



# Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 03:42 pm BST

PDB ID : 2PLS  
Title : Structural Genomics, the crystal structure of the CorC/HlyC transporter associated domain of a CBS domain protein from *Chlorobium tepidum* TLS  
Authors : Tan, K.; Volkart, L.; Clancy, S.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)  
Deposited on : 2007-04-20  
Resolution : 2.15 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 : 1.8.5 (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

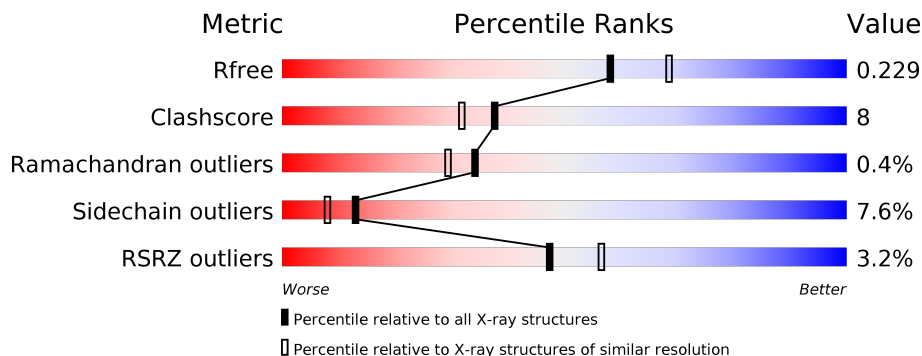
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.15 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	1479 (2.16-2.16)
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (2.16-2.16)

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	86	
1	B	86	
1	C	86	
1	D	86	
1	E	86	
1	F	86	

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Mol	Chain	Length	Quality of chain
1	G	86	 3% 72% 21% 6% •
1	H	86	 5% 67% 26% 5% ••
1	I	86	 5% 80% 15% ••
1	J	86	 2% 77% 20% •
1	K	86	 2% 79% 16% 5%
1	L	86	 5% 76% 19% 6%

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
4	FMT	I	805	-	-	X	-
4	FMT	L	806	-	-	X	-

## 2 Entry composition i

There are 6 unique types of molecules in this entry. The entry contains 8932 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 CBS domain protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	Se			
1	A	86	Total 699	C 446	N 117	O 133	Se 3	0	2	0
1	B	86	Total 688	C 439	N 116	O 130	Se 3	0	0	0
1	C	86	Total 693	C 442	N 116	O 132	Se 3	0	1	0
1	D	85	Total 686	C 439	N 115	O 129	Se 3	0	1	0
1	E	85	Total 696	C 445	N 121	O 127	Se 3	0	2	0
1	F	85	Total 693	C 443	N 119	O 128	Se 3	0	2	0
1	G	85	Total 680	C 435	N 115	O 127	Se 3	0	0	0
1	H	85	Total 687	C 439	N 115	O 130	Se 3	0	1	0
1	I	86	Total 688	C 439	N 116	O 130	Se 3	0	0	0
1	J	86	Total 688	C 439	N 116	O 130	Se 3	0	0	0
1	K	86	Total 688	C 439	N 116	O 130	Se 3	0	0	0
1	L	86	Total 695	C 444	N 118	O 130	Se 3	0	1	0

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	343	SER	-	CLONING ARTIFACT	UNP Q8KEZ1
A	344	ASN	-	CLONING ARTIFACT	UNP Q8KEZ1
A	345	ALA	-	CLONING ARTIFACT	UNP Q8KEZ1
A	387	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
A	389	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1

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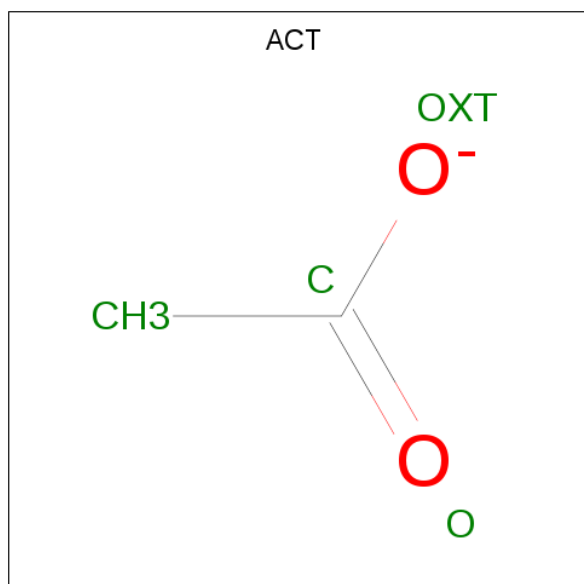
Chain	Residue	Modelled	Actual	Comment	Reference
A	414	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
B	343	SER	-	CLONING ARTIFACT	UNP Q8KEZ1
B	344	ASN	-	CLONING ARTIFACT	UNP Q8KEZ1
B	345	ALA	-	CLONING ARTIFACT	UNP Q8KEZ1
B	387	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
B	389	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
B	414	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
C	343	SER	-	CLONING ARTIFACT	UNP Q8KEZ1
C	344	ASN	-	CLONING ARTIFACT	UNP Q8KEZ1
C	345	ALA	-	CLONING ARTIFACT	UNP Q8KEZ1
C	387	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
C	389	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
C	414	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
D	343	SER	-	CLONING ARTIFACT	UNP Q8KEZ1
D	344	ASN	-	CLONING ARTIFACT	UNP Q8KEZ1
D	345	ALA	-	CLONING ARTIFACT	UNP Q8KEZ1
D	387	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
D	389	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
D	414	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
E	343	SER	-	CLONING ARTIFACT	UNP Q8KEZ1
E	344	ASN	-	CLONING ARTIFACT	UNP Q8KEZ1
E	345	ALA	-	CLONING ARTIFACT	UNP Q8KEZ1
E	387	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
E	389	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
E	414	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
F	343	SER	-	CLONING ARTIFACT	UNP Q8KEZ1
F	344	ASN	-	CLONING ARTIFACT	UNP Q8KEZ1
F	345	ALA	-	CLONING ARTIFACT	UNP Q8KEZ1
F	387	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
F	389	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
F	414	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
G	343	SER	-	CLONING ARTIFACT	UNP Q8KEZ1
G	344	ASN	-	CLONING ARTIFACT	UNP Q8KEZ1
G	345	ALA	-	CLONING ARTIFACT	UNP Q8KEZ1
G	387	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
G	389	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
G	414	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
H	343	SER	-	CLONING ARTIFACT	UNP Q8KEZ1
H	344	ASN	-	CLONING ARTIFACT	UNP Q8KEZ1
H	345	ALA	-	CLONING ARTIFACT	UNP Q8KEZ1
H	387	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
H	389	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1

