



# Full wwPDB X-ray Structure Validation Report ⓘ

May 31, 2022 – 06:13 pm BST

PDB ID : 7QIT  
Title : CRYSTAL STRUCTURE OF THE P1 trifluoroethylglycine (TfeGly) BPTI  
MUTANT- BOVINE CHYMOTRYPSIN COMPLEX  
Authors : Dimos, N.; Leppkes, J.; Kokschi, B.; Wahl, M.C.; Loll, B.  
Deposited on : 2021-12-15  
Resolution : 1.99 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.

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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 : 2.28.1  
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) : 2.28.1

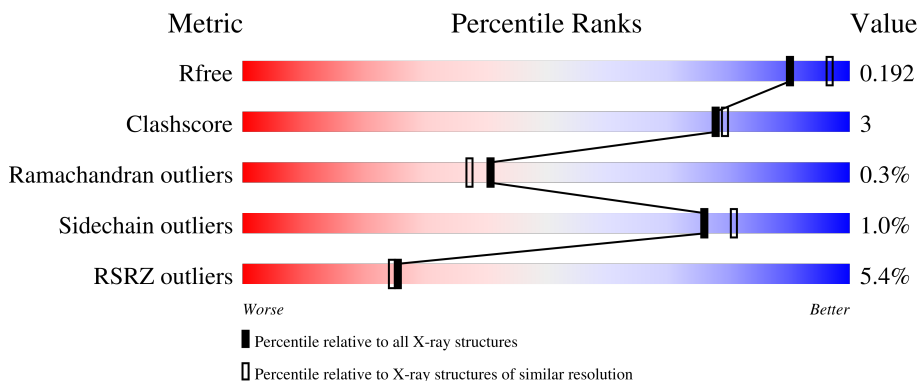
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.99 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (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  $\geq 3$ , 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	13	 8% 85% 15%
1	E	13	 8% 85% 15%
2	B	131	 4% 95% 5%
2	F	131	 6% 94% 6%
3	C	97	 6% 97%

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Mol	Chain	Length	Quality of chain
3	G	97	
4	D	58	
4	H	58	

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
5	GOL	B	305	-	-	-	X
5	GOL	D	102	-	-	X	-
5	GOL	F	202	-	-	-	X
5	GOL	G	304	-	-	-	X

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 5321 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 Chymotrypsin A chain A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	11	Total	C	N	O	S	0	1	0
			80	51	13	15	1			
1	E	11	Total	C	N	O	S	0	0	0
			74	48	12	13	1			

- Molecule 2 is a protein called Chymotrypsin A chain B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	131	Total	C	N	O	S	0	6	0
			1026	645	170	207	4			
2	F	131	Total	C	N	O	S	0	5	0
			1017	639	169	205	4			

- Molecule 3 is a protein called Chymotrypsin A chain C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	97	Total	C	N	O	S	0	5	0
			738	456	129	145	8			
3	G	97	Total	C	N	O	S	0	9	0
			769	474	139	149	7			

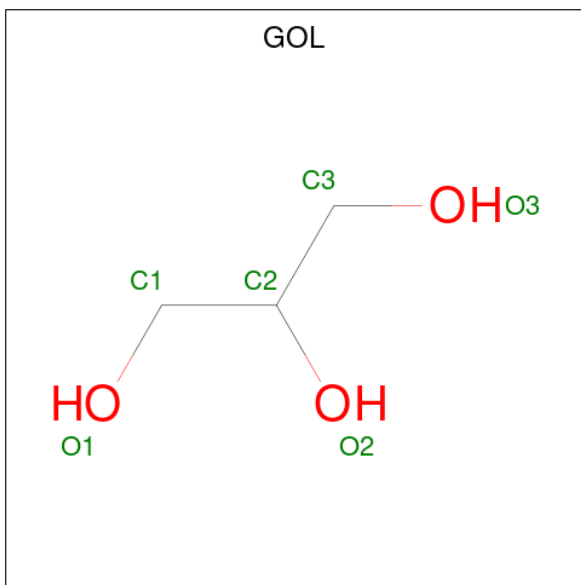
- Molecule 4 is a protein called Pancreatic trypsin inhibitor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	F	N	O				S
4	D	58	Total	C	F	N	O	S	0	3	0
			481	297	3	90	84	7			
4	H	58	Total	C	F	N	O	S	0	2	0
			474	293	3	89	82	7			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	15	3EG	LYS	engineered mutation	UNP P00974
H	15	3EG	LYS	engineered mutation	UNP P00974

