



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 03:58 am GMT

PDB ID : 4JD6
Title : Crystal structure of Mycobacterium tuberculosis Eis in complex with coenzyme A and tobramycin
Authors : Biswas, T.; Chen, W.; Garneau-Tsodikova, S.; Tsodikov, O.V.
Deposited on : 2013-02-23
Resolution : 3.50 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

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

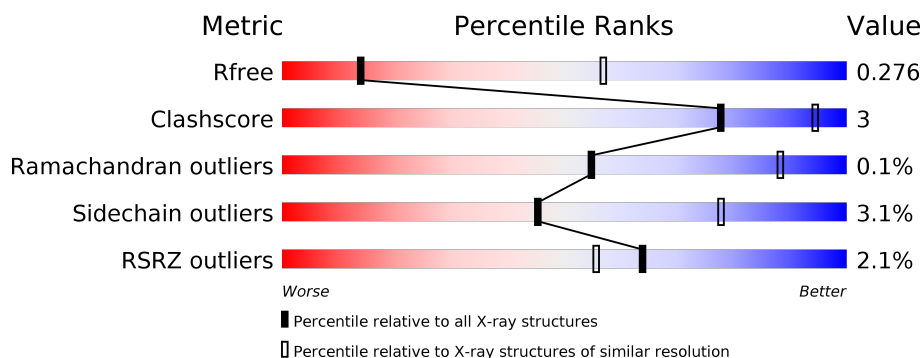
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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}	100719	1195 (3.60-3.40)
Clashscore	112137	1322 (3.60-3.40)
Ramachandran outliers	110173	1283 (3.60-3.40)
Sidechain outliers	110143	1284 (3.60-3.40)
RSRZ outliers	101464	1226 (3.60-3.40)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	428	<div> <div></div> <div>83% 9% 7%</div> </div>
1	B	428	<div> <div></div> <div>83% 9% 7%</div> </div>
1	C	428	<div> <div>4%</div> <div>84% 8% 7%</div> </div>
1	D	428	<div> <div></div> <div>82% 10% 7%</div> </div>
1	E	428	<div> <div>2%</div> <div>84% 9% 7%</div> </div>
1	F	428	<div> <div>4%</div> <div>84% 8% 7%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	COA	A	500	-	-	-	X
2	COA	B	500	-	-	-	X
2	COA	C	500	-	-	-	X
2	COA	E	500	-	-	-	X
2	COA	F	500	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 18716 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 Enhanced intracellular survival protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	396	Total	C	N	O	S	0	0	0
			3050	1919	560	560	11			
1	B	396	Total	C	N	O	S	0	0	0
			3050	1919	560	560	11			
1	C	396	Total	C	N	O	S	0	0	0
			3050	1919	560	560	11			
1	D	396	Total	C	N	O	S	0	0	0
			3050	1919	560	560	11			
1	E	396	Total	C	N	O	S	0	0	0
			3050	1919	560	560	11			
1	F	396	Total	C	N	O	S	0	0	0
			3050	1919	560	560	11			

There are 162 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-25	MET	-	EXPRESSION TAG	UNP I6X469
A	-24	GLY	-	EXPRESSION TAG	UNP I6X469
A	-23	SER	-	EXPRESSION TAG	UNP I6X469
A	-22	SER	-	EXPRESSION TAG	UNP I6X469
A	-21	HIS	-	EXPRESSION TAG	UNP I6X469
A	-20	HIS	-	EXPRESSION TAG	UNP I6X469
A	-19	HIS	-	EXPRESSION TAG	UNP I6X469
A	-18	HIS	-	EXPRESSION TAG	UNP I6X469
A	-17	HIS	-	EXPRESSION TAG	UNP I6X469
A	-16	HIS	-	EXPRESSION TAG	UNP I6X469
A	-15	SER	-	EXPRESSION TAG	UNP I6X469
A	-14	SER	-	EXPRESSION TAG	UNP I6X469
A	-13	GLY	-	EXPRESSION TAG	UNP I6X469
A	-12	LEU	-	EXPRESSION TAG	UNP I6X469
A	-11	VAL	-	EXPRESSION TAG	UNP I6X469
A	-10	PRO	-	EXPRESSION TAG	UNP I6X469
A	-9	ARG	-	EXPRESSION TAG	UNP I6X469