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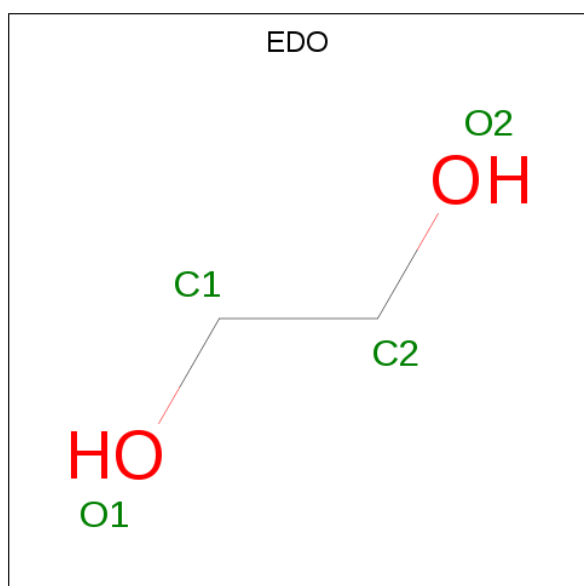
Chain	Residue	Modelled	Actual	Comment	Reference
H	414	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
I	343	SER	-	CLONING ARTIFACT	UNP Q8KEZ1
I	344	ASN	-	CLONING ARTIFACT	UNP Q8KEZ1
I	345	ALA	-	CLONING ARTIFACT	UNP Q8KEZ1
I	387	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
I	389	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
I	414	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
J	343	SER	-	CLONING ARTIFACT	UNP Q8KEZ1
J	344	ASN	-	CLONING ARTIFACT	UNP Q8KEZ1
J	345	ALA	-	CLONING ARTIFACT	UNP Q8KEZ1
J	387	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
J	389	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
J	414	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
K	343	SER	-	CLONING ARTIFACT	UNP Q8KEZ1
K	344	ASN	-	CLONING ARTIFACT	UNP Q8KEZ1
K	345	ALA	-	CLONING ARTIFACT	UNP Q8KEZ1
K	387	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
K	389	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
K	414	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
L	343	SER	-	CLONING ARTIFACT	UNP Q8KEZ1
L	344	ASN	-	CLONING ARTIFACT	UNP Q8KEZ1
L	345	ALA	-	CLONING ARTIFACT	UNP Q8KEZ1
L	387	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
L	389	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1
L	414	MSE	MET	MODIFIED RESIDUE	UNP Q8KEZ1

- Molecule 2 is ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 4 2 2	0	0
2	D	1	Total C O 4 2 2	0	0
2	E	1	Total C O 4 2 2	0	0
2	K	1	Total C O 4 2 2	0	0

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



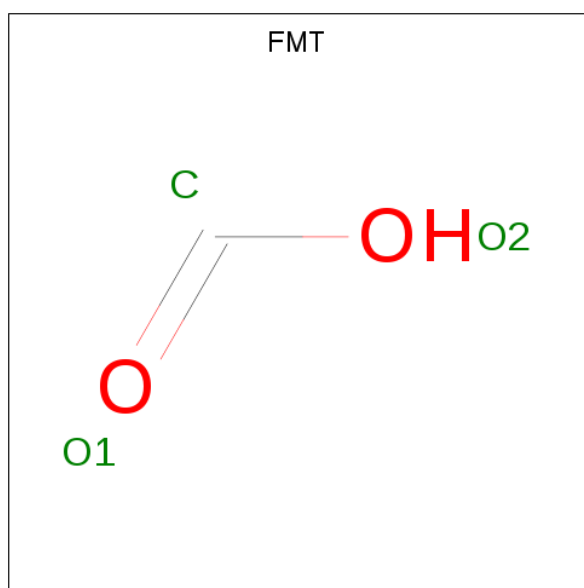
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0
3	C	1	Total C O 4 2 2	0	0
3	C	1	Total C O 4 2 2	0	0
3	C	1	Total C O 4 2 2	0	0
3	E	1	Total C O 4 2 2	0	0
3	E	1	Total C O 4 2 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	F	1	Total	C	O	0	0
			4	2	2		
3	F	1	Total	C	O	0	0
			4	2	2		
3	F	1	Total	C	O	0	0
			4	2	2		
3	I	1	Total	C	O	0	0
			4	2	2		
3	J	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is FORMIC ACID (three-letter code: FMT) (formula: CH<sub>2</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			3	1	2		
4	C	1	Total	C	O	0	0
			3	1	2		
4	D	1	Total	C	O	0	0
			3	1	2		
4	I	1	Total	C	O	0	0
			3	1	2		
4	I	1	Total	C	O	0	0
			3	1	2		
4	L	1	Total	C	O	0	0
			3	1	2		



- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	2	Total 2	Mg 2	0	0
5	G	1	Total 1	Mg 1	0	0
5	J	1	Total 1	Mg 1	0	0
5	I	2	Total 2	Mg 2	0	0

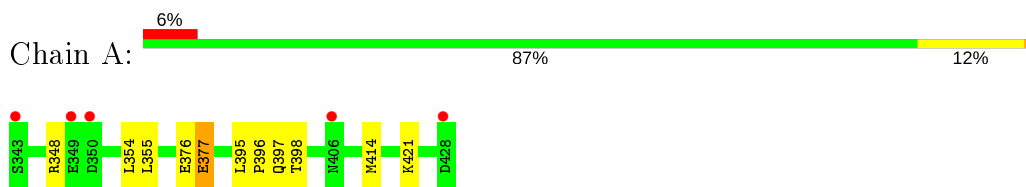
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	39	Total 39	O 39	0	0
6	B	54	Total 54	O 54	0	0
6	C	73	Total 73	O 73	0	0
6	D	38	Total 38	O 38	0	0
6	E	50	Total 50	O 50	0	0
6	F	71	Total 71	O 71	0	0
6	G	51	Total 51	O 51	0	0
6	H	21	Total 21	O 21	0	0
6	I	39	Total 39	O 39	0	0
6	J	56	Total 56	O 56	0	0
6	K	46	Total 46	O 46	0	0
6	L	21	Total 21	O 21	0	0

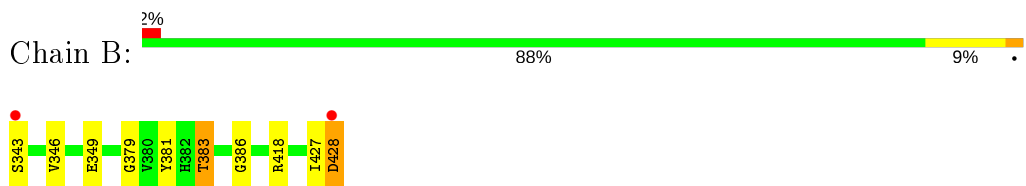
### 3 Residue-property plots [i](#)

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.

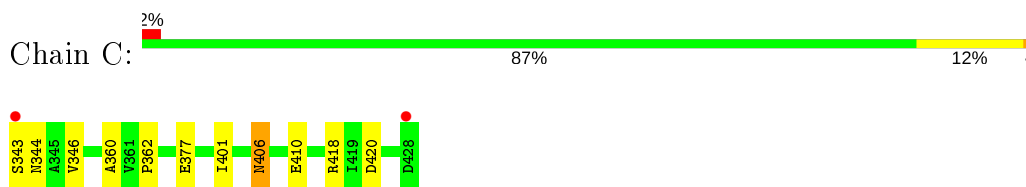
- Molecule 1: CBS domain protein



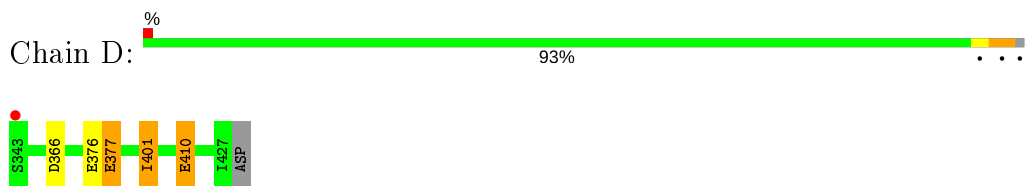
- Molecule 1: CBS domain protein



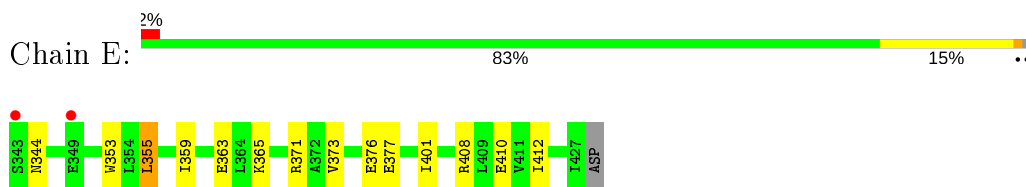
- Molecule 1: CBS domain protein



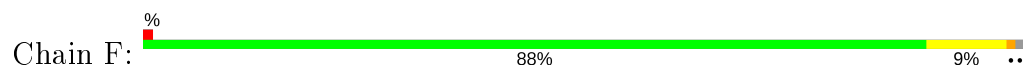
- Molecule 1: CBS domain protein



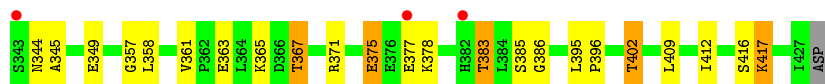
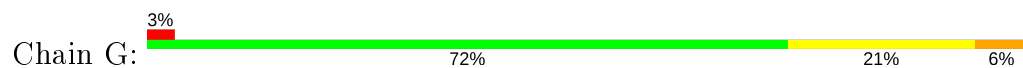
- Molecule 1: CBS domain protein



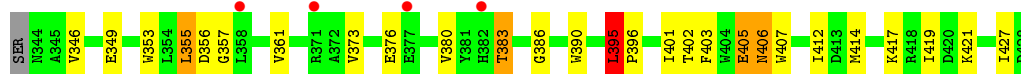
- Molecule 1: CBS domain protein



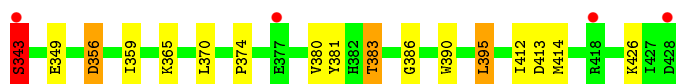
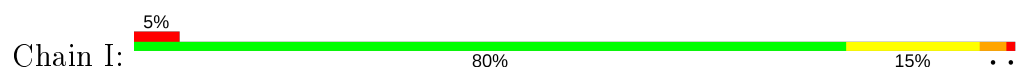
- Molecule 1: CBS domain protein



