



# wwPDB X-ray Structure Validation Summary Report

Apr 7, 2022 – 01:45 PM EDT

PDB ID : 2PD0  
Title : Protein cgd2\_2020 from *Cryptosporidium parvum*  
Authors : Cymborowski, M.; Chruszcz, M.; Hills, T.; Lew, J.; Melone, M.; Zhao, Y.; Artz, J.; Wernimont, A.; Edwards, A.; Sundstrom, M.; Weigelt, J.; Bochkarev, A.; Arrowsmith, C.; Hui, R.; Minor, W.; Structural Genomics Consortium (SGC)  
Deposited on : 2007-03-30  
Resolution : 2.30 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

<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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.27  
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) : 2.27

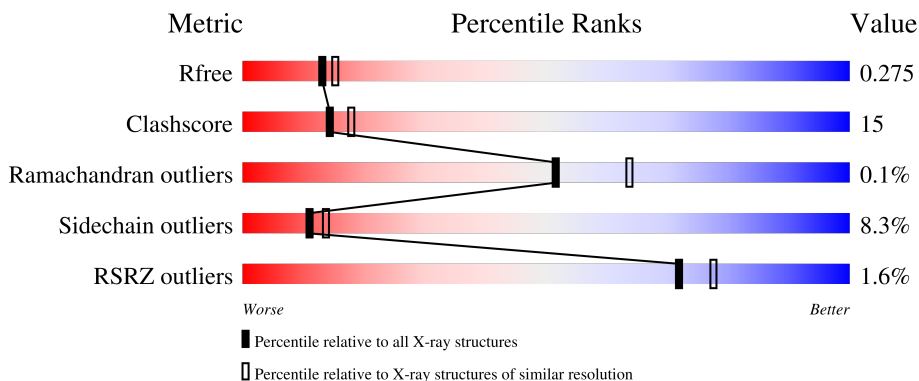
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	223	 2% 67% 20% • 8%
1	B	223	 2% 60% 27% • 8%
1	C	223	 59% 27% 6% 8%
1	D	223	 2% 65% 23% •• 9%

## 2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 7306 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 Hypothetical protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	205	1760	1126	290	338	3	3	0	10	0
1	B	205	1738	1115	288	328	4	3	0	8	0
1	C	205	1687	1083	280	319	2	3	0	3	0
1	D	203	1645	1058	271	311	2	3	0	1	0

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	MET	-	cloning artifact	UNP Q5CTR0
A	-17	GLY	-	cloning artifact	UNP Q5CTR0
A	-16	SER	-	cloning artifact	UNP Q5CTR0
A	-15	SER	-	cloning artifact	UNP Q5CTR0
A	-14	HIS	-	cloning artifact	UNP Q5CTR0
A	-13	HIS	-	cloning artifact	UNP Q5CTR0
A	-12	HIS	-	cloning artifact	UNP Q5CTR0
A	-11	HIS	-	cloning artifact	UNP Q5CTR0
A	-10	HIS	-	cloning artifact	UNP Q5CTR0
A	-9	HIS	-	cloning artifact	UNP Q5CTR0
A	-8	SER	-	cloning artifact	UNP Q5CTR0
A	-7	SER	-	cloning artifact	UNP Q5CTR0
A	-6	GLY	-	cloning artifact	UNP Q5CTR0
A	-5	LEU	-	cloning artifact	UNP Q5CTR0
A	-4	VAL	-	cloning artifact	UNP Q5CTR0
A	-3	PRO	-	cloning artifact	UNP Q5CTR0
A	-2	ARG	-	cloning artifact	UNP Q5CTR0
A	-1	GLY	-	cloning artifact	UNP Q5CTR0
A	0	SER	-	cloning artifact	UNP Q5CTR0
A	25	MSE	MET	modified residue	UNP Q5CTR0
A	131	MSE	MET	modified residue	UNP Q5CTR0

