wwPDB X-ray Structure Validation Summary Report (i)

Sep 28, 2024 – 09:43 PM EDT

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 wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

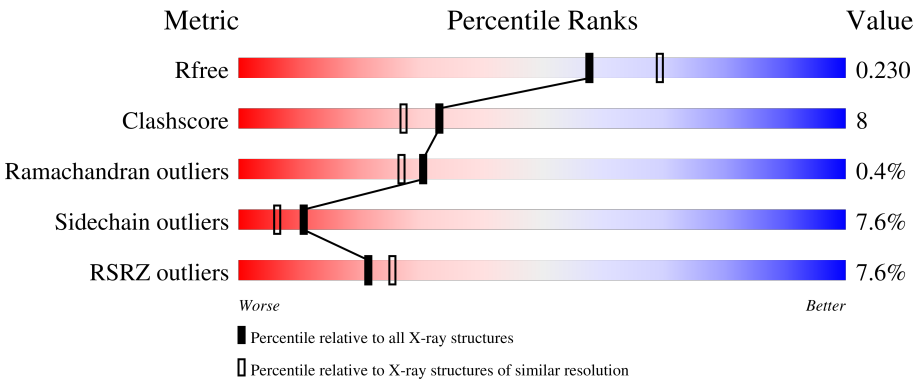
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

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 2.15 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}	164625	1881 (2.16-2.16)
Clashscore	180529	2047 (2.16-2.16)
Ramachandran outliers	177936	2027 (2.16-2.16)
Sidechain outliers	177891	2026 (2.16-2.16)
RSRZ outliers	164620	1882 (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 of the lower bar indicate the fraction of residues that contain outliers for >=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 <=5%

Mol	Chain	Length	Quality of chain
1	A	86	36% 87% 12% •
1	B	86	6% 88% 9% •
1	C	86	2% 87% 12% •
1	D	86	5% 93% • • •
1	E	86	2% 83% 15% ••
1	F	86	% 88% 9% ••

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Mol	Chain	Length	Quality of chain
1	G	86	2%, 72%, 21%, 6%
1	H	86	19%, 67%, 26%, 5%
1	I	86	6%, 80%, 15%
1	J	86	2%, 77%, 20%
1	K	86	2%, 79%, 16%, 5%
1	L	86	3%, 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	699	446	117	133	3	0	2	0
1	B	86	688	439	116	130	3	0	0	0
1	C	86	693	442	116	132	3	0	1	0
1	D	85	686	439	115	129	3	0	1	0
1	E	85	696	445	121	127	3	0	2	0
1	F	85	693	443	119	128	3	0	2	0
1	G	85	680	435	115	127	3	0	0	0
1	H	85	687	439	115	130	3	0	1	0
1	I	86	688	439	116	130	3	0	0	0
1	J	86	688	439	116	130	3	0	0	0
1	K	86	688	439	116	130	3	0	0	0
1	L	86	695	444	118	130	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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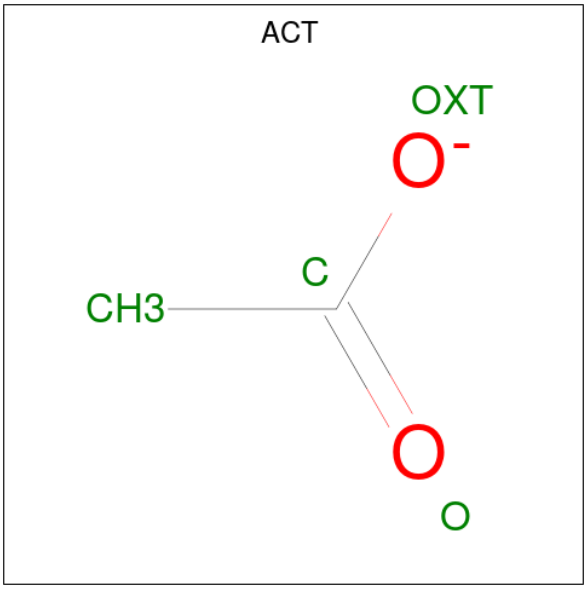
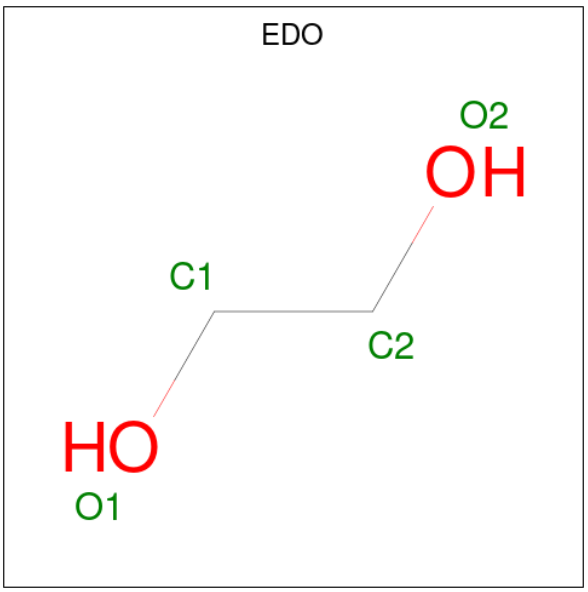
Chain	Residue	Modelled	Actual	Comment	Reference
H	414	MSE	MET	modified residue	UNP Q8KEZ1
I	343	SER	-	cloning artifact	UNP Q8KEZ1
I	344	ASN	-	cloning artifact	UNP Q8KEZ1
I	345	ALA	-	cloning artifact	UNP Q8KEZ1
I	387	MSE	MET	modified residue	UNP Q8KEZ1
I	389	MSE	MET	modified residue	UNP Q8KEZ1
I	414	MSE	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: $C_2H_3O_2$).