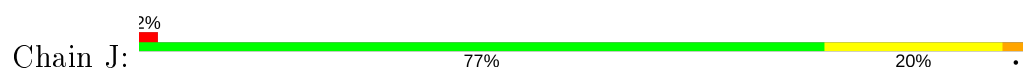
- Molecule 1: CBS domain protein



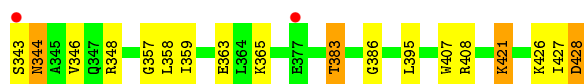
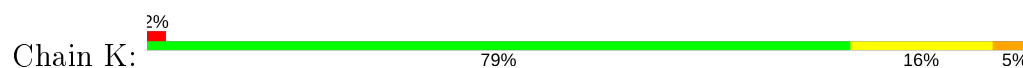
- Molecule 1: CBS domain protein



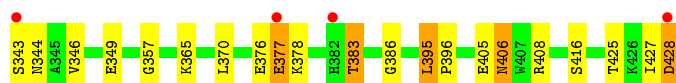
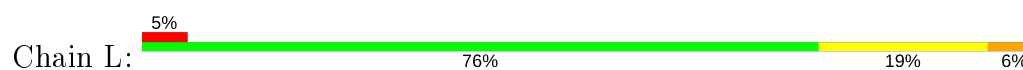
- Molecule 1: CBS domain protein



- Molecule 1: CBS domain protein



- Molecule 1: CBS domain protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	108.24Å 108.49Å 106.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.51 – 2.15 48.50 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.0 (48.51-2.15) 98.9 (48.50-2.15)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.38 (at 2.14Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.176 , 0.232 0.176 , 0.229	Depositor DCC
$R_{free}$ test set	3453 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	31.5	Xtriage
Anisotropy	0.141	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 50.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.015 for k,h,-l 0.017 for -h,-l,-k 0.015 for l,-k,h 0.006 for k,l,h 0.006 for l,h,k	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	8932	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.15% 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: MG, FMT, EDO, ACT

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	0.76	0/715	0.80	0/964
1	B	0.71	0/698	0.71	0/941
1	C	0.80	0/706	0.78	0/952
1	D	0.80	0/699	0.82	0/942
1	E	0.77	0/712	0.83	0/958
1	F	0.77	0/709	0.78	1/955 (0.1%)
1	G	0.73	0/690	0.80	0/930
1	H	0.71	0/700	0.82	1/944 (0.1%)
1	I	0.75	0/698	0.85	1/941 (0.1%)
1	J	0.85	0/698	0.81	0/941
1	K	0.78	0/698	0.92	3/941 (0.3%)
1	L	0.63	0/709	0.76	0/956
All	All	0.76	0/8432	0.81	6/11365 (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	B	0	1
1	C	0	1
1	D	0	1
1	I	0	1
All	All	0	4

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	348	ARG	NE-CZ-NH2	-8.92	115.84	120.30
1	K	348	ARG	NE-CZ-NH1	6.88	123.74	120.30
1	I	395	LEU	CA-CB-CG	6.70	130.71	115.30
1	F	408	ARG	NE-CZ-NH1	-5.94	117.33	120.30
1	K	408	ARG	NE-CZ-NH2	-5.30	117.65	120.30
1	H	395	LEU	CA-CB-CG	5.19	127.24	115.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	343	SER	Peptide
1	C	343	SER	Peptide
1	D	376	GLU	Peptide
1	I	343	SER	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	699	0	704	8	0
1	B	688	0	692	6	0
1	C	693	0	696	9	0
1	D	686	0	694	1	0
1	E	696	0	714	13	0
1	F	693	0	707	8	0
1	G	680	0	688	17	0
1	H	687	0	691	17	0
1	I	688	0	692	15	0
1	J	688	0	692	15	0
1	K	688	0	692	10	0
1	L	695	0	699	13	0
2	A	4	0	3	1	0
2	D	4	0	3	1	0
2	E	4	0	3	0	0
2	K	4	0	3	0	0
3	A	8	0	12	1	0
3	B	4	0	6	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	12	0	18	3	0
3	E	8	0	12	2	0
3	F	12	0	18	1	0
3	I	4	0	6	0	0
3	J	4	0	6	2	0
4	B	3	0	1	0	0
4	C	3	0	1	0	0
4	D	3	0	1	0	0
4	I	6	0	2	4	0
4	L	3	0	1	2	0
5	G	1	0	0	0	0
5	H	2	0	0	0	0
5	I	2	0	0	0	0
5	J	1	0	0	0	0
6	A	39	0	0	1	0
6	B	54	0	0	0	0
6	C	73	0	0	2	0
6	D	38	0	0	0	0
6	E	50	0	0	0	0
6	F	71	0	0	2	0
6	G	51	0	0	0	0
6	H	21	0	0	1	0
6	I	39	0	0	0	0
6	J	56	0	0	6	0
6	K	46	0	0	1	0
6	L	21	0	0	0	0
All	All	8932	0	8457	129	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 8.