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	GLY	-	EXPRESSION TAG	UNP I6X469
A	-7	SER	-	EXPRESSION TAG	UNP I6X469
A	-6	HIS	-	EXPRESSION TAG	UNP I6X469
A	-5	MET	-	EXPRESSION TAG	UNP I6X469
A	-4	LEU	-	EXPRESSION TAG	UNP I6X469
A	-3	GLN	-	EXPRESSION TAG	UNP I6X469
A	-2	SER	-	EXPRESSION TAG	UNP I6X469
A	-1	ASP	-	EXPRESSION TAG	UNP I6X469
A	0	SER	-	EXPRESSION TAG	UNP I6X469
A	204	ALA	CYS	ENGINEERED MUTATION	UNP I6X469
B	-25	MET	-	EXPRESSION TAG	UNP I6X469
B	-24	GLY	-	EXPRESSION TAG	UNP I6X469
B	-23	SER	-	EXPRESSION TAG	UNP I6X469
B	-22	SER	-	EXPRESSION TAG	UNP I6X469
B	-21	HIS	-	EXPRESSION TAG	UNP I6X469
B	-20	HIS	-	EXPRESSION TAG	UNP I6X469
B	-19	HIS	-	EXPRESSION TAG	UNP I6X469
B	-18	HIS	-	EXPRESSION TAG	UNP I6X469
B	-17	HIS	-	EXPRESSION TAG	UNP I6X469
B	-16	HIS	-	EXPRESSION TAG	UNP I6X469
B	-15	SER	-	EXPRESSION TAG	UNP I6X469
B	-14	SER	-	EXPRESSION TAG	UNP I6X469
B	-13	GLY	-	EXPRESSION TAG	UNP I6X469
B	-12	LEU	-	EXPRESSION TAG	UNP I6X469
B	-11	VAL	-	EXPRESSION TAG	UNP I6X469
B	-10	PRO	-	EXPRESSION TAG	UNP I6X469
B	-9	ARG	-	EXPRESSION TAG	UNP I6X469
B	-8	GLY	-	EXPRESSION TAG	UNP I6X469
B	-7	SER	-	EXPRESSION TAG	UNP I6X469
B	-6	HIS	-	EXPRESSION TAG	UNP I6X469
B	-5	MET	-	EXPRESSION TAG	UNP I6X469
B	-4	LEU	-	EXPRESSION TAG	UNP I6X469
B	-3	GLN	-	EXPRESSION TAG	UNP I6X469
B	-2	SER	-	EXPRESSION TAG	UNP I6X469
B	-1	ASP	-	EXPRESSION TAG	UNP I6X469
B	0	SER	-	EXPRESSION TAG	UNP I6X469
B	204	ALA	CYS	ENGINEERED MUTATION	UNP I6X469
C	-25	MET	-	EXPRESSION TAG	UNP I6X469
C	-24	GLY	-	EXPRESSION TAG	UNP I6X469
C	-23	SER	-	EXPRESSION TAG	UNP I6X469
C	-22	SER	-	EXPRESSION TAG	UNP I6X469
C	-21	HIS	-	EXPRESSION TAG	UNP I6X469

