O	S	0	0	0
			5057	1633	2522	420	470	12			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	238	SER	-	expression tag	UNP Q12996
A	239	ASN	-	expression tag	UNP Q12996
A	240	ALA	-	expression tag	UNP Q12996
B	238	SER	-	expression tag	UNP Q12996
B	239	ASN	-	expression tag	UNP Q12996
B	240	ALA	-	expression tag	UNP Q12996

- Molecule 2 is a protein called hFip1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	H	N	O			
2	C	9	Total	C	H	N	O	0	0	0
			143	52	61	10	20			
2	D	8	Total	C	H	N	O	0	0	0
			131	48	57	9	17			

- Molecule 3 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
3	A	1	Total	C	H	O	0	0
			14	3	8	3		
3	A	1	Total	C	H	O	0	0
			14	3	8	3		
3	A	1	Total	C	H	O	0	0
			14	3	8	3		
3	B	1	Total	C	H	O	0	0
			14	3	8	3		
3	B	1	Total	C	H	O	0	0
			14	3	8	3		
3	B	1	Total	C	H	O	0	0
			14	3	8	3		

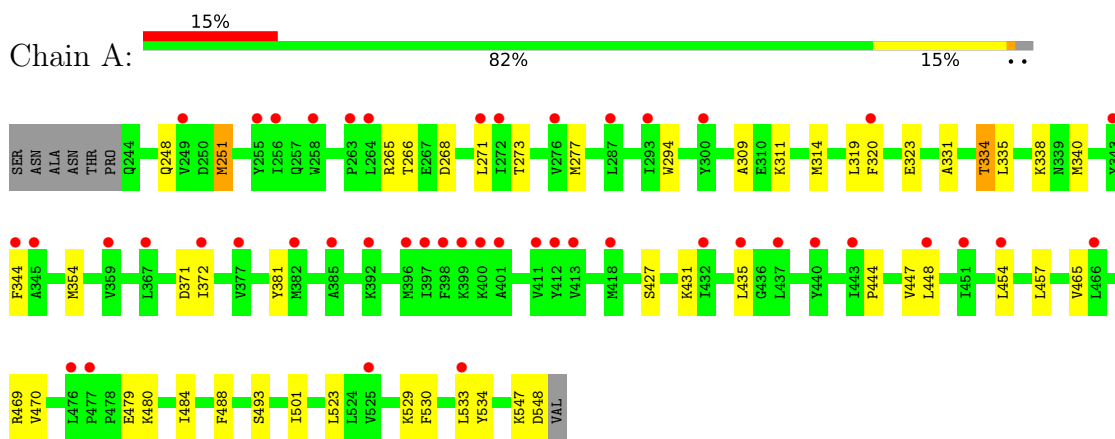
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	17	Total	O	0	0
			17	17		
4	B	18	Total	O	0	0
			18	18		
4	D	1	Total	O	0	0
			1	1		

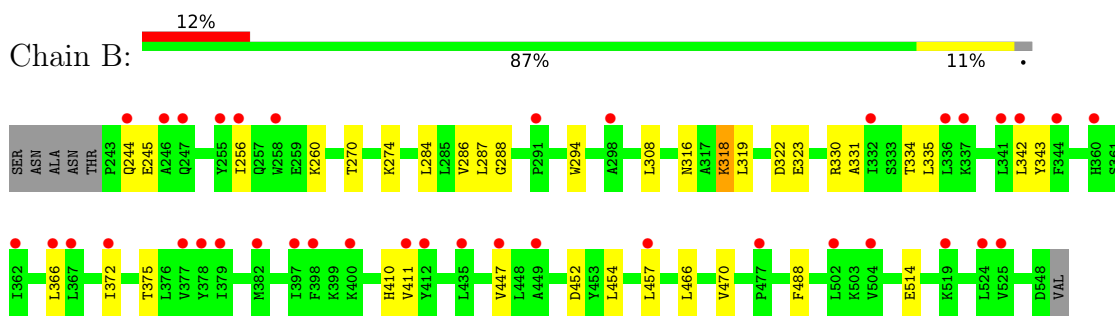
### 3 Residue-property plots [i](#)

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.