All (129) 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:377[A]:GLU:OE1	6:A:924:HOH:O	1.64	1.12
1:G:417:LYS:HA	1:G:417:LYS:HE3	1.36	1.08
1:C:360:ALA:HB3	3:C:714:EDO:H11	1.28	1.07
1:I:426:LYS:NZ	4:I:805:FMT:H	1.70	1.06
1:G:417:LYS:HA	1:G:417:LYS:CE	1.93	0.98
1:J:406:ASN:HB2	6:J:751:HOH:O	1.63	0.96
1:H:405:GLU:O	1:H:406:ASN:ND2	2.03	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:383:THR:HG22	1:G:386:GLY:H	1.37	0.90
1:I:426:LYS:HZ3	4:I:805:FMT:H	1.31	0.89
1:A:376:GLU:O	1:A:377[A]:GLU:HG2	1.73	0.87
1:B:383:THR:HG22	1:B:386:GLY:H	1.41	0.85
1:F:401:ILE:HD12	1:F:410:GLU:HG2	1.58	0.85
1:I:383:THR:HG22	1:I:386:GLY:H	1.41	0.84
1:C:362:PRO:HD2	3:C:714:EDO:H12	1.61	0.82
3:F:713:EDO:H21	6:F:767:HOH:O	1.77	0.82
1:L:425:THR:HG23	4:L:806:FMT:H	1.60	0.81
1:C:360:ALA:HB3	3:C:714:EDO:C1	2.10	0.80
1:G:416:SER:O	1:G:417:LYS:HE3	1.84	0.78
1:I:426:LYS:HZ1	4:I:805:FMT:H	1.49	0.77
1:C:401:ILE:HD12	1:C:410:GLU:HG2	1.68	0.75
1:B:427:ILE:O	1:B:428:ASP:HB2	1.87	0.75
1:K:383:THR:HG22	1:K:386:GLY:H	1.54	0.72
1:J:357:GLY:O	1:J:383:THR:HG23	1.89	0.71
1:C:406:ASN:H	1:C:406:ASN:HD22	1.37	0.70
1:E:359:ILE:CG1	1:E:363:GLU:HG2	2.23	0.69
1:G:375:GLU:HG3	1:G:378:LYS:HD2	1.74	0.68
1:C:420:ASP:OD2	6:C:873:HOH:O	2.12	0.67
1:G:417:LYS:CA	1:G:417:LYS:HE3	2.22	0.66
1:K:359:ILE:HD11	1:K:363:GLU:HG2	1.77	0.66
1:L:357:GLY:O	1:L:383:THR:HG23	1.95	0.65
1:E:359:ILE:HD11	1:E:363:GLU:HG2	1.79	0.64
1:F:401:ILE:CD1	1:F:410:GLU:HG2	2.30	0.61
1:D:401:ILE:HD13	1:D:410[B]:GLU:HG2	1.82	0.61
2:D:902:ACT:H3	6:F:769:HOH:O	2.00	0.61
1:H:357:GLY:O	1:H:383:THR:HG23	2.02	0.60
1:H:395:LEU:HD22	1:H:396:PRO:HD2	1.81	0.60
1:H:356[B]:ASP:OD1	6:H:617:HOH:O	2.16	0.60
1:G:363:GLU:O	1:G:367:THR:HG23	2.04	0.58
1:L:427:ILE:O	1:L:428:ASP:HB2	2.04	0.57
1:B:381:TYR:O	3:B:702:EDO:H12	2.05	0.57
1:J:383:THR:HG22	1:J:386:GLY:H	1.68	0.57
1:G:363:GLU:O	1:G:367:THR:CG2	2.53	0.57
1:E:365:LYS:HD3	1:E:373:VAL:HG13	1.87	0.57
1:G:417:LYS:HE2	1:G:417:LYS:HA	1.83	0.57
1:J:425:THR:HG23	3:J:711:EDO:H21	1.88	0.56
1:K:427:ILE:O	1:K:428:ASP:OD1	2.21	0.56
1:B:379:GLY:H	3:B:702:EDO:H22	1.71	0.56
1:I:343:SER:N	1:I:356:ASP:CG	2.59	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:359:ILE:CD1	1:E:363:GLU:HG2	2.36	0.55
1:F:373:VAL:CG2	1:F:376:GLU:HG2	2.36	0.55
1:K:427:ILE:O	1:K:428:ASP:HB2	2.07	0.55
1:I:412:ILE:HD12	1:J:412:ILE:HD12	1.90	0.54
1:E:353:TRP:HB3	1:E:355:LEU:HD13	1.90	0.54
1:A:376:GLU:C	1:A:377[A]:GLU:HG2	2.28	0.53
1:K:427:ILE:O	1:K:428:ASP:CB	2.55	0.53
1:L:383:THR:HG22	1:L:386:GLY:H	1.71	0.53
1:H:380:VAL:HG11	1:H:390:TRP:CD1	2.44	0.52
1:J:427:ILE:O	1:J:428:ASP:O	2.27	0.52
1:G:402:THR:HG22	1:G:409:LEU:HB2	1.91	0.52
1:G:395:LEU:HD12	1:G:396:PRO:HD2	1.90	0.52
1:C:401:ILE:CD1	1:C:410:GLU:HG2	2.39	0.52
1:H:383:THR:HG22	1:H:386:GLY:H	1.75	0.52
1:H:417:LYS:O	1:H:417:LYS:HG2	2.10	0.52
1:E:359:ILE:HD11	1:E:363:GLU:CG	2.42	0.50
1:F:343:SER:HA	1:F:359:ILE:HA	1.92	0.50
1:I:380:VAL:HG23	1:I:381:TYR:CD2	2.48	0.49
1:G:412:ILE:HD12	1:H:412:ILE:HD12	1.94	0.49
1:J:406:ASN:CB	6:J:751:HOH:O	2.38	0.48
1:K:357:GLY:O	1:K:383:THR:HG23	2.14	0.48