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Chain	Residue	Modelled	Actual	Comment	Reference
A	164	MSE	MET	modified residue	UNP Q5CTR0
B	-18	MET	-	cloning artifact	UNP Q5CTR0
B	-17	GLY	-	cloning artifact	UNP Q5CTR0
B	-16	SER	-	cloning artifact	UNP Q5CTR0
B	-15	SER	-	cloning artifact	UNP Q5CTR0
B	-14	HIS	-	cloning artifact	UNP Q5CTR0
B	-13	HIS	-	cloning artifact	UNP Q5CTR0
B	-12	HIS	-	cloning artifact	UNP Q5CTR0
B	-11	HIS	-	cloning artifact	UNP Q5CTR0
B	-10	HIS	-	cloning artifact	UNP Q5CTR0
B	-9	HIS	-	cloning artifact	UNP Q5CTR0
B	-8	SER	-	cloning artifact	UNP Q5CTR0
B	-7	SER	-	cloning artifact	UNP Q5CTR0
B	-6	GLY	-	cloning artifact	UNP Q5CTR0
B	-5	LEU	-	cloning artifact	UNP Q5CTR0
B	-4	VAL	-	cloning artifact	UNP Q5CTR0
B	-3	PRO	-	cloning artifact	UNP Q5CTR0
B	-2	ARG	-	cloning artifact	UNP Q5CTR0
B	-1	GLY	-	cloning artifact	UNP Q5CTR0
B	0	SER	-	cloning artifact	UNP Q5CTR0
B	25	MSE	MET	modified residue	UNP Q5CTR0
B	131	MSE	MET	modified residue	UNP Q5CTR0
B	164	MSE	MET	modified residue	UNP Q5CTR0
C	-18	MET	-	cloning artifact	UNP Q5CTR0
C	-17	GLY	-	cloning artifact	UNP Q5CTR0
C	-16	SER	-	cloning artifact	UNP Q5CTR0
C	-15	SER	-	cloning artifact	UNP Q5CTR0
C	-14	HIS	-	cloning artifact	UNP Q5CTR0
C	-13	HIS	-	cloning artifact	UNP Q5CTR0
C	-12	HIS	-	cloning artifact	UNP Q5CTR0
C	-11	HIS	-	cloning artifact	UNP Q5CTR0
C	-10	HIS	-	cloning artifact	UNP Q5CTR0
C	-9	HIS	-	cloning artifact	UNP Q5CTR0
C	-8	SER	-	cloning artifact	UNP Q5CTR0
C	-7	SER	-	cloning artifact	UNP Q5CTR0
C	-6	GLY	-	cloning artifact	UNP Q5CTR0
C	-5	LEU	-	cloning artifact	UNP Q5CTR0
C	-4	VAL	-	cloning artifact	UNP Q5CTR0
C	-3	PRO	-	cloning artifact	UNP Q5CTR0
C	-2	ARG	-	cloning artifact	UNP Q5CTR0
C	-1	GLY	-	cloning artifact	UNP Q5CTR0
C	0	SER	-	cloning artifact	UNP Q5CTR0

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Chain	Residue	Modelled	Actual	Comment	Reference
C	25	MSE	MET	modified residue	UNP Q5CTR0
C	131	MSE	MET	modified residue	UNP Q5CTR0
C	164	MSE	MET	modified residue	UNP Q5CTR0
D	-18	MET	-	cloning artifact	UNP Q5CTR0
D	-17	GLY	-	cloning artifact	UNP Q5CTR0
D	-16	SER	-	cloning artifact	UNP Q5CTR0
D	-15	SER	-	cloning artifact	UNP Q5CTR0
D	-14	HIS	-	cloning artifact	UNP Q5CTR0
D	-13	HIS	-	cloning artifact	UNP Q5CTR0
D	-12	HIS	-	cloning artifact	UNP Q5CTR0
D	-11	HIS	-	cloning artifact	UNP Q5CTR0
D	-10	HIS	-	cloning artifact	UNP Q5CTR0
D	-9	HIS	-	cloning artifact	UNP Q5CTR0
D	-8	SER	-	cloning artifact	UNP Q5CTR0
D	-7	SER	-	cloning artifact	UNP Q5CTR0
D	-6	GLY	-	cloning artifact	UNP Q5CTR0
D	-5	LEU	-	cloning artifact	UNP Q5CTR0
D	-4	VAL	-	cloning artifact	UNP Q5CTR0
D	-3	PRO	-	cloning artifact	UNP Q5CTR0
D	-2	ARG	-	cloning artifact	UNP Q5CTR0
D	-1	GLY	-	cloning artifact	UNP Q5CTR0
D	0	SER	-	cloning artifact	UNP Q5CTR0
D	25	MSE	MET	modified residue	UNP Q5CTR0
D	131	MSE	MET	modified residue	UNP Q5CTR0
D	164	MSE	MET	modified residue	UNP Q5CTR0