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-20	HIS	-	EXPRESSION TAG	UNP I6X469
C	-19	HIS	-	EXPRESSION TAG	UNP I6X469
C	-18	HIS	-	EXPRESSION TAG	UNP I6X469
C	-17	HIS	-	EXPRESSION TAG	UNP I6X469
C	-16	HIS	-	EXPRESSION TAG	UNP I6X469
C	-15	SER	-	EXPRESSION TAG	UNP I6X469
C	-14	SER	-	EXPRESSION TAG	UNP I6X469
C	-13	GLY	-	EXPRESSION TAG	UNP I6X469
C	-12	LEU	-	EXPRESSION TAG	UNP I6X469
C	-11	VAL	-	EXPRESSION TAG	UNP I6X469
C	-10	PRO	-	EXPRESSION TAG	UNP I6X469
C	-9	ARG	-	EXPRESSION TAG	UNP I6X469
C	-8	GLY	-	EXPRESSION TAG	UNP I6X469
C	-7	SER	-	EXPRESSION TAG	UNP I6X469
C	-6	HIS	-	EXPRESSION TAG	UNP I6X469
C	-5	MET	-	EXPRESSION TAG	UNP I6X469
C	-4	LEU	-	EXPRESSION TAG	UNP I6X469
C	-3	GLN	-	EXPRESSION TAG	UNP I6X469
C	-2	SER	-	EXPRESSION TAG	UNP I6X469
C	-1	ASP	-	EXPRESSION TAG	UNP I6X469
C	0	SER	-	EXPRESSION TAG	UNP I6X469
C	204	ALA	CYS	ENGINEERED MUTATION	UNP I6X469
D	-25	MET	-	EXPRESSION TAG	UNP I6X469
D	-24	GLY	-	EXPRESSION TAG	UNP I6X469
D	-23	SER	-	EXPRESSION TAG	UNP I6X469
D	-22	SER	-	EXPRESSION TAG	UNP I6X469
D	-21	HIS	-	EXPRESSION TAG	UNP I6X469
D	-20	HIS	-	EXPRESSION TAG	UNP I6X469
D	-19	HIS	-	EXPRESSION TAG	UNP I6X469
D	-18	HIS	-	EXPRESSION TAG	UNP I6X469
D	-17	HIS	-	EXPRESSION TAG	UNP I6X469
D	-16	HIS	-	EXPRESSION TAG	UNP I6X469
D	-15	SER	-	EXPRESSION TAG	UNP I6X469
D	-14	SER	-	EXPRESSION TAG	UNP I6X469
D	-13	GLY	-	EXPRESSION TAG	UNP I6X469
D	-12	LEU	-	EXPRESSION TAG	UNP I6X469
D	-11	VAL	-	EXPRESSION TAG	UNP I6X469
D	-10	PRO	-	EXPRESSION TAG	UNP I6X469
D	-9	ARG	-	EXPRESSION TAG	UNP I6X469
D	-8	GLY	-	EXPRESSION TAG	UNP I6X469
D	-7	SER	-	EXPRESSION TAG	UNP I6X469
D	-6	HIS	-	EXPRESSION TAG	UNP I6X469

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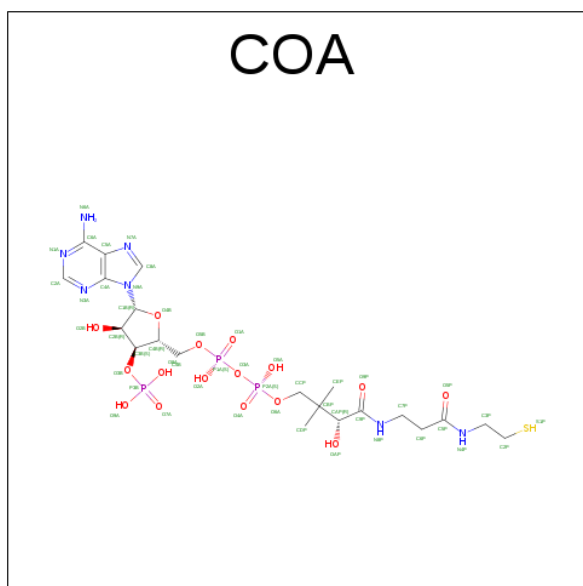
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D	-4	LEU	-	EXPRESSION TAG	UNP I6X469
D	-3	GLN	-	EXPRESSION TAG	UNP I6X469
D	-2	SER	-	EXPRESSION TAG	UNP I6X469
D	-1	ASP	-	EXPRESSION TAG	UNP I6X469
D	0	SER	-	EXPRESSION TAG	UNP I6X469
D	204	ALA	CYS	ENGINEERED MUTATION	UNP I6X469
E	-25	MET	-	EXPRESSION TAG	UNP I6X469
E	-24	GLY	-	EXPRESSION TAG	UNP I6X469
E	-23	SER	-	EXPRESSION TAG	UNP I6X469
E	-22	SER	-	EXPRESSION TAG	UNP I6X469
E	-21	HIS	-	EXPRESSION TAG	UNP I6X469
E	-20	HIS	-	EXPRESSION TAG	UNP I6X469
E	-19	HIS	-	EXPRESSION TAG	UNP I6X469
E	-18	HIS	-	EXPRESSION TAG	UNP I6X469
E	-17	HIS	-	EXPRESSION TAG	UNP I6X469
E	-16	HIS	-	EXPRESSION TAG	UNP I6X469
E	-15	SER	-	EXPRESSION TAG	UNP I6X469
E	-14	SER	-	EXPRESSION TAG	UNP I6X469
E	-13	GLY	-	EXPRESSION TAG	UNP I6X469
E	-12	LEU	-	EXPRESSION TAG	UNP I6X469
E	-11	VAL	-	EXPRESSION TAG	UNP I6X469
E	-10	PRO	-	EXPRESSION TAG	UNP I6X469
E	-9	ARG	-	EXPRESSION TAG	UNP I6X469
E	-8	GLY	-	EXPRESSION TAG	UNP I6X469
E	-7	SER	-	EXPRESSION TAG	UNP I6X469
E	-6	HIS	-	EXPRESSION TAG	UNP I6X469
E	-5	MET	-	EXPRESSION TAG	UNP I6X469
E	-4	LEU	-	EXPRESSION TAG	UNP I6X469
E	-3	GLN	-	EXPRESSION TAG	UNP I6X469
E	-2	SER	-	EXPRESSION TAG	UNP I6X469
E	-1	ASP	-	EXPRESSION TAG	UNP I6X469
E	0	SER	-	EXPRESSION TAG	UNP I6X469
E	204	ALA	CYS	ENGINEERED MUTATION	UNP I6X469
F	-25	MET	-	EXPRESSION TAG	UNP I6X469
F	-24	GLY	-	EXPRESSION TAG	UNP I6X469
F	-23	SER	-	EXPRESSION TAG	UNP I6X469
F	-22	SER	-	EXPRESSION TAG	UNP I6X469
F	-21	HIS	-	EXPRESSION TAG	UNP I6X469
F	-20	HIS	-	EXPRESSION TAG	UNP I6X469
F	-19	HIS	-	EXPRESSION TAG	UNP I6X469
F	-18	HIS	-	EXPRESSION TAG	UNP I6X469