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

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

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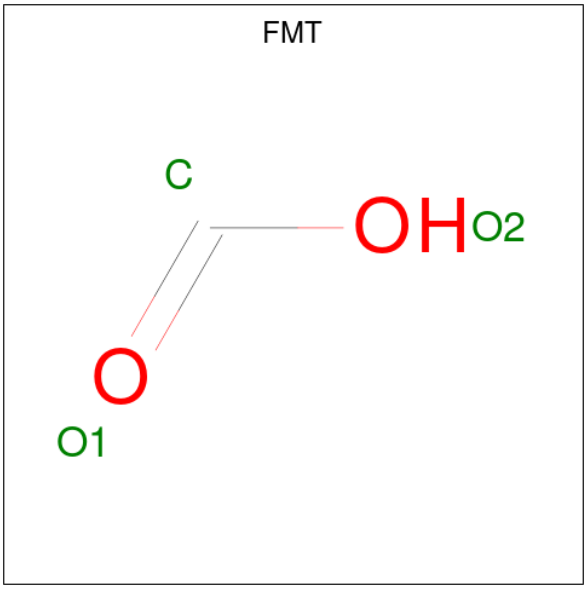
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	F	1	4	2	2	0	0
			Total	C	O		
3	F	1	4	2	2	0	0
			Total	C	O		
3	F	1	4	2	2	0	0
			Total	C	O		
3	I	1	4	2	2	0	0
			Total	C	O		
3	J	1	4	2	2	0	0

- Molecule 4 is FORMIC ACID (three-letter code: FMT) (formula: CH_2O_2).



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

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

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

- Molecule 6 is water.

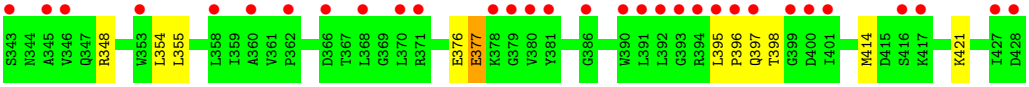
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	39	Total O 39 39	0	0
6	B	54	Total O 54 54	0	0
6	C	73	Total O 73 73	0	0
6	D	38	Total O 38 38	0	0
6	E	50	Total O 50 50	0	0
6	F	71	Total O 71 71	0	0
6	G	51	Total O 51 51	0	0
6	H	21	Total O 21 21	0	0
6	I	39	Total O 39 39	0	0
6	J	56	Total O 56 56	0	0
6	K	46	Total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

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. 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. 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.