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	C	1	Total 6	C 3	O 3	0	0
5	C	1	Total 6	C 3	O 3	0	0
5	C	1	Total 6	C 3	O 3	0	0
5	C	1	Total 6	C 3	O 3	0	0
5	C	1	Total 6	C 3	O 3	0	0
5	C	1	Total 6	C 3	O 3	0	0
5	C	1	Total 6	C 3	O 3	0	0
5	D	1	Total 6	C 3	O 3	0	0
5	D	1	Total 6	C 3	O 3	0	0
5	F	1	Total 6	C 3	O 3	0	0
5	F	1	Total 6	C 3	O 3	0	0
5	F	1	Total 6	C 3	O 3	0	0
5	F	1	Total 6	C 3	O 3	0	0
5	G	1	Total 6	C 3	O 3	0	0
5	G	1	Total 6	C 3	O 3	0	0
5	G	1	Total 6	C 3	O 3	0	0
5	G	1	Total 6	C 3	O 3	0	0
5	H	1	Total 6	C 3	O 3	0	0
5	H	1	Total 6	C 3	O 3	0	0

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
6	B	1	5	4	1	0	0
6	B	1	5	4	1	0	0
6	C	1	5	4	1	0	1
6	C	1	5	4	1	0	1
6	C	1	5	4	1	0	1
6	C	1	5	4	1	0	1
6	D	1	5	4	1	0	1
6	D	1	5	4	1	0	0
6	D	1	5	4	1	0	0
6	D	1	5	4	1	0	1
6	D	1	5	4	1	0	1
6	D	1	5	4	1	0	0
6	D	1	5	4	1	0	1
6	F	1	5	4	1	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	F	1	Total 5	O 4	S 1	0	0
6	F	1	Total 5	O 4	S 1	0	1
6	F	1	Total 5	O 4	S 1	0	1
6	G	1	Total 5	O 4	S 1	0	0
6	G	1	Total 5	O 4	S 1	0	0
6	H	1	Total 5	O 4	S 1	0	0

- Molecule 7 is water.

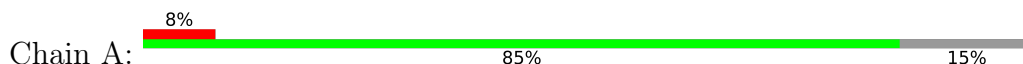
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	6	Total 6	O 6	0	0
7	B	82	Total 82	O 82	0	4
7	C	58	Total 58	O 58	0	3
7	D	54	Total 54	O 54	0	9
7	E	4	Total 4	O 4	0	0
7	F	88	Total 88	O 88	0	6
7	G	49	Total 49	O 49	0	8
7	H	41	Total 41	O 41	0	2



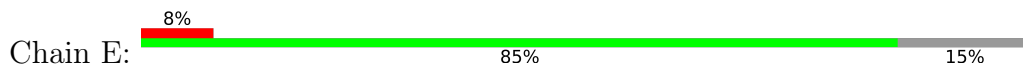
### 3 Residue-property plots [i](#)

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.

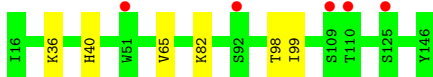
- Molecule 1: Chymotrypsin A chain A



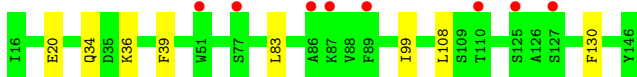
- Molecule 1: Chymotrypsin A chain A



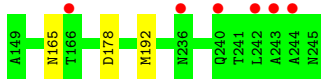
- Molecule 2: Chymotrypsin A chain B



- Molecule 2: Chymotrypsin A chain B



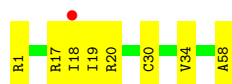
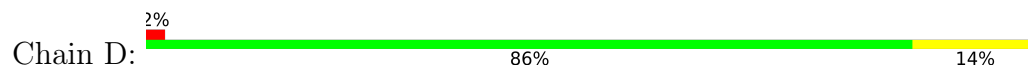
- Molecule 3: Chymotrypsin A chain C