- Molecule 2 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C<sub>6</sub>H<sub>13</sub>NO<sub>4</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
2	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
2	C	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
2	D	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

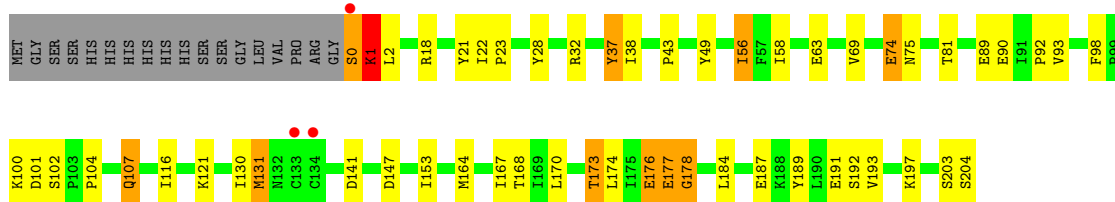
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	123	Total	O	0	0
			123	123		
3	B	130	Total	O	0	0
			130	130		
3	C	76	Total	O	0	0
			76	76		
3	D	99	Total	O	0	0
			99	99		

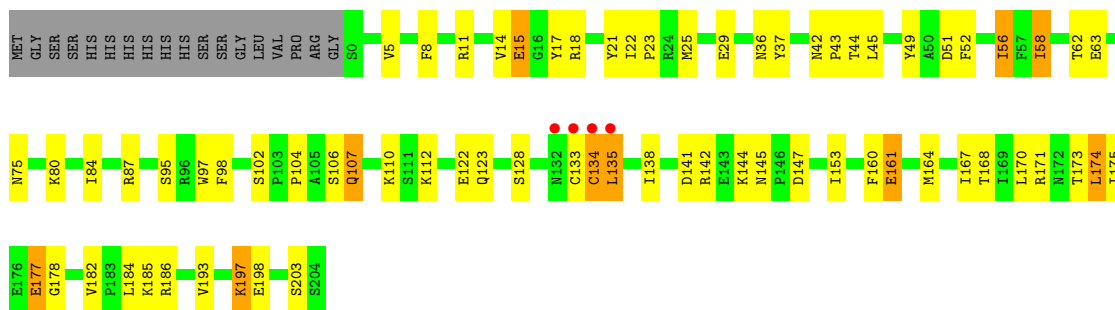
### 3 Residue-property plots [i](#)

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.