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-17	HIS	-	EXPRESSION TAG	UNP I6X469
F	-16	HIS	-	EXPRESSION TAG	UNP I6X469
F	-15	SER	-	EXPRESSION TAG	UNP I6X469
F	-14	SER	-	EXPRESSION TAG	UNP I6X469
F	-13	GLY	-	EXPRESSION TAG	UNP I6X469
F	-12	LEU	-	EXPRESSION TAG	UNP I6X469
F	-11	VAL	-	EXPRESSION TAG	UNP I6X469
F	-10	PRO	-	EXPRESSION TAG	UNP I6X469
F	-9	ARG	-	EXPRESSION TAG	UNP I6X469
F	-8	GLY	-	EXPRESSION TAG	UNP I6X469
F	-7	SER	-	EXPRESSION TAG	UNP I6X469
F	-6	HIS	-	EXPRESSION TAG	UNP I6X469
F	-5	MET	-	EXPRESSION TAG	UNP I6X469
F	-4	LEU	-	EXPRESSION TAG	UNP I6X469
F	-3	GLN	-	EXPRESSION TAG	UNP I6X469
F	-2	SER	-	EXPRESSION TAG	UNP I6X469
F	-1	ASP	-	EXPRESSION TAG	UNP I6X469
F	0	SER	-	EXPRESSION TAG	UNP I6X469
F	204	ALA	CYS	ENGINEERED MUTATION	UNP I6X469

- Molecule 2 is COENZYME A (three-letter code: COA) (formula: $C_{21}H_{36}N_7O_{16}P_3S$).



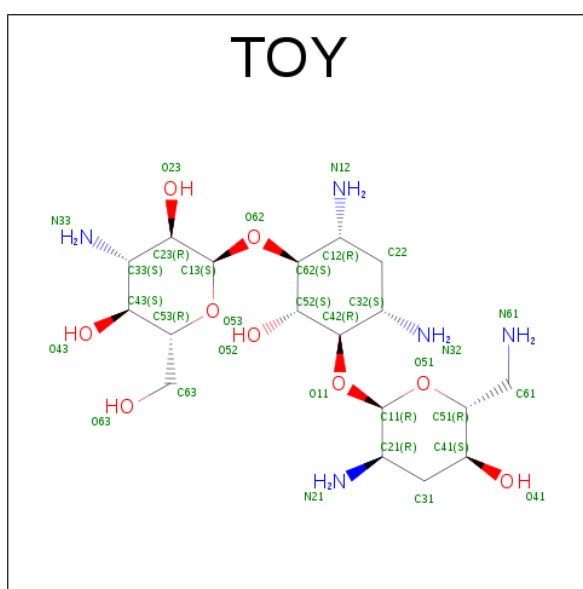
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	B	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	C	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	D	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	E	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	F	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		

- Molecule 3 is TOBRAMYCIN (three-letter code: TOY) (formula: $C_{18}H_{37}N_5O_9$).

