



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 19, 2020 – 07:45 pm BST

PDB ID : 5OTB  
Title : Structure of caprine serum albumin in P1 space group  
Authors : Talaj, J.A.; Bujacz, A.; Bujacz, G.  
Deposited on : 2017-08-21  
Resolution : 2.50 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 : 2.11  
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) : 2.11

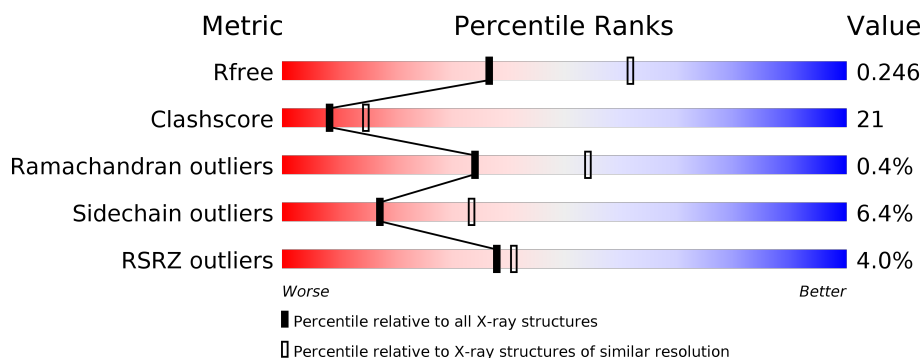
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 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	583	<div> <div>3%</div> <div>58% 38%</div> </div>
1	B	583	<div> <div>5%</div> <div>58% 40%</div> </div>
1	C	583	<div> <div>5%</div> <div>60% 36%</div> </div>
1	D	583	<div> <div>3%</div> <div>61% 36%</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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	PRO	A	602	-	-	X	-
3	PRO	B	602	-	-	X	-
3	PRO	D	602	-	-	X	-

## 2 Entry composition [i](#)

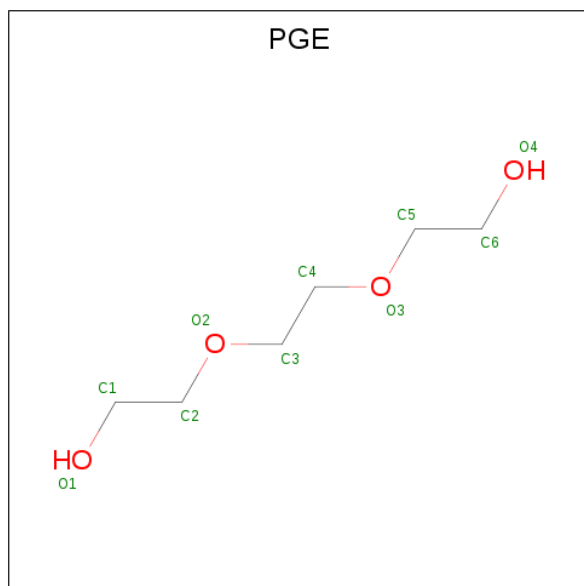
There are 5 unique types of molecules in this entry. The entry contains 19131 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Albumin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	581	Total	C	N	O	S	0	0	0
			4628	2922	777	890	39			
1	B	581	Total	C	N	O	S	0	0	0
			4627	2922	777	889	39			
1	C	581	Total	C	N	O	S	0	0	0
			4628	2922	777	890	39			
1	D	581	Total	C	N	O	S	0	1	0
			4634	2927	778	890	39			

- Molecule 2 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: C<sub>6</sub>H<sub>14</sub>O<sub>4</sub>).



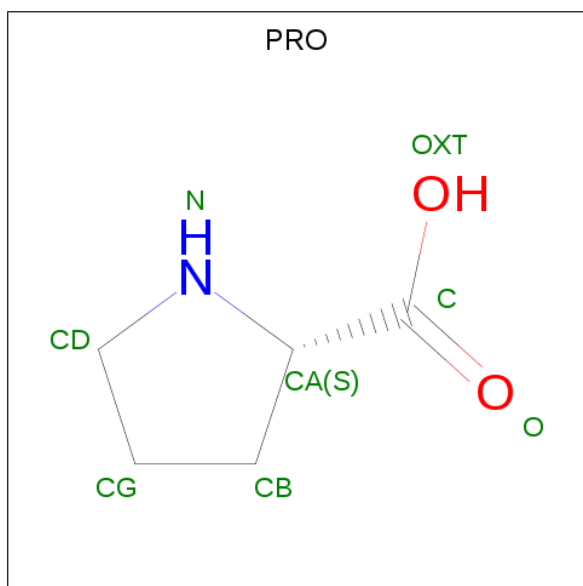
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			10	6	4		
2	B	1	Total	C	O	0	0
			10	6	4		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	C	O	0	0
			10	6	4		