1:E:410:GLU:HG2	1:E:412:ILE:HD12	1.94	0.47
1:L:376:GLU:O	1:L:377:GLU:HB2	2.14	0.47
1:B:427:ILE:O	1:B:428:ASP:CB	2.58	0.47
1:L:425:THR:CG2	4:L:806:FMT:H	2.37	0.47
1:G:357:GLY:O	1:G:383:THR:HG23	2.14	0.47
1:F:373:VAL:HG22	1:F:376:GLU:HG2	1.96	0.47
1:H:353:TRP:HB3	1:H:355:LEU:HD13	1.96	0.47
1:H:361:VAL:HG13	1:H:373:VAL:HG11	1.95	0.47
1:K:344:ASN:HB2	6:K:928:HOH:O	2.15	0.47
1:L:365:LYS:HA	1:L:370:LEU:HB2	1.97	0.47
1:F:359:ILE:HD11	1:F:363:GLU:HG2	1.95	0.46
1:B:418:ARG:NH1	1:H:401:ILE:O	2.47	0.46
1:J:426:LYS:H	3:J:711:EDO:C2	2.27	0.46
1:E:401:ILE:O	3:E:704:EDO:H11	2.14	0.46
1:F:373:VAL:HG23	1:F:376:GLU:HG2	1.97	0.46
1:I:365:LYS:HG2	1:I:370:LEU:HB2	1.98	0.46
1:J:427:ILE:O	1:J:428:ASP:C	2.55	0.46
1:C:406:ASN:HD22	1:C:406:ASN:N	2.10	0.45
1:J:406:ASN:CA	6:J:751:HOH:O	2.64	0.45
1:E:408[B]:ARG:HB3	1:E:408[B]:ARG:HH11	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:408:ARG:HB2	1:L:427:ILE:HD11	1.98	0.45
1:H:403:PHE:CE1	1:H:427:ILE:HD11	2.52	0.45
1:J:374:PRO:HB2	1:J:390:TRP:CZ3	2.51	0.45
1:G:361:VAL:O	1:G:365:LYS:HG3	2.17	0.45
1:H:406:ASN:ND2	1:H:407:TRP:CD1	2.85	0.45
1:L:376:GLU:O	1:L:377:GLU:CB	2.65	0.45
1:L:405:GLU:O	1:L:406:ASN:OD1	2.35	0.44
1:I:426:LYS:HZ3	4:I:805:FMT:C	2.16	0.44
1:A:398:THR:OG1	1:A:414:MSE:HG2	2.16	0.44
1:E:376:GLU:O	1:E:377:GLU:HB2	2.18	0.43
1:G:383:THR:HG23	1:G:385:SER:H	1.84	0.43
1:G:412:ILE:O	1:H:421:LYS:HE3	2.19	0.43
2:A:904:ACT:H3	6:C:842:HOH:O	2.18	0.43
1:A:397:GLN:HB3	3:A:712:EDO:H11	2.01	0.42
1:I:413:ASP:OD2	1:J:421:LYS:HE2	2.18	0.42
1:K:407:TRP:CH2	1:K:426:LYS:HG3	2.54	0.42
1:L:405:GLU:HG2	1:L:405:GLU:O	2.19	0.42
1:I:374:PRO:HB2	1:I:390:TRP:CZ3	2.55	0.42
1:A:395:LEU:HA	1:A:396:PRO:HD3	1.95	0.42
1:E:371[B]:ARG:HD3	1:G:345:ALA:HB3	2.01	0.42
1:J:426:LYS:HE3	6:J:751:HOH:O	2.20	0.42
1:H:373:VAL:HG22	1:H:376:GLU:HG3	2.01	0.42
1:L:395:LEU:HA	1:L:396:PRO:HD3	1.94	0.42
1:E:401:ILE:H	3:E:704:EDO:C1	2.33	0.41
1:E:359:ILE:HG12	1:E:363:GLU:HG2	2.01	0.41
1:I:380:VAL:HG23	1:I:381:TYR:HD2	1.84	0.41
1:I:343:SER:N	1:I:356:ASP:OD1	2.53	0.41
1:I:356:ASP:O	1:I:359:ILE:HG22	2.20	0.41
1:H:414:MSE:HG2	1:H:419:ILE:HA	2.02	0.41
1:J:344:ASN:HB2	6:J:752:HOH:O	2.20	0.41
1:F:408:ARG:HB2	1:F:427:ILE:HD11	2.03	0.41
1:J:406:ASN:N	6:J:751:HOH:O	2.53	0.41
1:L:376:GLU:O	1:L:378:LYS:NZ	2.52	0.41
1:C:406:ASN:H	1:C:406:ASN:ND2	2.13	0.41
1:K:365:LYS:HE3	1:K:365:LYS:HB3	1.84	0.41
1:H:395:LEU:HD21	1:H:417:LYS:HG2	2.03	0.40
1:I:414:MSE:HB3	1:I:414:MSE:HE3	1.92	0.40
1:K:421:LYS:HA	1:K:421:LYS:HD3	1.99	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	86/86 (100%)	81 (94%)	5 (6%)	0	100	100
1	B	84/86 (98%)	79 (94%)	4 (5%)	1 (1%)	13	7
1	C	85/86 (99%)	83 (98%)	2 (2%)	0	100	100
1	D	84/86 (98%)	80 (95%)	3 (4%)	1 (1%)	13	7
1	E	85/86 (99%)	80 (94%)	5 (6%)	0	100	100
1	F	85/86 (99%)	82 (96%)	3 (4%)	0	100	100
1	G	83/86 (96%)	81 (98%)	2 (2%)	0	100	100
1	H	84/86 (98%)	78 (93%)	4 (5%)	2 (2%)	6	1
1	I	84/86 (98%)	80 (95%)	4 (5%)	0	100	100
1	J	84/86 (98%)	82 (98%)	2 (2%)	0	100	100
1	K	84/86 (98%)	81 (96%)	3 (4%)	0	100	100
1	L	85/86 (99%)	82 (96%)	3 (4%)	0	100	100
All	All	1013/1032 (98%)	969 (96%)	40 (4%)	4 (0%)	34	29