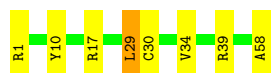
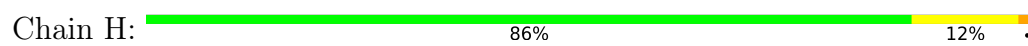
- Molecule 3: Chymotrypsin A chain C



- Molecule 4: Pancreatic trypsin inhibitor



- Molecule 4: Pancreatic trypsin inhibitor



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	99.96Å 99.96Å 206.52Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	43.29 – 1.99 48.58 – 1.99	Depositor EDS
% Data completeness (in resolution range)	99.0 (43.29-1.99) 99.3 (48.58-1.99)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.17 (at 1.98Å)	Xtrriage
Refinement program	PHENIX 1.19.1_4122	Depositor
R, $R_{free}$	0.170 , 0.191 0.171 , 0.192	Depositor DCC
$R_{free}$ test set	1058 reflections (1.34%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	39.0	Xtrriage
Anisotropy	0.513	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>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtrriage
Estimated twinning fraction	0.048 for h,-h-k,-l	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	5321	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.48% 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: 3EG, SO4, 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	0.38	0/80	0.60	0/108
1	E	0.38	0/75	0.58	0/103
2	B	0.57	0/1046	0.61	0/1424
2	F	0.61	0/1037	0.63	0/1411
3	C	0.58	0/751	0.63	0/1023
3	G	0.52	0/782	0.61	0/1062
4	D	0.73	1/482 (0.2%)	0.77	0/644
4	H	0.72	1/475 (0.2%)	0.79	0/634
All	All	0.60	2/4728 (0.0%)	0.65	0/6409

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	H	30	CYS	CB-SG	5.50	1.91	1.82
4	D	30	CYS	CB-SG	5.21	1.91	1.82

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	80	0	86	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	74	0	81	0	0
2	B	1026	0	988	3	0
2	F	1017	0	981	3	0
3	C	738	0	729	4	0
3	G	769	0	765	4	0
4	D	481	0	453	9	0
4	H	474	0	447	6	1
5	A	6	0	8	0	0
5	B	36	0	48	0	0
5	C	66	0	88	5	0
5	D	12	0	16	5	0
5	F	24	0	32	0	0
5	G	24	0	32	1	0
5	H	12	0	16	1	0
6	B	10	0	0	0	0
6	C	20	0	0	1	0
6	D	35	0	0	0	1
6	F	20	0	0	0	0
6	G	10	0	0	0	0
6	H	5	0	0	0	0
7	A	6	0	0	0	0
7	B	82	0	0	1	0
7	C	58	0	0	1	0
7	D	54	0	0	0	0
7	E	4	0	0	0	0
7	F	88	0	0	0	0
7	G	49	0	0	0	0
7	H	41	0	0	0	0
All	All	5321	0	4770	28	1

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 3.

