



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 03:45 pm GMT

PDB ID : 4TSQ  
Title : Crystal structure of FraC with DHPC bound (crystal form III)  
Authors : Caaveiro, J.M.M.; Tanaka, K.; Tsumoto, K.  
Deposited on : 2014-06-19  
Resolution : 1.60 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

<http://wwpdb.org/validation/2016/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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

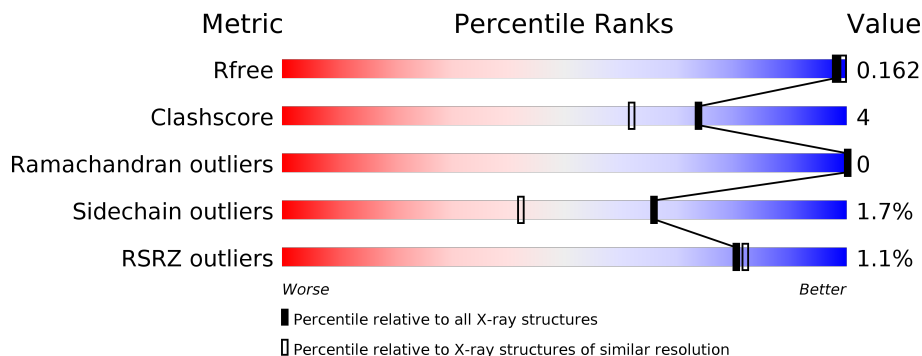
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.60 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))
$R_{free}$	100719	2696 (1.60-1.60)
Clashscore	112137	2967 (1.60-1.60)
Ramachandran outliers	110173	2887 (1.60-1.60)
Sidechain outliers	110143	2886 (1.60-1.60)
RSRZ outliers	101464	2714 (1.60-1.60)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	179	<div> <div>96%</div> <div> <div></div> <div></div> <div></div> <div></div> </div> <div>..</div> </div>
1	B	179	<div> <div>%</div> <div> <div></div> <div></div> <div></div> <div></div> </div> <div>94%</div> <div>5%</div> <div>..</div> </div>
1	C	179	<div> <div>%</div> <div> <div></div> <div></div> <div></div> <div></div> </div> <div>92%</div> <div>6%</div> <div>..</div> </div>
1	D	179	<div> <div>%</div> <div> <div></div> <div></div> <div></div> <div></div> </div> <div>92%</div> <div>7%</div> <div>..</div> </div>
1	E	179	<div> <div>3%</div> <div> <div></div> <div></div> <div></div> <div></div> </div> <div>93%</div> <div>6%</div> <div>..</div> </div>
1	F	179	<div> <div>%</div> <div> <div></div> <div></div> <div></div> <div></div> </div> <div>90%</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
2	HXG	A	201	-	-	-	X
2	HXG	A	202	-	-	-	X
2	HXG	A	203	-	-	-	X
2	HXG	A	204	-	-	-	X
2	HXG	A	205	-	-	-	X
2	HXG	B	202	-	-	-	X
2	HXG	B	203	-	-	-	X
2	HXG	B	204	-	-	-	X
2	HXG	C	201	-	-	-	X
2	HXG	C	202	-	-	-	X
2	HXG	D	201[A]	-	-	-	X
2	HXG	D	201[B]	-	-	-	X
2	HXG	D	202	-	-	-	X
2	HXG	E	201	-	-	-	X
2	HXG	E	202	-	-	-	X
2	HXG	F	201	-	-	-	X
3	PC	A	207	-	-	X	-
3	PC	C	203	-	-	-	X
3	PC	E	203	-	-	-	X
3	PC	E	204	-	-	-	X
3	PC	F	202	-	-	-	X
3	PC	F	203	-	-	-	X
4	SCN	B	205	-	-	-	X