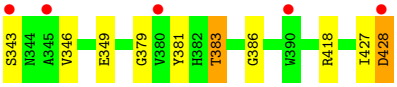
• Molecule 1: CBS domain protein

Chain A:



• Molecule 1: CBS domain protein

Chain B:

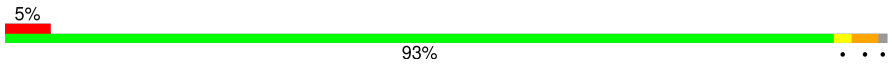


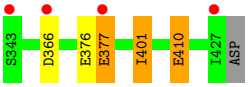
• Molecule 1: CBS domain protein

Chain C:

• Molecule 1: CBS domain protein

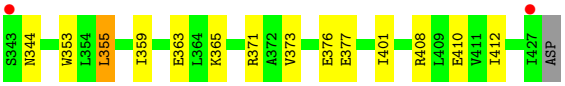
Chain D:





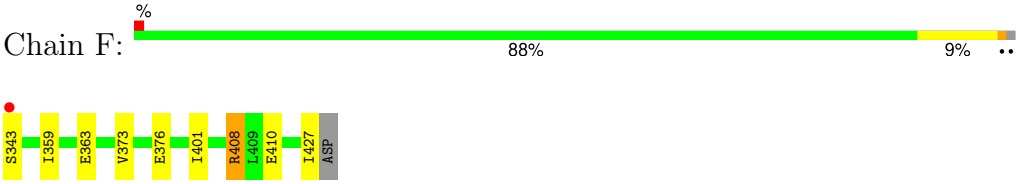
• Molecule 1: CBS domain protein

Chain E:



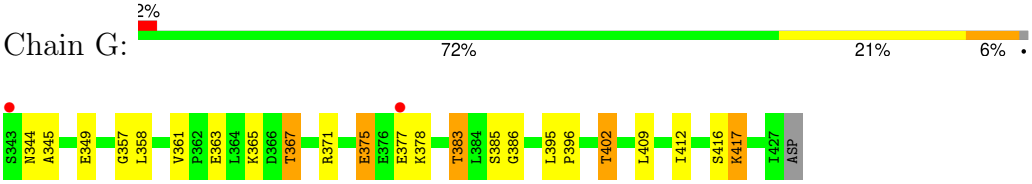
• Molecule 1: CBS domain protein

Chain F:



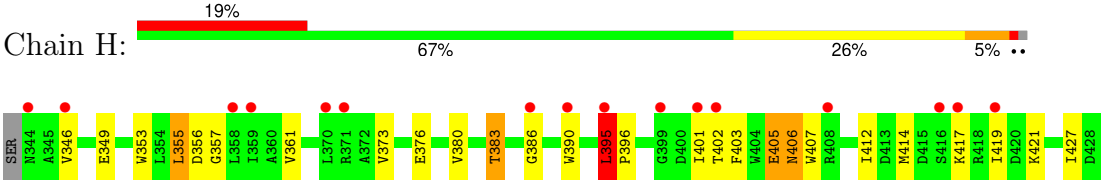
• Molecule 1: CBS domain protein

Chain G:



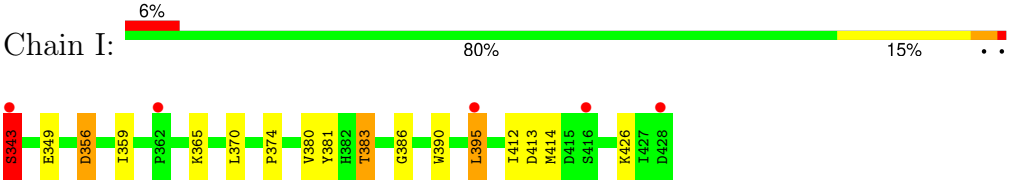
• Molecule 1: CBS domain protein

Chain H:



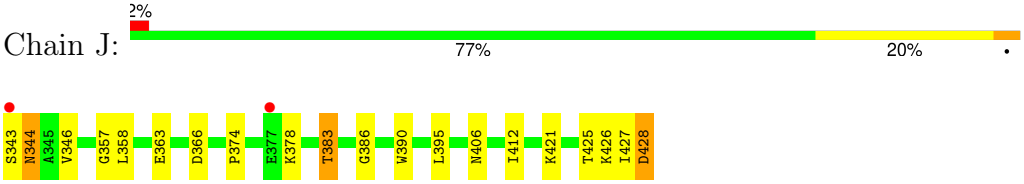
• Molecule 1: CBS domain protein

Chain I:



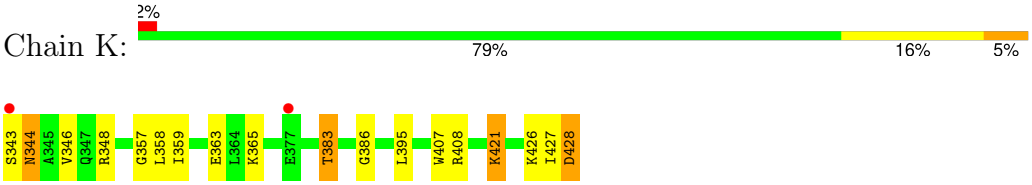
• Molecule 1: CBS domain protein

Chain J:



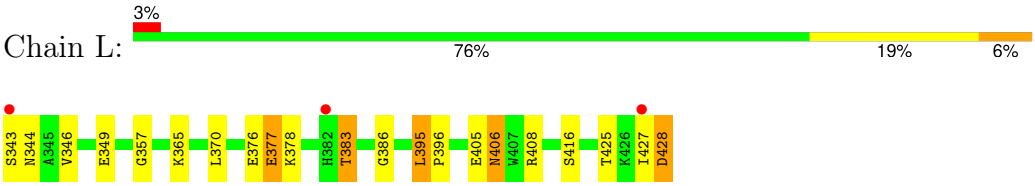
• Molecule 1: CBS domain protein

Chain K:



• Molecule 1: CBS domain protein

Chain L:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	108.24Å 108.49Å 106.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.51 – 2.15 48.51 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.0 (48.51-2.15) 99.1 (48.51-2.15)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.38 (at 2.14Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.176 , 0.232 0.176 , 0.230	Depositor DCC
R_{free} test set	3449 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	31.5	Xtriage
Anisotropy	0.141	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 47.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	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	0.93	EDS
Total number of atoms	8932	wwPDB-VP
Average B, all atoms (Å^2)	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.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: EDO, MG, ACT, FMT

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.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
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

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
3	C	12	0	18	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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.

The worst 5 of 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:HE3	1:G:417:LYS:HA	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

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%)	11	6
1	C	85/86 (99%)	83 (98%)	2 (2%)	0	100	100
1	D	84/86 (98%)	80 (95%)	3 (4%)	1 (1%)	11	6
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%)	5	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%)	30	27

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%)	10	6
1	B	75/72 (104%)	72 (96%)	3 (4%)	27	25
1	C	76/72 (106%)	71 (93%)	5 (7%)	14	9
1	D	75/72 (104%)	70 (93%)	5 (7%)	13	9
1	E	76/72 (106%)	74 (97%)	2 (3%)	41	43
1	F	76/72 (106%)	76 (100%)	0	100	100
1	G	74/72 (103%)	64 (86%)	10 (14%)	3	1
1	H	75/72 (104%)	69 (92%)	6 (8%)	10	6
1	I	75/72 (104%)	70 (93%)	5 (7%)	13	9
1	J	75/72 (104%)	65 (87%)	10 (13%)	3	1
1	K	75/72 (104%)	67 (89%)	8 (11%)	5	2
1	L	76/72 (106%)	66 (87%)	10 (13%)	3	1
All	All	905/864 (105%)	835 (92%)	70 (8%)	11	6