All (28) 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)
4:D:20:ARG:HE	5:D:102:GOL:H31	1.41	0.85
4:D:17[B]:ARG:HG3	4:D:34:VAL:HG11	1.67	0.75
4:H:17[B]:ARG:HG3	4:H:34:VAL:HG11	1.70	0.74
2:B:65[B]:VAL:HG11	2:B:82[B]:LYS:HG3	1.70	0.73
4:D:18:ILE:HG21	5:D:102:GOL:H12	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:178:ASP:H	5:C:308:GOL:H31	1.61	0.64
4:D:17[B]:ARG:HG3	4:D:34:VAL:CG1	2.31	0.60
4:H:17[B]:ARG:HG3	4:H:34:VAL:CG1	2.33	0.59
4:H:1:ARG:HB2	4:H:58:ALA:HB2	1.86	0.57
4:D:20:ARG:HE	5:D:102:GOL:C3	2.17	0.55
3:C:165:ASN:H	5:C:305:GOL:H11	1.73	0.54
7:B:410:HOH:O	5:D:102:GOL:H11	2.09	0.51
2:B:98:THR:HG21	5:C:309:GOL:H32	1.93	0.51
3:G:177:LYS:HD2	5:G:303:GOL:H2	1.93	0.51
4:D:18:ILE:CG2	5:D:102:GOL:H12	2.40	0.50
4:D:1:ARG:HB2	4:D:58:ALA:HB2	1.93	0.49
4:H:39:ARG:O	5:H:101:GOL:H12	2.13	0.48
4:D:19:ILE:HG12	4:H:29:LEU:HD23	1.96	0.46
2:F:130:PHE:CD1	3:G:203[A]:LYS:HE2	2.52	0.45
3:C:165:ASN:HB2	5:C:305:GOL:H32	1.99	0.45
6:C:313[A]:SO4:O4	7:C:402:HOH:O	2.21	0.44
4:H:1:ARG:CB	4:H:58:ALA:HB2	2.46	0.44
3:C:178:ASP:H	5:C:308:GOL:C3	2.30	0.43
3:G:202[A]:LYS:HA	3:G:206[A]:ALA:O	2.18	0.43
2:F:83:LEU:HD13	2:F:108:LEU:HD13	2.00	0.42
2:B:40:HIS:O	4:D:17[A]:ARG:HD3	2.20	0.42
3:G:211:GLY:HA2	3:G:229:ALA:O	2.21	0.41
2:F:34:GLN:HA	2:F:39:PHE:O	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:H:10:TYR:OH	6:D:109[B]:SO4:O2[6_455]	2.09	0.11

## 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	9/13 (69%)	9 (100%)	0	0	100	100
1	E	9/13 (69%)	9 (100%)	0	0	100	100
2	B	135/131 (103%)	131 (97%)	3 (2%)	1 (1%)	22	16
2	F	134/131 (102%)	131 (98%)	2 (2%)	1 (1%)	22	16
3	C	100/97 (103%)	99 (99%)	1 (1%)	0	100	100
3	G	104/97 (107%)	103 (99%)	1 (1%)	0	100	100
4	D	58/58 (100%)	55 (95%)	3 (5%)	0	100	100
4	H	57/58 (98%)	55 (96%)	2 (4%)	0	100	100
All	All	606/598 (101%)	592 (98%)	12 (2%)	2 (0%)	41	37

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	F	99	ILE
2	B	99	ILE

### 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	10/10 (100%)	10 (100%)	0	100	100
1	E	9/10 (90%)	9 (100%)	0	100	100
2	B	115/109 (106%)	114 (99%)	1 (1%)	78	83
2	F	114/109 (105%)	112 (98%)	2 (2%)	59	63
3	C	82/77 (106%)	80 (98%)	2 (2%)	49	51
3	G	84/77 (109%)	84 (100%)	0	100	100
4	D	48/45 (107%)	48 (100%)	0	100	100
4	H	47/45 (104%)	46 (98%)	1 (2%)	53	57
All	All	509/482 (106%)	503 (99%)	6 (1%)	76	76

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	36	LYS
3	C	192[A]	MET
3	C	192[B]	MET
2	F	20	GLU
2	F	36	LYS
4	H	29	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	236	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

2 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
4	3EG	D	15	4	7,8,9	1.13	0	6,11,13	0.91	0
4	3EG	H	15	4	7,8,9	1.17	0	6,11,13	0.95	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
4	3EG	D	15	4	-	1/4/7/9	-
4	3EG	H	15	4	-	0/4/7/9	-