## 2 Entry composition [i](#)

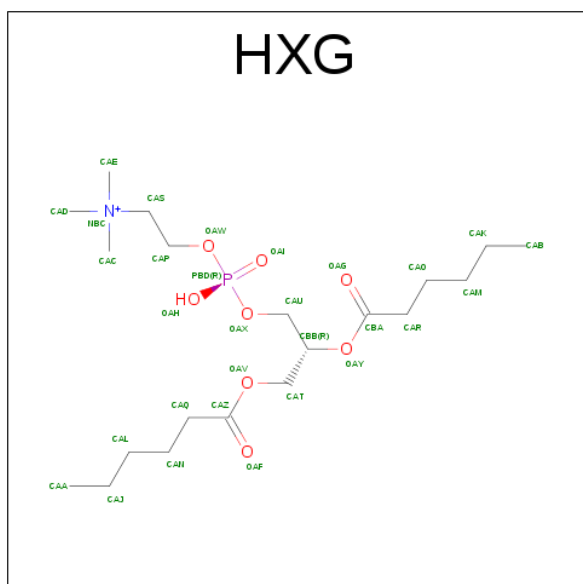
There are 6 unique types of molecules in this entry. The entry contains 10037 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Fragaceatoxin C.

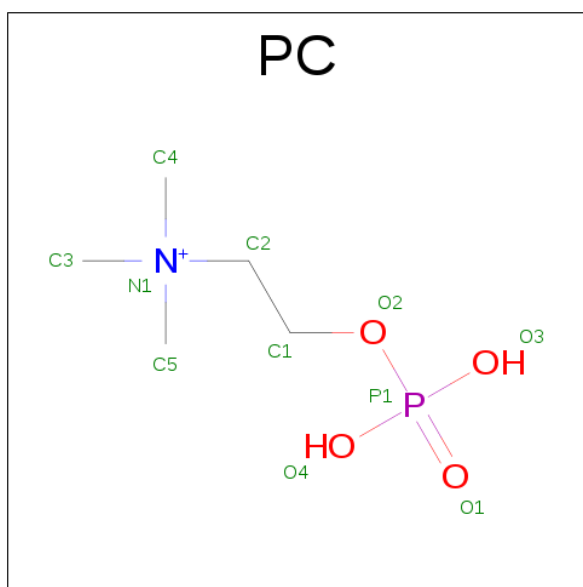
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	177	Total	C	N	O	S	0	5	0
			1415	902	256	253	4			
1	B	178	Total	C	N	O	S	0	9	0
			1437	916	258	259	4			
1	C	177	Total	C	N	O	S	0	7	0
			1425	910	255	256	4			
1	D	178	Total	C	N	O	S	0	6	0
			1427	912	259	252	4			
1	E	178	Total	C	N	O	S	0	5	0
			1419	907	253	255	4			
1	F	177	Total	C	N	O	S	0	7	0
			1422	905	257	256	4			

- Molecule 2 is 1,2-dihexanoyl-sn-glycero-3-phosphocholine (three-letter code: HXG) (formula:  $C_{20}H_{41}NO_8P$ ).