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	377	GLU
1	H	405	GLU
1	B	349	GLU
1	H	349	GLU

### 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	77/72 (107%)	71 (92%)	6 (8%)	12	7
1	B	75/72 (104%)	72 (96%)	3 (4%)	31	29
1	C	76/72 (106%)	71 (93%)	5 (7%)	16	11
1	D	75/72 (104%)	70 (93%)	5 (7%)	16	11
1	E	76/72 (106%)	74 (97%)	2 (3%)	46	47
1	F	76/72 (106%)	76 (100%)	0	100	100
1	G	74/72 (103%)	64 (86%)	10 (14%)	4	1
1	H	75/72 (104%)	69 (92%)	6 (8%)	12	7
1	I	75/72 (104%)	70 (93%)	5 (7%)	16	11
1	J	75/72 (104%)	65 (87%)	10 (13%)	4	1
1	K	75/72 (104%)	67 (89%)	8 (11%)	6	3
1	L	76/72 (106%)	66 (87%)	10 (13%)	4	1
All	All	905/864 (105%)	835 (92%)	70 (8%)	13	8

All (70) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	348	ARG
1	A	354	LEU
1	A	355	LEU
1	A	377[A]	GLU
1	A	377[B]	GLU
1	A	421	LYS
1	B	346	VAL
1	B	383	THR
1	B	428	ASP
1	C	344	ASN
1	C	346	VAL
1	C	377	GLU
1	C	406	ASN
1	C	418	ARG
1	D	366	ASP
1	D	377	GLU
1	D	401	ILE
1	D	410[A]	GLU
1	D	410[B]	GLU
1	E	344	ASN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	E	355	LEU
1	G	344	ASN
1	G	349	GLU
1	G	358	LEU
1	G	367	THR
1	G	371	ARG
1	G	375	GLU
1	G	377	GLU
1	G	383	THR
1	G	402	THR
1	G	417	LYS
1	H	346	VAL
1	H	355	LEU
1	H	383	THR
1	H	395	LEU
1	H	402	THR
1	H	406	ASN
1	I	343	SER
1	I	349	GLU
1	I	356	ASP
1	I	383	THR
1	I	395	LEU
1	J	343	SER
1	J	344	ASN
1	J	346	VAL
1	J	358	LEU
1	J	363	GLU
1	J	366	ASP
1	J	378	LYS
1	J	383	THR
1	J	395	LEU
1	J	428	ASP
1	K	343	SER
1	K	344	ASN
1	K	346	VAL
1	K	358	LEU
1	K	383	THR
1	K	395	LEU
1	K	421	LYS
1	K	428	ASP
1	L	343	SER
1	L	344	ASN

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Mol	Chain	Res	Type
1	L	346	VAL
1	L	349	GLU
1	L	377	GLU
1	L	383	THR
1	L	395	LEU
1	L	406	ASN
1	L	416	SER
1	L	428	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	347	GLN
1	B	406	ASN
1	C	344	ASN
1	C	406	ASN
1	J	344	ASN
1	K	344	ASN
1	L	344	ASN
1	L	406	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](#)

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 29 ligands modelled in this entry, 6 are monoatomic - leaving 23 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
3	EDO	E	705	-	3,3,3	0.61	0	2,2,2	0.34	0
2	ACT	A	904	-	1,3,3	3.04	1 (100%)	0,3,3	0.00	-
4	FMT	I	805	-	0,2,2	0.00	-	0,1,1	0.00	-
4	FMT	L	806	-	0,2,2	0.00	-	0,1,1	0.00	-
3	EDO	F	701	-	3,3,3	0.88	0	2,2,2	0.32	0
3	EDO	C	714	-	3,3,3	0.46	0	2,2,2	0.37	0
3	EDO	E	704	-	3,3,3	0.38	0	2,2,2	0.68	0
3	EDO	F	713	-	3,3,3	0.82	0	2,2,2	0.23	0
3	EDO	J	711	-	3,3,3	0.62	0	2,2,2	0.52	0
2	ACT	K	901	-	1,3,3	1.27	0	0,3,3	0.00	-
4	FMT	B	804	-	0,2,2	0.00	-	0,1,1	0.00	-
3	EDO	F	710	-	3,3,3	0.40	0	2,2,2	0.51	0
3	EDO	I	708	-	3,3,3	0.63	0	2,2,2	0.23	0
4	FMT	I	801	-	0,2,2	0.00	-	0,1,1	0.00	-
3	EDO	A	706	-	3,3,3	0.57	0	2,2,2	0.42	0
3	EDO	C	703	-	3,3,3	0.63	0	2,2,2	0.31	0
4	FMT	C	802	-	0,2,2	0.00	-	0,1,1	0.00	-
2	ACT	E	903	-	1,3,3	2.26	1 (100%)	0,3,3	0.00	-
3	EDO	A	712	-	3,3,3	0.48	0	2,2,2	0.37	0
3	EDO	C	709	-	3,3,3	0.59	0	2,2,2	0.61	0
3	EDO	B	702	-	3,3,3	0.63	0	2,2,2	0.33	0
4	FMT	D	803	-	0,2,2	0.00	-	0,1,1	0.00	-
2	ACT	D	902	-	1,3,3	1.93	0	0,3,3	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
3	EDO	E	705	-	-	0/1/1/1	-
3	EDO	J	711	-	-	0/1/1/1	-
3	EDO	F	710	-	-	1/1/1/1	-
3	EDO	C	709	-	-	1/1/1/1	-
3	EDO	I	708	-	-	0/1/1/1	-
3	EDO	B	702	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	A	706	-	-	0/1/1/1	-
3	EDO	A	712	-	-	1/1/1/1	-
3	EDO	C	703	-	-	1/1/1/1	-
3	EDO	F	701	-	-	0/1/1/1	-
3	EDO	C	714	-	-	1/1/1/1	-
3	EDO	E	704	-	-	0/1/1/1	-
3	EDO	F	713	-	-	1/1/1/1	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	904	ACT	CH3-C	3.04	1.52	1.48
2	E	903	ACT	CH3-C	2.26	1.51	1.48

There are no bond angle outliers.