There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	15	3EG	O-C-CA-CB

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

50 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
5	GOL	F	201	-	5,5,5	1.09	1 (20%)	5,5,5	0.97	0
5	GOL	B	302	-	5,5,5	1.37	0	5,5,5	0.80	0
5	GOL	H	101	-	5,5,5	1.35	1 (20%)	5,5,5	0.85	0
6	SO4	F	206	-	4,4,4	0.20	0	6,6,6	0.50	0
5	GOL	F	204	-	5,5,5	0.64	0	5,5,5	1.06	0
5	GOL	H	102	-	5,5,5	0.99	0	5,5,5	1.03	0
5	GOL	C	307	-	5,5,5	0.78	0	5,5,5	0.88	0
6	SO4	D	105	-	4,4,4	0.24	0	6,6,6	0.29	0
6	SO4	D	109[B]	-	4,4,4	0.28	0	6,6,6	0.18	0
6	SO4	B	307	-	4,4,4	0.20	0	6,6,6	0.23	0
6	SO4	G	306	-	4,4,4	0.16	0	6,6,6	0.24	0
5	GOL	B	306	-	5,5,5	0.77	0	5,5,5	1.16	0
6	SO4	G	305	-	4,4,4	0.17	0	6,6,6	0.51	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	SO4	H	103	-	4,4,4	0.25	0	6,6,6	0.48	0
6	SO4	C	313[A]	-	4,4,4	0.18	0	6,6,6	0.57	0
6	SO4	C	312[A]	-	4,4,4	0.17	0	6,6,6	0.69	0
5	GOL	G	303	-	5,5,5	1.25	0	5,5,5	0.87	0
6	SO4	D	106[A]	-	4,4,4	0.24	0	6,6,6	0.32	0
6	SO4	F	207[A]	-	4,4,4	0.15	0	6,6,6	0.30	0
5	GOL	C	303	-	5,5,5	1.15	0	5,5,5	1.03	0
5	GOL	C	306	-	5,5,5	1.11	0	5,5,5	1.29	0
5	GOL	C	310	-	5,5,5	1.88	2 (40%)	5,5,5	1.64	2 (40%)
5	GOL	B	303	-	5,5,5	1.02	0	5,5,5	0.95	0
6	SO4	F	208[B]	-	4,4,4	0.21	0	6,6,6	0.52	0
5	GOL	C	305	-	5,5,5	1.28	1 (20%)	5,5,5	0.92	0
5	GOL	G	301	-	5,5,5	1.01	0	5,5,5	0.97	0
5	GOL	D	101	-	5,5,5	1.31	1 (20%)	5,5,5	0.83	0
5	GOL	B	305	-	5,5,5	1.43	1 (20%)	5,5,5	0.73	0
5	GOL	B	301	-	5,5,5	0.76	0	5,5,5	1.01	0
6	SO4	C	315[B]	-	4,4,4	0.18	0	6,6,6	0.25	0
5	GOL	C	309	-	5,5,5	1.06	0	5,5,5	0.74	0
5	GOL	C	304	-	5,5,5	0.75	0	5,5,5	1.18	0
5	GOL	F	203	-	5,5,5	1.16	0	5,5,5	0.79	0
5	GOL	G	302	-	5,5,5	1.00	0	5,5,5	1.03	0
5	GOL	C	301	-	5,5,5	1.42	1 (20%)	5,5,5	0.90	0
5	GOL	D	102	-	5,5,5	1.33	0	5,5,5	1.11	0
5	GOL	F	202	-	5,5,5	1.06	0	5,5,5	0.94	0
5	GOL	G	304	-	5,5,5	1.32	1 (20%)	5,5,5	0.74	0
5	GOL	C	308	-	5,5,5	1.21	1 (20%)	5,5,5	0.85	0
6	SO4	C	314[B]	-	4,4,4	0.23	0	6,6,6	0.24	0
6	SO4	D	104	-	4,4,4	0.17	0	6,6,6	0.43	0
6	SO4	F	205	-	4,4,4	0.20	0	6,6,6	0.17	0
5	GOL	C	311	-	5,5,5	1.30	1 (20%)	5,5,5	1.08	0
5	GOL	C	302	-	5,5,5	1.16	0	5,5,5	0.82	0
6	SO4	D	108	-	4,4,4	0.45	0	6,6,6	0.67	0
5	GOL	B	304	-	5,5,5	1.02	0	5,5,5	0.95	0
6	SO4	D	103[A]	-	4,4,4	0.32	0	6,6,6	0.52	0
6	SO4	B	308	-	4,4,4	0.22	0	6,6,6	0.35	0
5	GOL	A	101	-	5,5,5	1.07	1 (20%)	5,5,5	1.08	0
6	SO4	D	107[B]	-	4,4,4	0.17	0	6,6,6	0.30	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	GOL	F	201	-	-	2/4/4/4	-
5	GOL	B	302	-	-	4/4/4/4	-
5	GOL	H	101	-	-	2/4/4/4	-
5	GOL	F	204	-	-	2/4/4/4	-
5	GOL	H	102	-	-	4/4/4/4	-
5	GOL	C	307	-	-	2/4/4/4	-
5	GOL	B	306	-	-	3/4/4/4	-
5	GOL	G	303	-	-	4/4/4/4	-
5	GOL	C	303	-	-	2/4/4/4	-
5	GOL	C	306	-	-	1/4/4/4	-
5	GOL	C	310	-	-	1/4/4/4	-
5	GOL	B	303	-	-	2/4/4/4	-
5	GOL	C	305	-	-	2/4/4/4	-
5	GOL	G	301	-	-	2/4/4/4	-
5	GOL	D	101	-	-	0/4/4/4	-
5	GOL	B	305	-	-	2/4/4/4	-
5	GOL	B	301	-	-	0/4/4/4	-
5	GOL	C	309	-	-	3/4/4/4	-
5	GOL	C	304	-	-	1/4/4/4	-
5	GOL	F	203	-	-	2/4/4/4	-
5	GOL	G	302	-	-	2/4/4/4	-
5	GOL	C	301	-	-	2/4/4/4	-
5	GOL	D	102	-	-	1/4/4/4	-
5	GOL	F	202	-	-	2/4/4/4	-
5	GOL	G	304	-	-	4/4/4/4	-
5	GOL	C	308	-	-	3/4/4/4	-
5	GOL	C	311	-	-	3/4/4/4	-
5	GOL	C	302	-	-	0/4/4/4	-
5	GOL	B	304	-	-	2/4/4/4	-
5	GOL	A	101	-	-	3/4/4/4	-