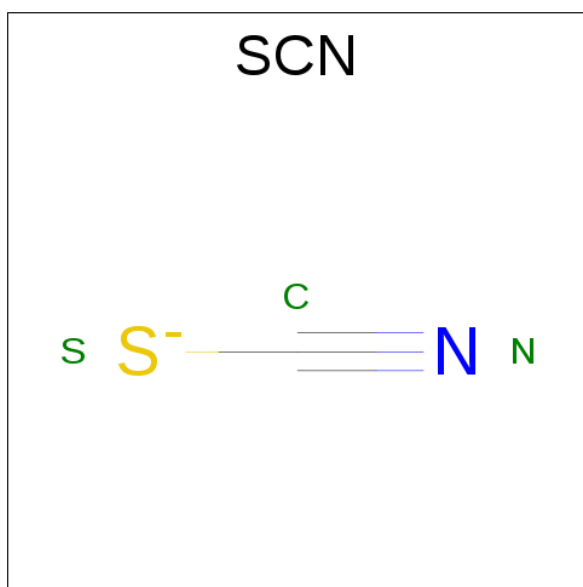
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			30	20	1	8	1		
2	A	1	Total	C	N	O	P	0	0
			30	20	1	8	1		
2	A	1	Total	C	N	O	P	0	0
			30	20	1	8	1		
2	A	1	Total	C	N	O	P	0	0
			30	20	1	8	1		
2	A	1	Total	C	N	O	P	0	0
			30	20	1	8	1		
2	B	1	Total	C	N	O	P	0	0
			30	20	1	8	1		
2	B	1	Total	C	N	O	P	0	0
			30	20	1	8	1		
2	B	1	Total	C	N	O	P	0	0
			30	20	1	8	1		
2	B	1	Total	C	N	O	P	0	0
			30	20	1	8	1		
2	C	1	Total	C	N	O	P	0	0
			30	20	1	8	1		
2	C	1	Total	C	N	O	P	0	0
			30	20	1	8	1		
2	D	1	Total	C	N	O	P	0	1
			60	40	2	16	2		
2	D	1	Total	C	N	O	P	0	0
			30	20	1	8	1		
2	E	1	Total	C	N	O	P	0	0
			30	20	1	8	1		
2	E	1	Total	C	N	O	P	0	0
			30	20	1	8	1		
2	F	1	Total	C	N	O	P	0	0
			30	20	1	8	1		

- Molecule 3 is PHOSPHOCHOLINE (three-letter code: PC) (formula: C<sub>5</sub>H<sub>15</sub>NO<sub>4</sub>P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			11	5	1	4	1		
3	A	1	Total	C	N	O	P	0	0
			11	5	1	4	1		
3	C	1	Total	C	N	O	P	0	0
			11	5	1	4	1		
3	D	1	Total	C	N	O	P	0	0
			11	5	1	4	1		
3	E	1	Total	C	N	O	P	0	0
			11	5	1	4	1		
3	E	1	Total	C	N	O	P	0	0
			11	5	1	4	1		
3	F	1	Total	C	N	O	P	0	0
			11	5	1	4	1		
3	F	1	Total	C	N	O	P	0	0
			11	5	1	4	1		

- Molecule 4 is THIOCYANATE ION (three-letter code: SCN) (formula: CNS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	S	0	0
			3	1	1	1		
4	B	1	Total	C	N	S	0	0
			3	1	1	1		
4	D	1	Total	C	N	S	0	0
			3	1	1	1		
4	E	1	Total	C	N	S	0	0
			3	1	1	1		
4	F	1	Total	C	N	S	0	0
			3	1	1	1		

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Cl	0	0
			1	1		
5	E	1	Total	Cl	0	0
			1	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	173	Total	O	0	6
			176	176		
6	B	137	Total	O	0	5
			141	141		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	C	140	Total 143	O 143	0	4
6	D	149	Total 153	O 153	0	5
6	E	132	Total 134	O 134	0	3
6	F	126	Total 130	O 130	0	6



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

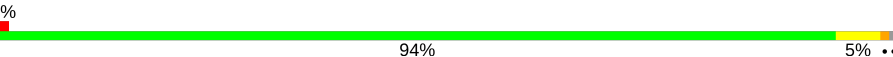
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: Fragaceatoxin C

Chain A: 



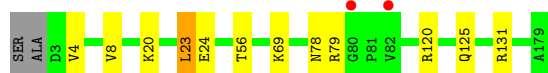
- Molecule 1: Fragaceatoxin C

Chain B: 




- Molecule 1: Fragaceatoxin C

Chain C: 



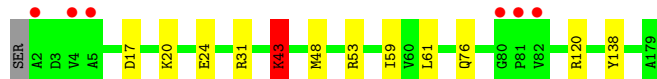
- Molecule 1: Fragaceatoxin C

Chain D: 




- Molecule 1: Fragaceatoxin C

Chain E: 