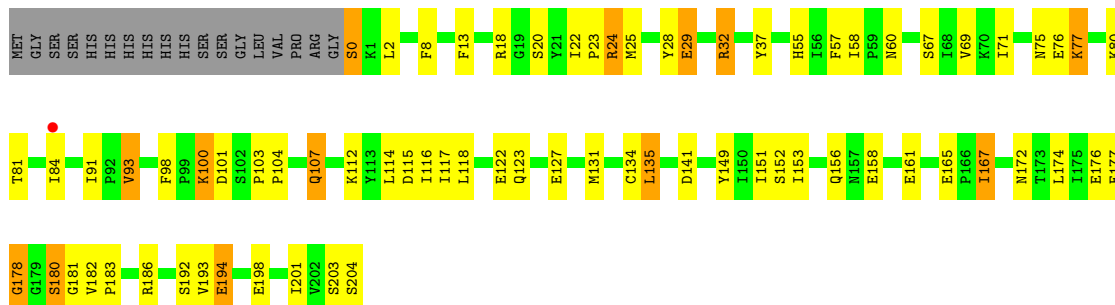
- Molecule 1: Hypothetical protein



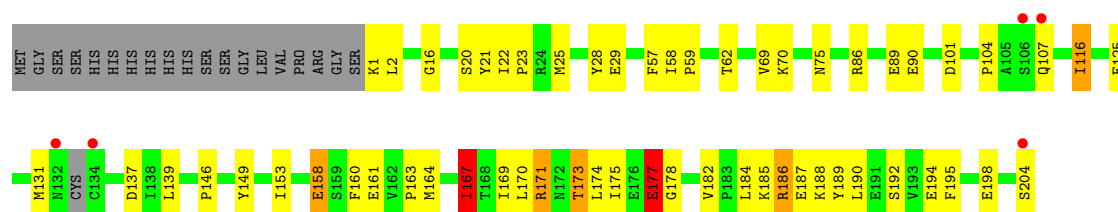
- Molecule 1: Hypothetical protein



- Molecule 1: Hypothetical protein



- Molecule 1: Hypothetical protein





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	49.53Å 68.52Å 79.57Å 69.29° 75.14° 93.73°	Depositor
Resolution (Å)	20.00 – 2.30 20.00 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.2 (20.00-2.30) 98.1 (20.00-2.30)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.69 (at 2.30Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.220 , 0.280 0.224 , 0.275	Depositor DCC
$R_{free}$ test set	2091 reflections (5.15%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	28.8	Xtrriage
Anisotropy	0.047	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 37.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	7306	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.17% 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: MES

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	0.92	2/1796 (0.1%)	0.81	0/2420
1	B	1.04	4/1773 (0.2%)	0.91	2/2391 (0.1%)
1	C	0.87	1/1722 (0.1%)	0.82	0/2325
1	D	0.96	1/1680 (0.1%)	0.85	3/2272 (0.1%)
All	All	0.95	8/6971 (0.1%)	0.85	5/9408 (0.1%)

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	A	0	5
1	B	0	2
1	C	0	4
1	D	0	1
All	All	0	12

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	131	MSE	SE-CE	-7.25	1.52	1.95
1	B	134	CYS	CB-SG	6.68	1.93	1.82
1	B	17	TYR	CD1-CE1	-6.66	1.29	1.39
1	B	17	TYR	CD2-CE2	-5.95	1.30	1.39
1	A	37	TYR	CD1-CE1	-5.93	1.30	1.39

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	171	ARG	NE-CZ-NH2	-5.97	117.32	120.30
1	D	167	ILE	CB-CA-C	-5.80	100.00	111.60
1	B	171	ARG	NE-CZ-NH2	-5.31	117.64	120.30
1	B	147	ASP	CB-CG-OD2	-5.12	113.69	118.30
1	D	171	ARG	NE-CZ-NH1	5.11	122.85	120.30

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	0	SER	Peptide
1	A	1	LYS	Peptide
1	A	131	MSE	Peptide
1	A	177	GLU	Peptide
1	A	178	GLY	Peptide

## 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	1760	0	1729	52	0
1	B	1738	0	1716	50	0
1	C	1687	0	1650	68	0
1	D	1645	0	1594	48	0
2	A	12	0	12	0	0
2	B	12	0	12	3	0
2	C	12	0	12	2	0
2	D	12	0	12	1	0
3	A	123	0	0	8	0
3	B	130	0	0	7	0
3	C	76	0	0	11	0
3	D	99	0	0	14	0
All	All	7306	0	6737	211	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 15.