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	F	713	EDO	O1-C1-C2-O2
3	C	709	EDO	O1-C1-C2-O2
3	B	702	EDO	O1-C1-C2-O2
3	C	714	EDO	O1-C1-C2-O2
3	A	712	EDO	O1-C1-C2-O2
3	C	703	EDO	O1-C1-C2-O2
3	F	710	EDO	O1-C1-C2-O2

There are no ring outliers.

10 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	904	ACT	1	0
4	I	805	FMT	4	0
4	L	806	FMT	2	0
3	C	714	EDO	3	0
3	E	704	EDO	2	0
3	F	713	EDO	1	0
3	J	711	EDO	2	0
3	A	712	EDO	1	0
3	B	702	EDO	2	0
2	D	902	ACT	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	83/86 (96%)	0.52	5 (6%) 21 29	34, 43, 57, 68	0
1	B	83/86 (96%)	0.06	2 (2%) 59 67	32, 36, 50, 59	0
1	C	83/86 (96%)	-0.01	2 (2%) 59 67	25, 29, 43, 53	0
1	D	82/86 (95%)	-0.07	1 (1%) 79 83	27, 31, 43, 53	0
1	E	82/86 (95%)	-0.06	2 (2%) 59 67	30, 34, 46, 55	0
1	F	82/86 (95%)	-0.12	1 (1%) 79 83	28, 32, 40, 53	0
1	G	82/86 (95%)	-0.07	3 (3%) 41 49	31, 39, 53, 57	0
1	H	82/86 (95%)	0.21	4 (4%) 29 38	38, 45, 53, 58	0
1	I	83/86 (96%)	0.04	4 (4%) 30 39	28, 36, 47, 54	0
1	J	83/86 (96%)	-0.08	2 (2%) 59 67	26, 33, 47, 53	0
1	K	83/86 (96%)	0.01	2 (2%) 59 67	30, 37, 48, 51	0
1	L	83/86 (96%)	0.21	4 (4%) 30 39	38, 46, 53, 59	0
All	All	991/1032 (96%)	0.05	32 (3%) 47 56	25, 37, 52, 68	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	428	ASP	5.5
1	L	343	SER	5.0
1	A	343	SER	4.8
1	J	343	SER	4.4
1	K	377	GLU	4.3
1	F	343	SER	4.2
1	B	343	SER	4.0
1	K	343	SER	3.8
1	A	428	ASP	3.7
1	G	343	SER	3.6
1	B	428	ASP	3.6

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Mol	Chain	Res	Type	RSRZ
1	J	377	GLU	3.3
1	A	350	ASP	3.3
1	E	343	SER	3.3
1	G	377	GLU	3.2
1	L	377	GLU	3.1
1	D	343	SER	3.0
1	I	377	GLU	2.9
1	I	428	ASP	2.9
1	H	371	ARG	2.8
1	H	358	LEU	2.6
1	H	377	GLU	2.6
1	L	428	ASP	2.4
1	A	349	GLU	2.4
1	I	343	SER	2.4
1	I	418	ARG	2.4
1	C	343	SER	2.3
1	L	382[A]	HIS	2.3
1	E	349	GLU	2.2
1	A	406[A]	ASN	2.2
1	G	382	HIS	2.2
1	H	382	HIS	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates [i](#)

There are no 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(Å <sup>2</sup> )	Q<0.9
2	ACT	A	904	4/4	0.75	0.20	42,44,45,45	0
4	FMT	I	805	3/3	0.75	0.40	52,52,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	FMT	C	802	3/3	0.84	0.20	44,44,46,46	0
2	ACT	D	902	4/4	0.84	0.15	41,41,42,42	0
4	FMT	I	801	3/3	0.85	0.21	64,64,64,64	0
3	EDO	A	706	4/4	0.85	0.12	47,48,48,50	0
4	FMT	L	806	3/3	0.85	0.36	46,46,46,46	0
2	ACT	E	903	4/4	0.85	0.15	52,52,52,53	0
4	FMT	D	803	3/3	0.85	0.23	62,62,63,63	0
3	EDO	F	701	4/4	0.85	0.13	31,36,38,39	0
3	EDO	J	711	4/4	0.86	0.31	33,39,45,48	0
3	EDO	A	712	4/4	0.86	0.23	36,41,42,46	0
3	EDO	F	710	4/4	0.87	0.32	41,47,47,50	0
3	EDO	I	708	4/4	0.88	0.21	44,46,46,47	0
2	ACT	K	901	4/4	0.88	0.11	67,67,67,67	0
3	EDO	F	713	4/4	0.90	0.30	23,37,37,43	0
5	MG	H	601	1/1	0.92	0.13	47,47,47,47	0
3	EDO	C	714	4/4	0.92	0.25	38,39,40,41	0
3	EDO	C	703	4/4	0.93	0.09	37,42,42,44	0
4	FMT	B	804	3/3	0.93	0.07	60,60,61,61	0
3	EDO	C	709	4/4	0.94	0.19	30,39,41,44	0
3	EDO	B	702	4/4	0.94	0.09	27,35,36,37	0
5	MG	H	602	1/1	0.94	0.18	38,38,38,38	0
3	EDO	E	705	4/4	0.94	0.13	29,36,36,40	0
3	EDO	E	704	4/4	0.95	0.30	25,25,27,28	0
5	MG	G	603	1/1	0.95	0.11	51,51,51,51	0
5	MG	J	604	1/1	0.96	0.15	32,32,32,32	0
5	MG	I	606	1/1	0.97	0.06	35,35,35,35	0
5	MG	I	605	1/1	0.97	0.10	25,25,25,25	0

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

There are no such residues in this entry.