- Molecule 1: Fragaceatoxin C

Chain F: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	70.27 Å 70.27 Å 202.97 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	45.25 – 1.60 45.25 – 1.60	Depositor EDS
% Data completeness (in resolution range)	95.4 (45.25-1.60) 95.4 (45.25-1.60)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.05 (at 1.60 Å)	Xtriage
Refinement program	REFMAC 5.8.0069	Depositor
R, $R_{free}$	0.132 , 0.154 0.141 , 0.162	Depositor DCC
$R_{free}$ test set	4325 reflections (3.16%)	DCC
Wilson B-factor (Å <sup>2</sup> )	17.0	Xtriage
Anisotropy	0.005	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 37.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.045 for -h,-k,l 0.139 for h,-h-k,-l 0.048 for -k,-h,-l	Xtriage
Reported twinning fraction	0.833 for H, K, L 0.167 for K, H, -L	Depositor
Outliers	0 of 141077 reflections	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	10037	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.36% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PC, SCN, HXG, CL

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	0.93	0/1463	1.05	4/1977 (0.2%)
1	B	0.87	0/1499	0.99	4/2025 (0.2%)
1	C	0.92	0/1482	0.99	1/2004 (0.0%)
1	D	0.92	0/1480	1.06	6/1997 (0.3%)
1	E	0.96	0/1472	1.11	8/1990 (0.4%)
1	F	0.94	2/1475 (0.1%)	1.00	4/1994 (0.2%)
All	All	0.92	2/8871 (0.0%)	1.03	27/11987 (0.2%)

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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	17	ASP	CB-CG	7.61	1.67	1.51
1	F	58	ASP	CB-CG	5.83	1.64	1.51

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	48	MET	CG-SD-CE	-13.27	78.96	100.20
1	E	53	ARG	NE-CZ-NH2	12.04	126.32	120.30
1	F	152	ARG	NE-CZ-NH2	-9.73	115.43	120.30
1	F	152	ARG	NE-CZ-NH1	8.64	124.62	120.30
1	D	53	ARG	NE-CZ-NH2	-8.51	116.05	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	27	GLY	Peptide

## 5.2 Too-close contacts ⓘ

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	1415	0	1400	1	0
1	B	1437	0	1432	8	0
1	C	1425	0	1413	11	0
1	D	1427	0	1432	13	0
1	E	1419	0	1412	5	0
1	F	1422	0	1410	9	0
2	A	150	0	200	13	0
2	B	120	0	160	6	0
2	C	60	0	80	0	0
2	D	90	0	120	5	0
2	E	60	0	80	2	0
2	F	30	0	40	1	0
3	A	22	0	26	7	0
3	C	11	0	13	0	0
3	D	11	0	13	0	0
3	E	22	0	26	1	0
3	F	22	0	26	4	0
4	A	3	0	0	0	0
4	B	3	0	0	0	0
4	D	3	0	0	0	0
4	E	3	0	0	1	0
4	F	3	0	0	1	0
5	B	1	0	0	0	0
5	E	1	0	0	0	0
6	A	176	0	0	0	0
6	B	141	0	0	0	0
6	C	143	0	0	3	0
6	D	153	0	0	3	0
6	E	134	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	F	130	0	0	3	0
All	All	10037	0	9283	70	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.

The worst 5 of 70 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:64[B]:LYS:NZ	1:D:64[B]:LYS:HB3	1.27	1.22
1:D:64[B]:LYS:CB	1:D:64[B]:LYS:NZ	2.12	1.09
1:D:64[B]:LYS:HB3	1:D:64[B]:LYS:HZ3	1.24	0.97
1:D:64[B]:LYS:CB	1:D:64[B]:LYS:HZ2	1.78	0.89
1:C:56[B]:THR:OG1	6:C:401:HOH:O	1.91	0.88