The worst 5 of 211 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:A:93:VAL:HG11	1:A:167[B]:ILE:HG12	1.28	1.15
1:A:56[A]:ILE:HD11	1:A:58:ILE:CG2	1.79	1.12
1:A:56[A]:ILE:HD11	1:A:58:ILE:HG23	1.28	1.11
1:D:1:LYS:CB	1:D:2:LEU:HA	1.82	1.10
1:C:135:LEU:N	1:C:135:LEU:HD23	1.71	1.05

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	213/223 (96%)	205 (96%)	8 (4%)	0	100	100
1	B	211/223 (95%)	204 (97%)	7 (3%)	0	100	100
1	C	206/223 (92%)	199 (97%)	5 (2%)	2 (1%)	15	17
1	D	200/223 (90%)	197 (98%)	3 (2%)	0	100	100
All	All	830/892 (93%)	805 (97%)	23 (3%)	2 (0%)	51	58

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	24[A]	ARG
1	C	24[B]	ARG

#### 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	197/203 (97%)	186 (94%)	11 (6%)	21	29
1	B	193/203 (95%)	175 (91%)	18 (9%)	9	10
1	C	185/203 (91%)	163 (88%)	22 (12%)	5	5
1	D	178/203 (88%)	163 (92%)	15 (8%)	11	13
All	All	753/812 (93%)	687 (91%)	66 (9%)	11	12

5 of 66 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	158	GLU
1	D	173	THR
1	D	194	GLU
1	B	161[A]	GLU
1	B	135	LEU

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

Mol	Chain	Res	Type
1	B	107	GLN

### 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](#)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	MES	A	502	-	12,12,12	2.11	1 (8%)	14,16,16	2.61	7 (50%)
2	MES	B	503	-	12,12,12	2.38	1 (8%)	14,16,16	2.28	4 (28%)
2	MES	C	504	-	12,12,12	2.04	1 (8%)	14,16,16	2.45	7 (50%)
2	MES	D	501	-	12,12,12	1.52	1 (8%)	14,16,16	2.62	5 (35%)

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	MES	A	502	-	-	4/6/14/14	0/1/1/1
2	MES	B	503	-	-	4/6/14/14	0/1/1/1
2	MES	C	504	-	-	1/6/14/14	0/1/1/1
2	MES	D	501	-	-	4/6/14/14	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	503	MES	C8-S	-7.68	1.66	1.77
2	C	504	MES	C8-S	-6.63	1.68	1.77
2	A	502	MES	C8-S	-6.60	1.68	1.77
2	D	501	MES	C8-S	-4.58	1.71	1.77

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	501	MES	C5-N4-C3	6.52	123.51	108.83
2	A	502	MES	C5-N4-C3	6.34	123.09	108.83
2	C	504	MES	C5-N4-C3	5.75	121.77	108.83
2	B	503	MES	C5-N4-C3	5.65	121.56	108.83
2	A	502	MES	O1S-S-C8	4.05	111.79	106.92

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	502	MES	C7-C8-S-O1S
2	A	502	MES	C7-C8-S-O3S
2	B	503	MES	C8-C7-N4-C3
2	D	501	MES	C8-C7-N4-C3
2	D	501	MES	C7-C8-S-O2S

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	503	MES	3	0
2	C	504	MES	2	0
2	D	501	MES	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	202/223 (90%)	-0.22	3 (1%) 73 79	11, 25, 41, 59	0
1	B	202/223 (90%)	-0.25	4 (1%) 65 71	13, 24, 39, 53	0
1	C	202/223 (90%)	-0.07	1 (0%) 91 94	15, 29, 46, 61	0
1	D	200/223 (89%)	-0.12	5 (2%) 57 64	16, 30, 44, 63	0
All	All	806/892 (90%)	-0.17	13 (1%) 72 77	11, 27, 44, 63	0

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	134	CYS	7.2
1	A	0	SER	4.9
1	B	135	LEU	4.5
1	B	133	CYS	4.2
1	D	134	CYS	3.8

### 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
2	MES	C	504	12/12	0.89	0.21	54,56,57,59	0
2	MES	B	503	12/12	0.91	0.22	39,41,43,43	0
2	MES	D	501	12/12	0.93	0.23	36,38,41,42	0
2	MES	A	502	12/12	0.94	0.16	31,37,49,50	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.