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	310	GOL	C3-C2	2.80	1.63	1.51
5	C	310	GOL	O2-C2	2.79	1.51	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	305	GOL	C3-C2	2.47	1.61	1.51
5	C	301	GOL	C1-C2	2.34	1.61	1.51
5	C	305	GOL	C3-C2	2.31	1.61	1.51
5	C	311	GOL	C3-C2	2.30	1.61	1.51
5	D	101	GOL	C1-C2	2.17	1.60	1.51
5	H	101	GOL	C3-C2	2.11	1.60	1.51
5	A	101	GOL	C1-C2	2.10	1.60	1.51
5	F	201	GOL	O2-C2	-2.08	1.37	1.43
5	C	308	GOL	C3-C2	2.05	1.60	1.51
5	G	304	GOL	C3-C2	2.05	1.60	1.51

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	310	GOL	O2-C2-C3	2.31	119.30	109.12
5	C	310	GOL	O2-C2-C1	2.06	118.20	109.12

There are no chirality outliers.

All (63) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	302	GOL	O1-C1-C2-C3
5	B	302	GOL	C1-C2-C3-O3
5	B	302	GOL	O2-C2-C3-O3
5	B	303	GOL	O1-C1-C2-C3
5	B	304	GOL	C1-C2-C3-O3
5	B	304	GOL	O2-C2-C3-O3
5	B	306	GOL	C1-C2-C3-O3
5	C	301	GOL	C1-C2-C3-O3
5	C	303	GOL	O1-C1-C2-C3
5	C	305	GOL	O1-C1-C2-C3
5	C	309	GOL	C1-C2-C3-O3
5	C	309	GOL	O2-C2-C3-O3
5	C	311	GOL	C1-C2-C3-O3
5	D	102	GOL	O1-C1-C2-C3
5	F	203	GOL	C1-C2-C3-O3
5	F	204	GOL	O1-C1-C2-C3
5	G	302	GOL	O1-C1-C2-C3
5	G	304	GOL	O1-C1-C2-O2
5	G	304	GOL	O1-C1-C2-C3
5	G	304	GOL	C1-C2-C3-O3
5	H	102	GOL	C1-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
5	B	302	GOL	O1-C1-C2-O2
5	B	306	GOL	O2-C2-C3-O3
5	C	305	GOL	O1-C1-C2-O2
5	A	101	GOL	O1-C1-C2-C3
5	B	305	GOL	C1-C2-C3-O3
5	B	306	GOL	O1-C1-C2-C3
5	C	304	GOL	C1-C2-C3-O3
5	C	307	GOL	O1-C1-C2-C3
5	C	308	GOL	O1-C1-C2-C3
5	C	310	GOL	O1-C1-C2-C3
5	C	311	GOL	O1-C1-C2-C3
5	F	201	GOL	C1-C2-C3-O3
5	F	202	GOL	O1-C1-C2-C3
5	G	301	GOL	O1-C1-C2-C3
5	G	303	GOL	C1-C2-C3-O3
5	H	101	GOL	O1-C1-C2-C3
5	H	102	GOL	O1-C1-C2-C3
5	B	305	GOL	O2-C2-C3-O3
5	C	303	GOL	O1-C1-C2-O2
5	C	307	GOL	O1-C1-C2-O2
5	C	311	GOL	O2-C2-C3-O3
5	F	203	GOL	O2-C2-C3-O3
5	G	302	GOL	O1-C1-C2-O2
5	G	303	GOL	O2-C2-C3-O3
5	G	304	GOL	O2-C2-C3-O3
5	H	102	GOL	O2-C2-C3-O3
5	B	303	GOL	O1-C1-C2-O2