- Molecule 3 is PROLINE (three-letter code: PRO) (formula:  $C_5H_9NO_2$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			8	5	1	2		
3	A	1	Total	C	N	O	0	0
			8	5	1	2		
3	B	1	Total	C	N	O	0	0
			8	5	1	2		
3	B	1	Total	C	N	O	0	0
			8	5	1	2		
3	C	1	Total	C	N	O	0	0
			8	5	1	2		
3	C	1	Total	C	N	O	0	0
			8	5	1	2		
3	C	1	Total	C	N	O	0	0
			8	5	1	2		
3	D	1	Total	C	N	O	0	0
			8	5	1	2		
3	D	1	Total	C	N	O	0	0
			8	5	1	2		
3	D	1	Total	C	N	O	0	0
			8	5	1	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	D	1	Total	C	N	O	0	0
			8	5	1	2		

- Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	O	0	0
			7	4	3		
4	D	1	Total	C	O	0	0
			7	4	3		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	108	Total	O	0	0
			108	108		
5	B	124	Total	O	0	0
			124	124		
5	C	124	Total	O	0	0
			124	124		
5	D	126	Total	O	0	0
			126	126		

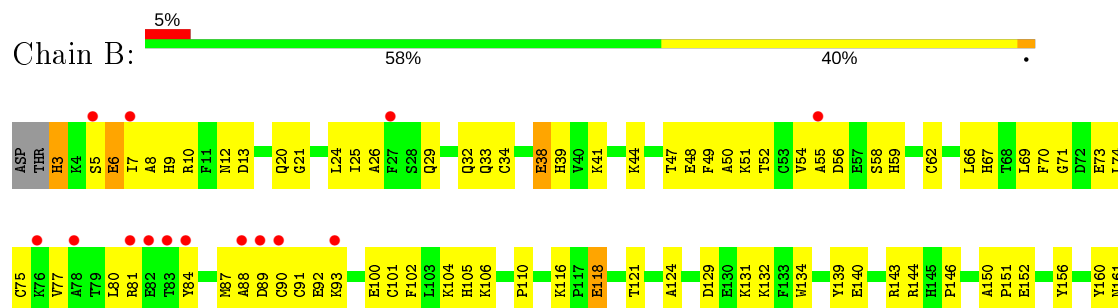
### 3 Residue-property plots

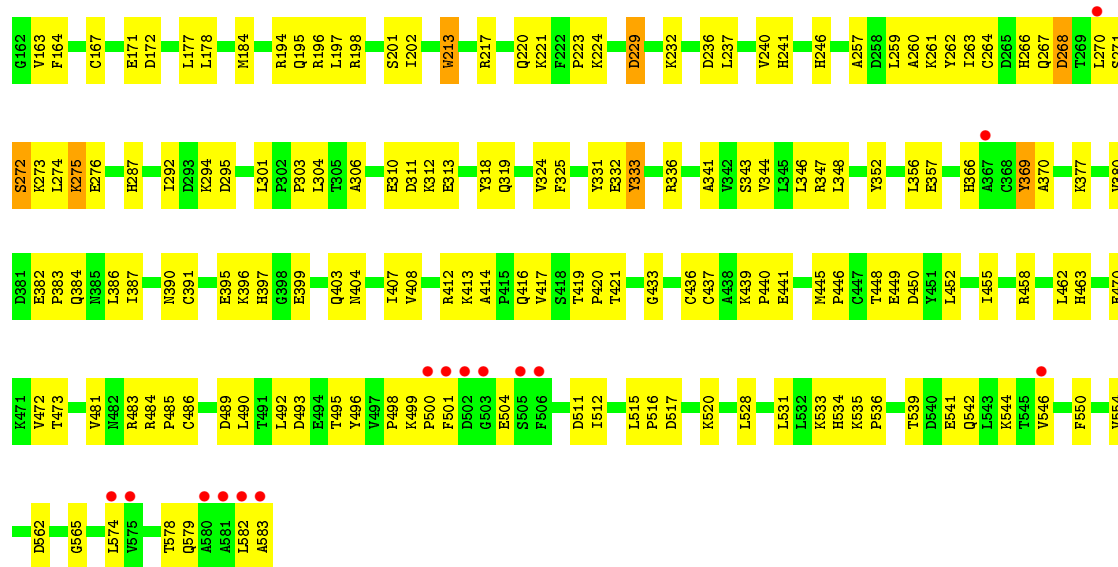
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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 ( $\text{RSRZ} > 2$ ). 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: Albumin