5 of 70 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	K	395	LEU
1	K	428	ASP
1	L	383	THR
1	G	367	THR
1	G	358	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	L	406	ASN
1	L	344	ASN
1	J	344	ASN
1	C	406	ASN
1	K	344	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 oligosaccharides 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	A	712	-	3,3,3	0.45	0	2,2,2	0.40	0
4	FMT	I	805	-	2,2,2	0.62	0	1,1,1	0.23	0
4	FMT	D	803	-	2,2,2	0.66	0	1,1,1	0.13	0
3	EDO	B	702	-	3,3,3	0.62	0	2,2,2	0.28	0
3	EDO	C	703	-	3,3,3	0.61	0	2,2,2	0.33	0
4	FMT	C	802	-	2,2,2	0.74	0	1,1,1	0.11	0
3	EDO	E	705	-	3,3,3	0.56	0	2,2,2	0.38	0
3	EDO	E	704	-	3,3,3	0.36	0	2,2,2	0.70	0
2	ACT	A	904	-	3,3,3	1.10	0	3,3,3	1.15	0
3	EDO	A	706	-	3,3,3	0.53	0	2,2,2	0.46	0
4	FMT	B	804	-	2,2,2	0.62	0	1,1,1	0.19	0
4	FMT	I	801	-	2,2,2	0.65	0	1,1,1	0.17	0
2	ACT	D	902	-	3,3,3	1.05	0	3,3,3	0.91	0
3	EDO	F	713	-	3,3,3	0.79	0	2,2,2	0.16	0
3	EDO	F	701	-	3,3,3	0.86	0	2,2,2	0.30	0
3	EDO	I	708	-	3,3,3	0.61	0	2,2,2	0.27	0
3	EDO	C	714	-	3,3,3	0.42	0	2,2,2	0.41	0
2	ACT	K	901	-	3,3,3	0.84	0	3,3,3	1.20	0
4	FMT	L	806	-	2,2,2	0.64	0	1,1,1	0.16	0
3	EDO	J	711	-	3,3,3	0.59	0	2,2,2	0.49	0
3	EDO	C	709	-	3,3,3	0.57	0	2,2,2	0.62	0
2	ACT	E	903	-	3,3,3	0.98	0	3,3,3	1.03	0
3	EDO	F	710	-	3,3,3	0.37	0	2,2,2	0.54	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
3	EDO	F	701	-	-	0/1/1/1	-
3	EDO	I	708	-	-	0/1/1/1	-
3	EDO	C	703	-	-	1/1/1/1	-
3	EDO	A	706	-	-	0/1/1/1	-
3	EDO	A	712	-	-	1/1/1/1	-
3	EDO	C	714	-	-	1/1/1/1	-
3	EDO	E	705	-	-	0/1/1/1	-
3	EDO	E	704	-	-	0/1/1/1	-
3	EDO	J	711	-	-	0/1/1/1	-
3	EDO	C	709	-	-	1/1/1/1	-
3	EDO	F	710	-	-	1/1/1/1	-
3	EDO	B	702	-	-	1/1/1/1	-
3	EDO	F	713	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	702	EDO	O1-C1-C2-O2
3	C	709	EDO	O1-C1-C2-O2
3	F	713	EDO	O1-C1-C2-O2
3	C	714	EDO	O1-C1-C2-O2
3	A	712	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
3	A	712	EDO	1	0
4	I	805	FMT	4	0
3	B	702	EDO	2	0
3	E	704	EDO	2	0
2	A	904	ACT	1	0
2	D	902	ACT	1	0
3	F	713	EDO	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	714	EDO	3	0
4	L	806	FMT	2	0
3	J	711	EDO	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)

Warning: The R factor obtained from EDS is 0.2433,which does not match the depositor's R factor of 0.17582. Please interpret the results in this section carefully.