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	180/179 (101%)	176 (98%)	4 (2%)	0	100	100
1	B	185/179 (103%)	183 (99%)	2 (1%)	0	100	100
1	C	182/179 (102%)	180 (99%)	2 (1%)	0	100	100
1	D	182/179 (102%)	178 (98%)	4 (2%)	0	100	100
1	E	182/179 (102%)	179 (98%)	3 (2%)	0	100	100
1	F	182/179 (102%)	178 (98%)	4 (2%)	0	100	100
All	All	1093/1074 (102%)	1074 (98%)	19 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	146/142 (103%)	146 (100%)	0	100	100
1	B	150/142 (106%)	148 (99%)	2 (1%)	73	55
1	C	148/142 (104%)	144 (97%)	4 (3%)	50	22
1	D	147/142 (104%)	143 (97%)	4 (3%)	50	22
1	E	147/142 (104%)	144 (98%)	3 (2%)	60	34
1	F	148/142 (104%)	145 (98%)	3 (2%)	60	34
All	All	886/852 (104%)	870 (98%)	16 (2%)	66	40

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	79	ARG
1	D	127[A]	ARG
1	E	76	GLN
1	D	28	ASN
1	F	125	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	76	GLN
1	B	130	GLN
1	D	28	ASN
1	E	76	GLN

### 5.3.3 RNA ⓘ

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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 32 ligands modelled in this entry, 2 are monoatomic - leaving 30 for Mogul analysis.

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	HXG	A	201	-	29,29,29	1.04	1 (3%)	34,37,37	1.10	1 (2%)
2	HXG	A	202	-	29,29,29	1.09	1 (3%)	34,37,37	2.08	6 (17%)
2	HXG	A	203	-	29,29,29	1.00	3 (10%)	34,37,37	1.54	7 (20%)
2	HXG	A	204	-	29,29,29	1.20	3 (10%)	34,37,37	1.40	3 (8%)
2	HXG	A	205	-	29,29,29	1.01	3 (10%)	34,37,37	1.13	2 (5%)
3	PC	A	206	-	10,10,10	1.13	0	15,15,15	1.35	3 (20%)
3	PC	A	207	-	10,10,10	0.91	0	15,15,15	1.23	1 (6%)
4	SCN	A	208	-	1,2,2	0.64	0	0,1,1	0.00	-
2	HXG	B	201	-	29,29,29	0.97	1 (3%)	34,37,37	1.32	6 (17%)
2	HXG	B	202	-	29,29,29	0.83	1 (3%)	34,37,37	1.23	4 (11%)
2	HXG	B	203	-	29,29,29	1.07	3 (10%)	34,37,37	1.05	3 (8%)
2	HXG	B	204	-	29,29,29	0.97	2 (6%)	34,37,37	0.90	2 (5%)
4	SCN	B	205	-	1,2,2	0.67	0	0,1,1	0.00	-
2	HXG	C	201	-	29,29,29	1.37	3 (10%)	34,37,37	1.39	6 (17%)
2	HXG	C	202	-	29,29,29	0.84	0	34,37,37	0.98	2 (5%)
3	PC	C	203	-	10,10,10	0.90	0	15,15,15	1.59	3 (20%)
2	HXG	D	201[A]	-	29,29,29	0.86	1 (3%)	34,37,37	1.25	4 (11%)
2	HXG	D	201[B]	-	29,29,29	1.11	2 (6%)	34,37,37	1.47	5 (14%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	HXG	D	202	-	29,29,29	1.09	2 (6%)	34,37,37	1.32	5 (14%)
3	PC	D	203	-	10,10,10	0.95	0	15,15,15	1.15	1 (6%)
4	SCN	D	204	-	1,2,2	0.69	0	0,1,1	0.00	-
2	HXG	E	201	-	29,29,29	1.13	2 (6%)	34,37,37	1.29	3 (8%)
2	HXG	E	202	-	29,29,29	1.08	2 (6%)	34,37,37	1.23	3 (8%)
3	PC	E	203	-	10,10,10	0.99	0	15,15,15	1.06	1 (6%)
3	PC	E	204	-	10,10,10	0.99	0	15,15,15	1.16	1 (6%)
4	SCN	E	205	-	1,2,2	0.68	0	0,1,1	0.00	-
2	HXG	F	201	-	29,29,29	1.70	4 (13%)	34,37,37	1.43	7 (20%)
3	PC	F	202	-	10,10,10	1.26	2 (20%)	15,15,15	2.78	4 (26%)
3	PC	F	203	-	10,10,10	0.89	0	15,15,15	1.34	2 (13%)
4	SCN	F	204	-	1,2,2	1.12	0	0,1,1	0.00	-