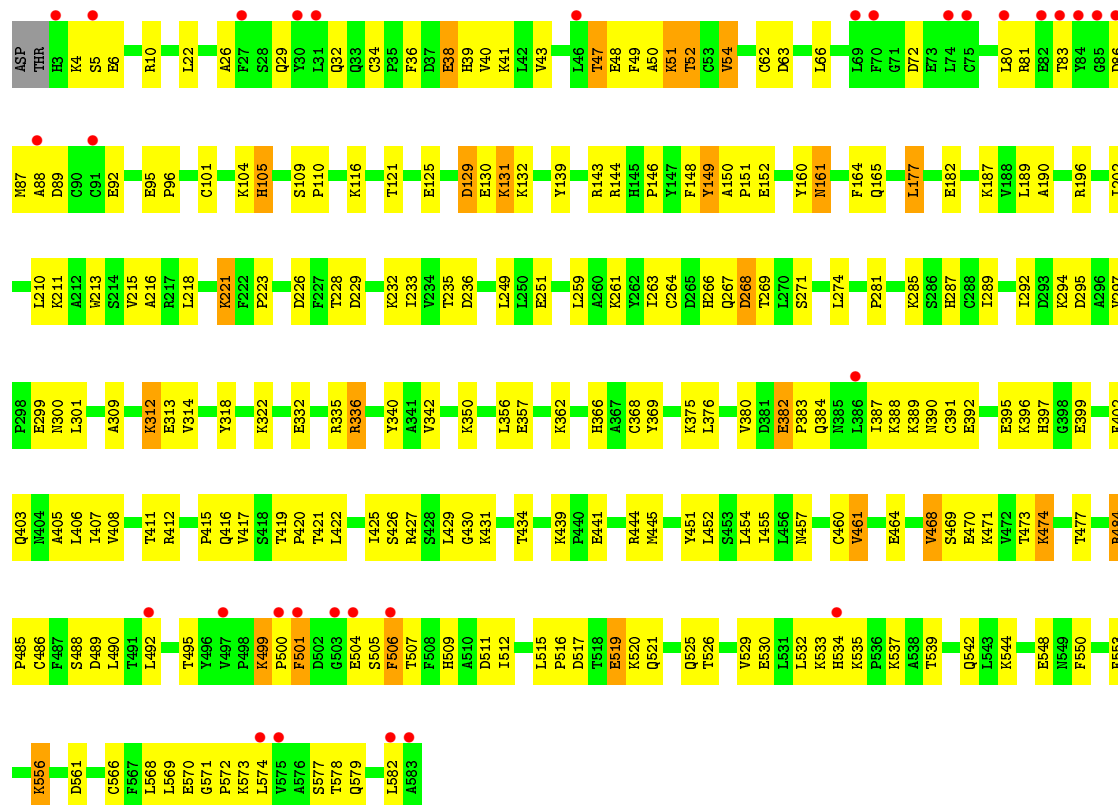


#### • Molecule 1: Albumin





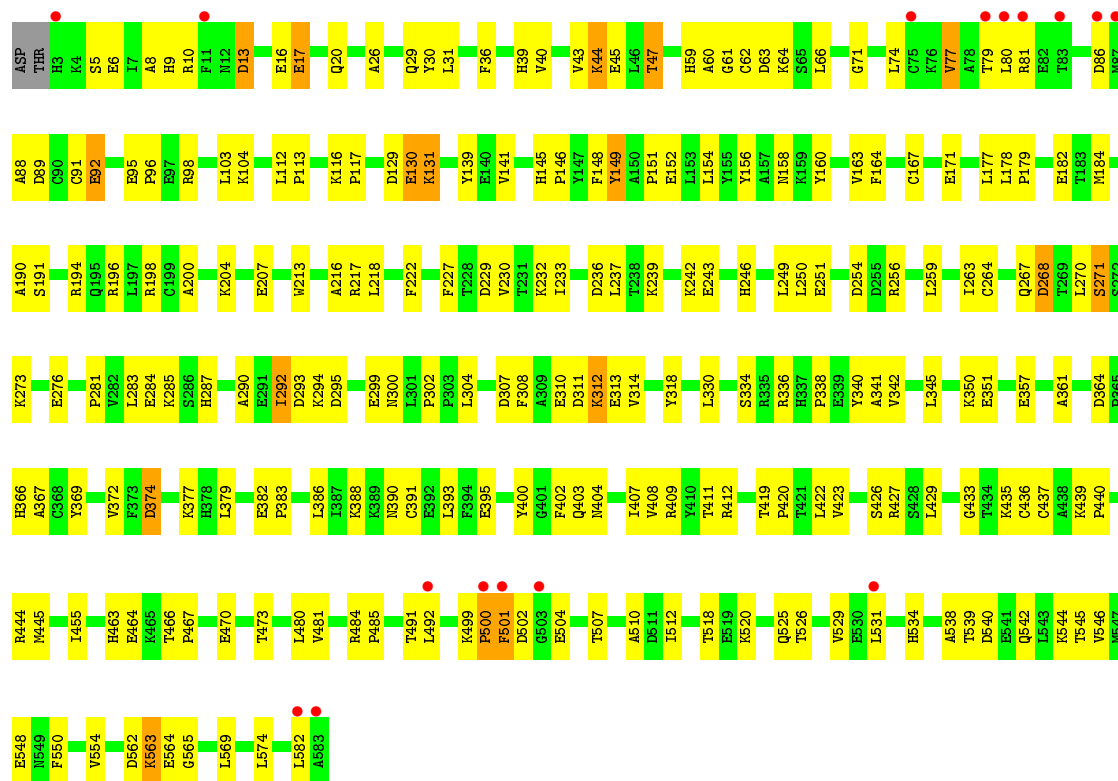
• Molecule 1: Albumin



• Molecule 1: Albumin







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	78.75Å 80.93Å 110.53Å 90.01° 75.90° 72.22°	Depositor
Resolution (Å)	40.00 – 2.50 39.47 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.2 (40.00-2.50) 98.2 (39.47-2.50)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.06 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, $R_{free}$	0.197 , 0.246 0.198 , 0.246	Depositor DCC
$R_{free}$ test set	1707 reflections (2.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	57.8	Xtriage
Anisotropy	0.046	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 61.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	19131	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.27% 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: PEG, PGE

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	0/4724	1.03	0/6376
1	B	0.93	0/4723	1.04	0/6374