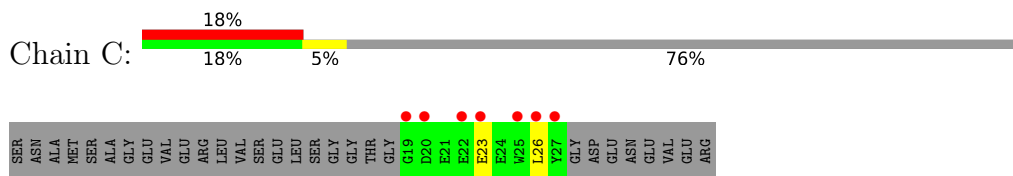
- Molecule 1: Cleavage stimulation factor subunit 3



- Molecule 1: Cleavage stimulation factor subunit 3



- Molecule 2: hFip1



- Molecule 2: hFip1



SER	ASN	ALA	MET	SER	ALA	GLY	GLU	VAL	GLU	ARG	LEU	VAL	SER	GLU	LEU	SER	GLY	GLY	THR	GLY	GLY	ASP	E21	L26	Y27	G28	ASP	GLU	ASN	GLU	VAL	GLU	ARG
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## 4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	157.61Å 157.61Å 161.00Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	56.31 – 2.55 104.12 – 2.55	Depositor EDS
% Data completeness (in resolution range)	100.0 (56.31-2.55) 100.0 (104.12-2.55)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.40 (at 2.55Å)	Xtrriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, $R_{free}$	0.212 , 0.247 0.198 , 0.231	Depositor DCC
$R_{free}$ test set	1916 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	71.0	Xtrriage
Anisotropy	0.025	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	10507	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	77.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.93% 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: 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	0.64	0/2584	0.80	3/3479 (0.1%)
1	B	0.64	0/2592	0.80	1/3490 (0.0%)
2	C	0.52	0/84	0.58	0/113
2	D	0.52	0/76	0.48	0/102
All	All	0.64	0/5336	0.79	4/7184 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	265	ARG	NE-CZ-NH2	-7.43	116.58	120.30
1	B	466	LEU	CB-CG-CD1	5.32	120.05	111.00
1	A	354	MET	CG-SD-CE	5.26	108.61	100.20
1	A	523	LEU	CB-CG-CD1	5.24	119.91	111.00

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	2528	2514	2513	28	0
1	B	2535	2522	2521	23	0
2	C	82	61	60	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	74	57	56	0	0
3	A	18	24	24	1	0
3	B	24	32	32	1	0
4	A	17	0	0	0	0
4	B	18	0	0	0	0
4	D	1	0	0	0	0
All	All	5297	5210	5206	50	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 5.