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	HXG	A	201	-	-	1/33/33/33	0/0/0/0
2	HXG	A	202	-	-	0/33/33/33	0/0/0/0
2	HXG	A	203	-	-	0/33/33/33	0/0/0/0
2	HXG	A	204	-	-	0/33/33/33	0/0/0/0
2	HXG	A	205	-	-	0/33/33/33	0/0/0/0
3	PC	A	206	-	-	0/8/8/8	0/0/0/0
3	PC	A	207	-	-	0/8/8/8	0/0/0/0
4	SCN	A	208	-	-	0/0/0/0	0/0/0/0
2	HXG	B	201	-	-	0/33/33/33	0/0/0/0
2	HXG	B	202	-	-	0/33/33/33	0/0/0/0
2	HXG	B	203	-	-	0/33/33/33	0/0/0/0
2	HXG	B	204	-	-	0/33/33/33	0/0/0/0
4	SCN	B	205	-	-	0/0/0/0	0/0/0/0
2	HXG	C	201	-	-	0/33/33/33	0/0/0/0
2	HXG	C	202	-	-	0/33/33/33	0/0/0/0
3	PC	C	203	-	-	0/8/8/8	0/0/0/0
2	HXG	D	201[A]	-	-	0/33/33/33	0/0/0/0
2	HXG	D	201[B]	-	-	0/33/33/33	0/0/0/0
2	HXG	D	202	-	-	0/33/33/33	0/0/0/0
3	PC	D	203	-	-	0/8/8/8	0/0/0/0
4	SCN	D	204	-	-	0/0/0/0	0/0/0/0
2	HXG	E	201	-	-	0/33/33/33	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HXG	E	202	-	-	2/33/33/33	0/0/0/0
3	PC	E	203	-	-	0/8/8/8	0/0/0/0
3	PC	E	204	-	-	0/8/8/8	0/0/0/0
4	SCN	E	205	-	-	0/0/0/0	0/0/0/0
2	HXG	F	201	-	-	0/33/33/33	0/0/0/0
3	PC	F	202	-	-	0/8/8/8	0/0/0/0
3	PC	F	203	-	-	0/8/8/8	0/0/0/0
4	SCN	F	204	-	-	0/0/0/0	0/0/0/0

The worst 5 of 36 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	204	HXG	OAV-CAT	-3.16	1.38	1.45
2	E	201	HXG	CAC-NBC	-3.08	1.41	1.50
2	A	201	HXG	OAY-CBB	-2.90	1.39	1.46
3	F	202	PC	P1-O4	-2.56	1.44	1.54
2	A	203	HXG	OAY-CBB	-2.28	1.40	1.46

The worst 5 of 85 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	202	HXG	CAT-OAV-CAZ	-7.81	93.63	117.13
2	D	201[B]	HXG	CBB-OAY-CBA	-5.79	104.19	117.88
2	A	203	HXG	CBB-OAY-CBA	-4.73	106.69	117.88
2	A	201	HXG	CAT-OAV-CAZ	-4.55	103.46	117.13
2	A	204	HXG	CAT-OAV-CAZ	-4.33	104.10	117.13

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	201	HXG	CBB-OAY-CBA-CAR
2	E	202	HXG	CBB-OAY-CBA-OAG
2	E	202	HXG	CBB-OAY-CBA-CAR

There are no ring outliers.