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, 95th 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^2)	Q<0.9
1	A	83/86 (96%)	1.83	31 (37%)	1	1	26, 42, 57, 68	2 (2%)
1	B	83/86 (96%)	0.81	5 (6%)	29	34	32, 36, 50, 59	0
1	C	83/86 (96%)	-0.02	2 (2%)	59	64	20, 29, 43, 53	1 (1%)
1	D	82/86 (95%)	0.20	4 (4%)	36	41	18, 31, 43, 53	1 (1%)
1	E	82/86 (95%)	0.30	2 (2%)	59	64	19, 34, 46, 55	2 (2%)
1	F	82/86 (95%)	0.07	1 (1%)	76	79	18, 32, 40, 53	2 (2%)
1	G	82/86 (95%)	0.49	2 (2%)	59	64	31, 39, 53, 57	0
1	H	82/86 (95%)	1.46	16 (19%)	4	5	26, 45, 53, 58	1 (1%)
1	I	83/86 (96%)	0.86	5 (6%)	29	34	28, 36, 47, 54	0
1	J	83/86 (96%)	0.33	2 (2%)	59	64	26, 33, 47, 53	0
1	K	83/86 (96%)	0.42	2 (2%)	59	64	30, 37, 48, 51	0
1	L	83/86 (96%)	0.93	3 (3%)	46	52	27, 46, 53, 59	1 (1%)
All	All	991/1032 (96%)	0.64	75 (7%)	21	25	18, 37, 52, 68	10 (1%)

The worst 5 of 75 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	395	LEU	4.4
1	J	343	SER	4.3
1	A	343	SER	4.2
1	C	343	SER	4.0
1	A	380	VAL	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, 95th 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^2)	Q<0.9
2	ACT	E	903	4/4	0.71	0.20	52,52,52,53	0
4	FMT	I	801	3/3	0.71	0.19	64,64,64,64	0
2	ACT	A	904	4/4	0.75	0.20	42,44,45,45	0
4	FMT	C	802	3/3	0.76	0.19	44,44,46,46	0
3	EDO	A	706	4/4	0.76	0.17	47,48,48,50	0
4	FMT	I	805	3/3	0.76	0.25	52,52,53,53	0
4	FMT	B	804	3/3	0.77	0.15	60,60,61,61	0
2	ACT	K	901	4/4	0.78	0.17	67,67,67,67	0
4	FMT	D	803	3/3	0.78	0.15	62,62,63,63	0
3	EDO	F	710	4/4	0.80	0.26	41,47,47,50	0
3	EDO	F	701	4/4	0.81	0.15	31,36,38,39	0
3	EDO	E	705	4/4	0.84	0.18	29,36,36,40	0
3	EDO	C	703	4/4	0.85	0.13	37,42,42,44	0
2	ACT	D	902	4/4	0.86	0.16	41,41,42,42	0
3	EDO	C	714	4/4	0.86	0.24	38,39,40,41	0
3	EDO	A	712	4/4	0.88	0.21	36,41,42,46	0
3	EDO	C	709	4/4	0.89	0.20	30,39,41,44	0
3	EDO	B	702	4/4	0.89	0.15	27,35,36,37	0
4	FMT	L	806	3/3	0.89	0.27	46,46,46,46	0
3	EDO	I	708	4/4	0.90	0.17	44,46,46,47	0
3	EDO	F	713	4/4	0.91	0.26	23,37,37,43	0
3	EDO	E	704	4/4	0.91	0.29	25,25,27,28	0
3	EDO	J	711	4/4	0.93	0.17	33,39,45,48	0
5	MG	J	604	1/1	0.93	0.17	32,32,32,32	0
5	MG	G	603	1/1	0.95	0.07	51,51,51,51	0
5	MG	H	602	1/1	0.96	0.18	38,38,38,38	0
5	MG	I	606	1/1	0.98	0.10	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	MG	H	601	1/1	0.98	0.11	47,47,47,47	0
5	MG	I	605	1/1	0.99	0.17	25,25,25,25	0

6.5 Other polymers (i)

There are no such residues in this entry.