5	C	301	GOL	O2-C2-C3-O3
5	F	201	GOL	O2-C2-C3-O3
5	F	204	GOL	O1-C1-C2-O2
5	F	202	GOL	O2-C2-C3-O3
5	G	301	GOL	O1-C1-C2-O2
5	G	303	GOL	O1-C1-C2-O2
5	A	101	GOL	O1-C1-C2-O2
5	H	101	GOL	O1-C1-C2-O2
5	C	306	GOL	O2-C2-C3-O3
5	A	101	GOL	C1-C2-C3-O3
5	C	309	GOL	O1-C1-C2-C3
5	C	308	GOL	O2-C2-C3-O3
5	G	303	GOL	O1-C1-C2-C3
5	C	308	GOL	O1-C1-C2-O2
5	H	102	GOL	O1-C1-C2-O2

There are no ring outliers.

8 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	H	101	GOL	1	0
6	D	109[B]	SO4	0	1
6	C	313[A]	SO4	1	0
5	G	303	GOL	1	0
5	C	305	GOL	2	0
5	C	309	GOL	1	0
5	D	102	GOL	5	0
5	C	308	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	11/13 (84%)	0.54	1 (9%) 9 8	53, 56, 72, 97	0
1	E	11/13 (84%)	0.70	1 (9%) 9 8	58, 62, 80, 101	0
2	B	131/131 (100%)	0.38	5 (3%) 40 39	34, 51, 71, 91	0
2	F	131/131 (100%)	0.48	8 (6%) 21 20	36, 52, 76, 88	0
3	C	97/97 (100%)	0.45	6 (6%) 20 19	34, 46, 67, 70	0
3	G	97/97 (100%)	0.63	10 (10%) 6 6	36, 50, 73, 80	0
4	D	57/58 (98%)	0.58	1 (1%) 68 66	33, 39, 58, 76	0
4	H	57/58 (98%)	0.53	0 100 100	33, 37, 56, 78	0
All	All	592/598 (98%)	0.50	32 (5%) 25 24	33, 49, 72, 101	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	G	240	GLN	5.0
3	C	244	ALA	4.6
1	E	11	SER	4.5
2	F	86	ALA	3.9
2	F	125[A]	SER	3.8
3	G	242	LEU	3.8
1	A	11[A]	SER	3.5
3	G	241	THR	3.4
3	G	204[A]	ASN	3.3
2	F	110	THR	3.3
3	C	240	GLN	3.3
3	G	244	ALA	3.1
2	F	51	TRP	3.1
3	G	205[A]	GLY	3.0
2	B	110	THR	3.0
3	C	243	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
3	C	236	ASN	2.7
3	G	203[A]	LYS	2.7
3	G	245	ASN	2.7
4	D	18	ILE	2.7
3	G	243	ALA	2.6
2	B	51	TRP	2.5
3	C	242	LEU	2.5
2	F	87	LYS	2.4
2	F	89	PHE	2.3
2	F	127	SER	2.3
3	C	166[A]	THR	2.3
3	G	236	ASN	2.3
2	B	109	SER	2.2
2	B	125	SER	2.2
2	B	92	SER	2.1
2	F	77	SER	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, 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
4	3EG	D	15	9/10	0.99	0.14	36,38,41,44	0
4	3EG	H	15	9/10	0.99	0.13	35,38,40,41	0