All (50) 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:318:LYS:HE3	1:B:322:ASP:OD2	1.75	0.87
1:A:266:THR:HG21	1:A:271:LEU:HD23	1.68	0.75
1:A:248:GLN:HA	1:A:251:MET:HE3	1.69	0.74
1:A:454:LEU:HD12	1:A:457:LEU:HD12	1.69	0.72
1:A:447:VAL:HG11	1:A:470:VAL:HG11	1.74	0.70
1:A:338:LYS:NZ	1:A:371:ASP:OD2	2.25	0.69
1:A:319:LEU:O	1:A:323:GLU:HG3	1.93	0.69
1:B:447:VAL:HG11	1:B:470:VAL:HG11	1.75	0.68
1:B:334:THR:O	1:B:335:LEU:HB2	1.94	0.67
1:A:266:THR:HG22	1:A:268:ASP:H	1.61	0.66
1:A:448:LEU:CD1	1:A:484:ILE:HD13	2.29	0.62
1:A:448:LEU:HD13	1:A:484:ILE:HD13	1.83	0.59
1:B:319:LEU:O	1:B:323:GLU:HG3	2.03	0.59
1:A:479:GLU:OE1	1:A:479:GLU:N	2.34	0.56
1:A:444:PRO:HG3	1:A:480:LYS:HB3	1.89	0.55
1:B:454:LEU:HD12	1:B:457:LEU:HD12	1.92	0.51
1:A:311:LYS:O	1:A:311:LYS:HG3	2.11	0.50
1:B:318:LYS:CE	1:B:322:ASP:OD2	2.52	0.50
1:B:366:LEU:HD11	1:B:372:ILE:HD13	1.93	0.50
1:B:288:GLY:HA3	1:B:335:LEU:HD13	1.93	0.50
1:B:514:GLU:N	1:B:514:GLU:OE1	2.46	0.49
1:B:256:ILE:HG22	1:B:260:LYS:HE2	1.95	0.49
1:A:334:THR:O	1:A:335:LEU:HB2	2.14	0.48
1:B:447:VAL:HG11	1:B:470:VAL:CG1	2.43	0.48
1:A:529:LYS:HE3	1:A:534:TYR:CZ	2.49	0.48
1:B:308:LEU:HD13	1:B:316:ASN:HB3	1.95	0.48
1:A:493:SER:HA	1:A:501:ILE:HD11	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:273:THR:HG21	1:A:320:PHE:CE2	2.50	0.47
1:A:309:ALA:O	1:A:314:MET:HE1	2.14	0.47
1:B:284:LEU:HD22	1:B:294:TRP:CE2	2.51	0.46
1:A:547:LYS:O	1:A:548:ASP:HB3	2.16	0.46
1:B:331:ALA:HB1	1:B:342:LEU:HD13	1.99	0.46
1:A:533:LEU:HD11	1:B:410:HIS:CG	2.52	0.45
1:A:294:TRP:CE3	1:A:331:ALA:HB2	2.52	0.45
1:A:277:MET:HG3	3:A:602:GOL:H12	1.97	0.45
1:A:435:LEU:HD22	2:C:26:LEU:HD11	1.99	0.44
1:B:286:VAL:HG23	1:B:287:LEU:HG	1.99	0.44
1:B:375:THR:HG23	1:B:411:VAL:HG13	1.98	0.44
1:B:244:GLN:HG3	1:B:245:GLU:N	2.33	0.43
1:B:270:THR:O	1:B:274:LYS:HG3	2.18	0.43
1:A:311:LYS:O	1:A:311:LYS:CG	2.66	0.43
1:B:343:TYR:CD1	1:B:366:LEU:HB2	2.55	0.42
1:B:323:GLU:OE1	3:B:602:GOL:H31	2.20	0.42
1:A:529:LYS:HG2	1:A:530:PHE:N	2.34	0.42
1:A:340:MET:HG2	1:A:344:PHE:CZ	2.55	0.41
1:B:366:LEU:HD11	1:B:372:ILE:CD1	2.50	0.41
1:A:454:LEU:HD12	1:A:454:LEU:HA	1.89	0.41
1:A:427:SER:O	1:A:431:LYS:HG3	2.20	0.41
1:B:330:ARG:O	1:B:334:THR:HG22	2.21	0.41
1:A:465:VAL:O	1:A:469:ARG:HG3	2.20	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	303/312 (97%)	298 (98%)	5 (2%)	0	100	100
1	B	304/312 (97%)	298 (98%)	6 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C	7/38 (18%)	7 (100%)	0	0	100	100
2	D	6/38 (16%)	6 (100%)	0	0	100	100
All	All	620/700 (89%)	609 (98%)	11 (2%)	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	268/274 (98%)	263 (98%)	5 (2%)	57	72
1	B	269/274 (98%)	266 (99%)	3 (1%)	73	83
2	C	8/30 (27%)	7 (88%)	1 (12%)	4	4
2	D	7/30 (23%)	7 (100%)	0	100	100
All	All	552/608 (91%)	543 (98%)	9 (2%)	62	77

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	251	MET
1	A	334	THR
1	A	372	ILE
1	A	381	TYR
1	A	488	PHE
1	B	318	LYS
1	B	452	ASP
1	B	488	PHE
2	C	23	GLU

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

### 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

7 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	$\# Z  > 2$
3	GOL	B	603	-	5,5,5	0.78	0	5,5,5	1.84	2 (40%)
3	GOL	A	601	-	5,5,5	0.64	0	5,5,5	0.71	0
3	GOL	B	604	-	5,5,5	0.71	0	5,5,5	1.03	0
3	GOL	A	603	-	5,5,5	0.68	0	5,5,5	0.64	0
3	GOL	B	602	-	5,5,5	0.51	0	5,5,5	1.09	0
3	GOL	B	601	-	5,5,5	0.60	0	5,5,5	0.69	0
3	GOL	A	602	-	5,5,5	0.76	0	5,5,5	0.98	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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	B	603	-	-	2/4/4/4	-
3	GOL	A	601	-	-	0/4/4/4	-
3	GOL	B	604	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	A	603	-	-	1/4/4/4	-
3	GOL	B	602	-	-	2/4/4/4	-
3	GOL	B	601	-	-	0/4/4/4	-
3	GOL	A	602	-	-	2/4/4/4	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	603	GOL	C3-C2-C1	2.47	121.29	111.70
3	B	603	GOL	O1-C1-C2	2.12	120.37	110.20