18 monomers are involved in 35 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	203	HXG	5	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	204	HXG	6	0
2	A	205	HXG	2	0
3	A	206	PC	1	0
3	A	207	PC	6	0
2	B	201	HXG	2	0
2	B	202	HXG	3	0
2	B	203	HXG	2	0
2	B	204	HXG	1	0
2	D	201[A]	HXG	2	0
2	D	201[B]	HXG	3	0
2	E	202	HXG	2	0
3	E	204	PC	1	0
4	E	205	SCN	1	0
2	F	201	HXG	1	0
3	F	202	PC	2	0
3	F	203	PC	3	0
4	F	204	SCN	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 [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	177/179 (98%)	-0.76	0 100 100	10, 15, 26, 34	0
1	B	178/179 (99%)	-0.60	1 (0%) 89 89	12, 20, 34, 42	0
1	C	177/179 (98%)	-0.63	2 (1%) 80 82	10, 18, 30, 56	0
1	D	178/179 (99%)	-0.62	2 (1%) 80 82	11, 17, 32, 45	0
1	E	178/179 (99%)	-0.52	6 (3%) 46 44	10, 17, 33, 58	0
1	F	177/179 (98%)	-0.50	1 (0%) 89 89	11, 22, 36, 53	0
All	All	1065/1074 (99%)	-0.60	12 (1%) 80 82	10, 18, 33, 58	0

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	2	ALA	5.2
1	D	112	TRP	2.8
1	E	81	PRO	2.8
1	E	80	GLY	2.7
1	B	2	ALA	2.6

### 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 carbohydrates in this entry.

## 6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	HXG	F	201	30/30	0.90	0.22	14.59	24,59,82,82	0
2	HXG	A	203	30/30	0.96	0.17	7.19	19,49,78,82	0
2	HXG	B	202	30/30	0.96	0.14	6.79	18,44,66,67	0
2	HXG	D	202	30/30	0.96	0.15	5.79	17,46,83,83	0
3	PC	F	202	11/11	0.91	0.13	5.21	12,20,22,25	11
3	PC	C	203	11/11	0.95	0.17	5.00	22,41,57,58	0
2	HXG	A	204	30/30	0.93	0.19	4.86	28,46,64,66	0
3	PC	E	203	11/11	0.94	0.17	4.52	17,23,27,29	11
2	HXG	C	202	30/30	0.97	0.12	4.30	15,32,62,63	0
3	PC	F	203	11/11	0.85	0.21	4.16	24,33,36,39	11
3	PC	E	204	11/11	0.96	0.17	3.98	14,19,26,27	11
2	HXG	A	201	30/30	0.97	0.14	3.85	15,47,88,91	0
2	HXG	E	202	30/30	0.97	0.12	3.66	15,42,74,76	0
2	HXG	D	201[B]	30/30	0.91	0.23	3.60	15,32,69,70	30
2	HXG	B	204	30/30	0.94	0.14	3.48	26,42,76,76	0
2	HXG	E	201	30/30	0.94	0.14	3.46	15,32,67,69	0
2	HXG	C	201	30/30	0.93	0.14	3.39	13,27,54,59	0
2	HXG	D	201[A]	30/30	0.91	0.23	3.34	16,47,73,73	30
4	SCN	B	205	3/3	0.97	0.10	3.07	22,22,23,26	0
2	HXG	A	205	30/30	0.93	0.14	2.43	20,28,36,40	0
2	HXG	A	202	30/30	0.94	0.13	2.42	16,39,70,72	0
2	HXG	B	203	30/30	0.94	0.17	2.09	24,47,65,68	0
3	PC	A	206	11/11	0.89	0.16	1.70	17,19,21,23	11
2	HXG	B	201	30/30	0.95	0.11	1.54	21,33,56,57	0
4	SCN	F	204	3/3	0.98	0.09	1.03	12,12,24,26	0
4	SCN	D	204	3/3	0.99	0.07	0.87	15,15,15,17	0
4	SCN	E	205	3/3	0.99	0.05	-0.86	17,17,20,21	0
4	SCN	A	208	3/3	0.99	0.04	-2.22	13,13,14,15	0
5	CL	B	206	1/1	0.97	0.05	-	59,59,59,59	0
5	CL	E	206	1/1	0.88	0.07	-	56,56,56,56	0
3	PC	A	207	11/11	0.79	0.28	-	34,36,39,40	11
3	PC	D	203	11/11	0.97	0.15	-	17,24,27,28	11

## 6.5 Other polymers [i](#)

There are no such residues in this entry.