## 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
5	GOL	G	304	6/6	0.46	0.41	82,86,94,98	0
5	GOL	B	305	6/6	0.57	0.43	74,81,85,90	0
5	GOL	F	202	6/6	0.64	0.58	85,92,98,100	0
5	GOL	C	311	6/6	0.68	0.35	81,90,92,95	0
5	GOL	D	102	6/6	0.74	0.27	50,59,77,82	0
5	GOL	F	203	6/6	0.75	0.17	83,87,90,93	0
6	SO4	C	314[B]	5/5	0.75	0.27	46,47,55,68	5
5	GOL	C	301	6/6	0.76	0.27	66,76,82,85	0
5	GOL	C	303	6/6	0.76	0.34	79,84,89,90	0
5	GOL	C	310	6/6	0.76	0.21	42,61,64,68	0
5	GOL	B	301	6/6	0.77	0.18	78,81,88,92	0
5	GOL	B	303	6/6	0.78	0.28	72,81,87,90	0
5	GOL	G	301	6/6	0.78	0.30	71,92,94,94	0
5	GOL	A	101	6/6	0.80	0.22	56,75,82,86	0
5	GOL	C	309	6/6	0.81	0.18	63,69,83,91	0
5	GOL	G	303	6/6	0.81	0.17	52,78,90,91	0
5	GOL	B	304	6/6	0.83	0.32	70,73,75,83	0
5	GOL	F	201	6/6	0.83	0.26	62,78,89,91	0
6	SO4	F	207[A]	5/5	0.83	0.21	52,61,68,83	5
5	GOL	D	101	6/6	0.84	0.32	60,70,76,85	0
5	GOL	H	101	6/6	0.84	0.22	47,52,58,67	0
5	GOL	G	302	6/6	0.85	0.17	77,84,96,96	0
5	GOL	B	302	6/6	0.85	0.28	67,72,80,86	0
5	GOL	C	305	6/6	0.86	0.14	72,75,80,86	0
5	GOL	C	308	6/6	0.87	0.26	43,70,83,93	0
5	GOL	C	304	6/6	0.88	0.14	68,80,89,101	0
5	GOL	C	302	6/6	0.88	0.20	60,78,89,97	0
5	GOL	H	102	6/6	0.89	0.17	43,65,67,77	0
6	SO4	F	208[B]	5/5	0.89	0.18	52,63,68,80	5
5	GOL	C	307	6/6	0.91	0.22	65,83,96,105	0
5	GOL	F	204	6/6	0.92	0.16	72,81,84,86	0
5	GOL	B	306	6/6	0.93	0.17	61,74,86,86	0
6	SO4	G	306	5/5	0.93	0.13	69,73,88,104	5
6	SO4	F	206	5/5	0.95	0.26	67,70,84,88	0
6	SO4	G	305	5/5	0.95	0.12	47,52,67,70	5
5	GOL	C	306	6/6	0.95	0.16	58,64,70,84	0
6	SO4	D	109[B]	5/5	0.96	0.18	41,44,45,46	5
6	SO4	B	308	5/5	0.96	0.20	59,67,76,79	0
6	SO4	D	108	5/5	0.96	0.10	50,52,78,87	0
6	SO4	C	312[A]	5/5	0.97	0.16	42,43,44,49	5
6	SO4	D	106[A]	5/5	0.98	0.16	42,45,47,49	5
6	SO4	D	107[B]	5/5	0.98	0.14	40,44,46,48	5
6	SO4	B	307	5/5	0.98	0.21	60,65,78,90	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
6	SO4	C	315[B]	5/5	0.98	0.18	40,41,48,49	5
6	SO4	F	205	5/5	0.98	0.11	61,72,77,93	0
6	SO4	D	104	5/5	0.99	0.15	46,50,58,60	0
6	SO4	D	105	5/5	0.99	0.14	39,39,47,49	0
6	SO4	C	313[A]	5/5	0.99	0.15	36,43,47,49	5
6	SO4	D	103[A]	5/5	0.99	0.16	33,37,42,46	5
6	SO4	H	103	5/5	0.99	0.15	45,48,57,58	0

## 6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.