1	C	0.90	0/4724	1.00	0/6376
1	D	0.96	0/4733	1.04	0/6387
All	All	0.93	0/18904	1.03	0/25513

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4628	0	4537	210	0
1	B	4627	0	4537	200	1
1	C	4628	0	4537	191	1
1	D	4634	0	4550	177	2
2	A	10	0	14	1	0
2	B	10	0	14	1	0
2	C	10	0	14	0	0
3	A	16	0	14	12	0
3	B	16	0	14	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	24	0	21	6	0
3	D	32	0	28	15	0
4	C	7	0	10	1	0
4	D	7	0	10	2	0
5	A	108	0	0	6	0
5	B	124	0	0	5	0
5	C	124	0	0	9	0
5	D	126	0	0	10	0
All	All	19131	0	18300	773	2

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 21.

The worst 5 of 773 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:498:PRO:O	1:B:500:PRO:HD3	1.31	1.26
1:A:116:LYS:HE3	1:B:116:LYS:HE3	1.28	1.08
1:C:86:ASP:O	1:C:89:ASP:HB2	1.60	1.02
1:B:539:THR:HB	1:B:542:GLN:HB2	1.44	0.99
1:C:499:LYS:HG3	1:C:500:PRO:HD2	1.45	0.98

All (2) 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)
1:B:41:LYS:NZ	1:D:313:GLU:OE2[1_545]	2.05	0.15
1:C:312:LYS:NZ	1:D:361:ALA:O[1_546]	2.15	0.05