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	602	GOL	C1-C2-C3-O3
3	B	603	GOL	O1-C1-C2-C3
3	B	604	GOL	O1-C1-C2-C3
3	A	602	GOL	C1-C2-C3-O3
3	B	603	GOL	O2-C2-C3-O3
3	B	602	GOL	O2-C2-C3-O3
3	A	602	GOL	O2-C2-C3-O3
3	A	603	GOL	O1-C1-C2-O2
3	B	604	GOL	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	602	GOL	1	0
3	A	602	GOL	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	305/312 (97%)	1.11	46 (15%) 2 2	51, 67, 102, 138	0
1	B	306/312 (98%)	1.11	38 (12%) 4 5	49, 64, 94, 127	0
2	C	9/38 (23%)	4.92	7 (77%) 0 0	97, 108, 126, 128	0
2	D	8/38 (21%)	1.53	2 (25%) 0 0	95, 107, 119, 127	0
All	All	628/700 (89%)	1.17	93 (14%) 2 2	49, 66, 104, 138	0

All (93) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	25	TRP	10.1
2	C	26	LEU	9.0
2	C	27	TYR	7.7
2	C	20	ASP	5.8
2	D	26	LEU	4.5
1	A	249	VAL	4.3
2	C	23	GLU	3.9
1	B	372	ILE	3.6
1	A	476	LEU	3.5
1	A	392	LYS	3.5
1	A	411	VAL	3.4
1	B	477	PRO	3.3
1	A	276	VAL	3.3
1	A	396	MET	3.2
1	A	477	PRO	3.2
1	A	451	ILE	3.2
1	A	440	TYR	3.1
1	A	287	LEU	3.1
1	B	244	GLN	3.1
1	B	367	LEU	3.1
1	B	524	LEU	3.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	435	LEU	3.0
1	A	399	LYS	3.0
1	A	258	TRP	3.0
1	B	411	VAL	3.0
1	B	397	ILE	3.0
1	A	382	MET	3.0
1	B	336	LEU	2.9
1	A	256	ILE	2.9
1	A	432	ILE	2.8
1	A	264	LEU	2.8
1	A	320	PHE	2.8
1	B	379	ILE	2.8
1	A	255	TYR	2.8
1	A	412	TYR	2.7
1	A	397	ILE	2.7
1	A	400	LYS	2.7
1	A	293	ILE	2.7
1	A	533	LEU	2.6
1	B	435	LEU	2.6
1	A	272	ILE	2.6
1	A	448	LEU	2.6
1	A	372	ILE	2.5
1	A	413	VAL	2.5
1	A	359	VAL	2.5
1	A	263	PRO	2.5
1	A	466	LEU	2.5
1	B	502	LEU	2.5
1	A	344	PHE	2.5
2	D	27	TYR	2.5
1	B	398	PHE	2.5
1	B	256	ILE	2.4
1	B	332	ILE	2.4
1	B	360	HIS	2.4
1	B	255	TYR	2.4
1	B	519	LYS	2.4
1	A	271	LEU	2.4
2	C	22	GLU	2.4
1	B	449	ALA	2.4
1	B	247	GLN	2.4
1	A	437	LEU	2.4
1	A	443	ILE	2.3
1	B	341	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	525	VAL	2.3
1	B	298	ALA	2.3
1	A	367	LEU	2.3
1	B	400	LYS	2.3
1	B	447	VAL	2.3
1	B	378	TYR	2.3
1	A	418	MET	2.3
2	C	19	GLY	2.3
1	A	401	ALA	2.3
1	B	362	ILE	2.3
1	A	398	PHE	2.3
1	A	300	TYR	2.3
1	B	457	LEU	2.3
1	B	377	VAL	2.2
1	A	345	ALA	2.2
1	A	454	LEU	2.2
1	B	412	TYR	2.2
1	B	246	ALA	2.2
1	B	525	VAL	2.2
1	A	385	ALA	2.2
1	B	344	PHE	2.2
1	B	337	LYS	2.2
1	A	377	VAL	2.2
1	B	382	MET	2.1
1	B	291	PRO	2.1
1	B	504	VAL	2.1
1	A	343	TYR	2.1
1	B	258	TRP	2.1
1	B	366	LEU	2.1
1	B	342	LEU	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(Å <sup>2</sup> )	Q<0.9
3	GOL	B	602	6/6	0.59	0.37	84,106,123,127	0
3	GOL	B	603	6/6	0.61	0.42	54,70,86,86	0
3	GOL	B	601	6/6	0.67	0.44	88,123,148,148	0
3	GOL	A	602	6/6	0.70	0.91	80,96,111,124	0
3	GOL	A	601	6/6	0.71	0.38	76,106,132,132	0
3	GOL	B	604	6/6	0.85	0.91	77,93,112,112	0
3	GOL	A	603	6/6	0.95	0.30	55,67,80,81	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.