## 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	579/583 (99%)	518 (90%)	58 (10%)	3 (0%)	29	48
1	B	579/583 (99%)	523 (90%)	54 (9%)	2 (0%)	41	61
1	C	579/583 (99%)	515 (89%)	62 (11%)	2 (0%)	41	61
1	D	580/583 (100%)	517 (89%)	60 (10%)	3 (0%)	29	48
All	All	2317/2332 (99%)	2073 (90%)	234 (10%)	10 (0%)	34	54

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	499	LYS
1	A	269	THR
1	B	441	GLU
1	D	79	THR
1	A	360	CYS

### 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	515/517 (100%)	477 (93%)	38 (7%)	13	27
1	B	515/517 (100%)	487 (95%)	28 (5%)	22	42
1	C	515/517 (100%)	482 (94%)	33 (6%)	17	33
1	D	516/517 (100%)	483 (94%)	33 (6%)	17	33
All	All	2061/2068 (100%)	1929 (94%)	132 (6%)	17	33

5 of 132 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	343	SER
1	C	105	HIS
1	D	377	LYS
1	B	369	TYR
1	C	38	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	67	HIS
1	B	463	HIS
1	D	20	GLN
1	B	33	GLN
1	C	509	HIS

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

16 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	PGE	A	601	-	9,9,9	0.60	0	8,8,8	0.29	0
4	PEG	C	602	-	6,6,6	0.47	0	5,5,5	0.52	0
2	PGE	C	601	-	9,9,9	0.59	0	8,8,8	0.68	0
2	PGE	B	601	-	9,9,9	0.56	0	8,8,8	0.78	0
4	PEG	D	601	-	6,6,6	0.45	0	5,5,5	0.34	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
2	PGE	A	601	-	-	4/7/7/7	-
4	PEG	C	602	-	-	3/4/4/4	-
2	PGE	C	601	-	-	3/7/7/7	-
2	PGE	B	601	-	-	5/7/7/7	-
4	PEG	D	601	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	601	PEG	O2-C3-C4-O4
2	A	601	PGE	O1-C1-C2-O2
2	C	601	PGE	O3-C5-C6-O4
2	A	601	PGE	O3-C5-C6-O4
4	C	602	PEG	O1-C1-C2-O2

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	PGE	1	0
4	C	602	PEG	1	0
2	B	601	PGE	1	0
4	D	601	PEG	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 [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	581/583 (99%)	-0.16	16 (2%) 53 56	33, 62, 96, 118	0
1	B	581/583 (99%)	-0.01	29 (4%) 28 30	33, 60, 104, 138	0
1	C	581/583 (99%)	0.02	31 (5%) 26 28	36, 62, 106, 154	0
1	D	581/583 (99%)	-0.19	16 (2%) 53 56	32, 60, 97, 133	0
All	All	2324/2332 (99%)	-0.09	92 (3%) 38 41	32, 61, 102, 154	0

The worst 5 of 92 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	70	PHE	5.3
1	C	501	PHE	5.1
1	C	500	PRO	4.8
1	B	89	ASP	4.7
1	D	81	ARG	4.4

### 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 [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
3	PRO	B	603	8/8	0.79	0.17	80,86,91,92	0
3	PRO	D	603	8/8	0.85	0.29	74,86,104,105	0
3	PRO	B	602	8/8	0.87	0.25	75,88,94,97	0
3	PRO	D	604	8/8	0.88	0.14	66,77,83,86	0
3	PRO	A	603	8/8	0.89	0.14	81,82,90,92	0
3	PRO	C	604	8/8	0.90	0.17	68,74,81,90	0
3	PRO	C	603	8/8	0.92	0.21	74,84,86,90	0
3	PRO	D	605	8/8	0.92	0.13	80,83,100,100	0
3	PRO	A	602	8/8	0.93	0.21	78,84,88,92	0
3	PRO	C	605	8/8	0.93	0.28	78,88,91,91	0
2	PGE	C	601	10/10	0.94	0.14	52,61,68,75	0
4	PEG	D	601	7/7	0.94	0.15	52,53,62,63	0
3	PRO	D	602	8/8	0.95	0.16	61,70,89,100	0
4	PEG	C	602	7/7	0.95	0.20	55,66,77,83	0
2	PGE	A	601	10/10	0.96	0.20	47,71,85,97	0
2	PGE	B	601	10/10	0.97	0.16	45,55,86,87	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.