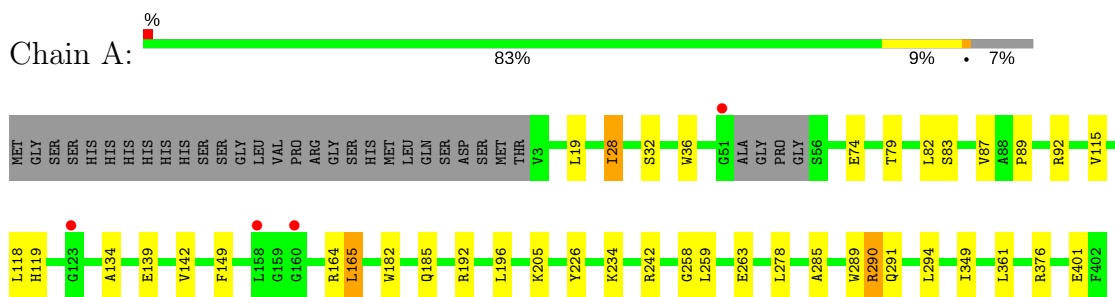


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	1
			64	36	10	18		
3	B	1	Total	C	N	O	0	1
			64	36	10	18		

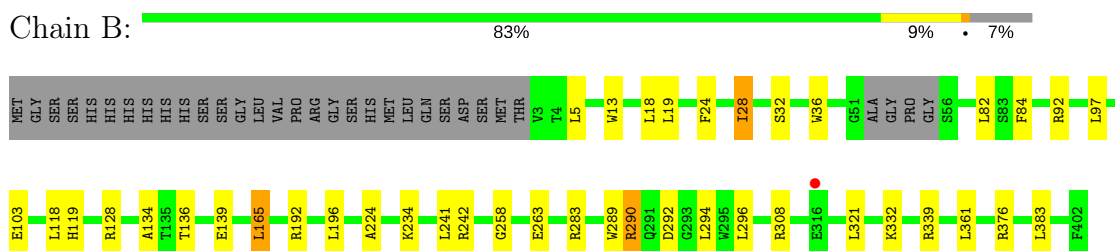
3 Residue-property plots

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 ($RSRZ > 2$). 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.

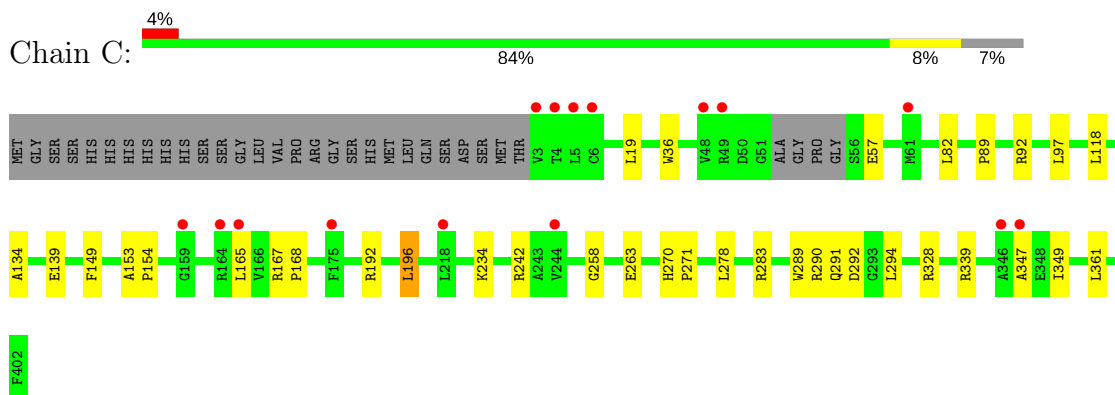
- Molecule 1: Enhanced intracellular survival protein



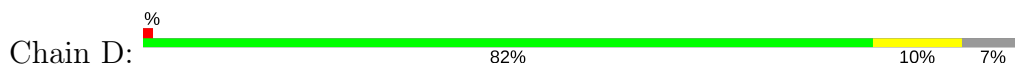
- Molecule 1: Enhanced intracellular survival protein

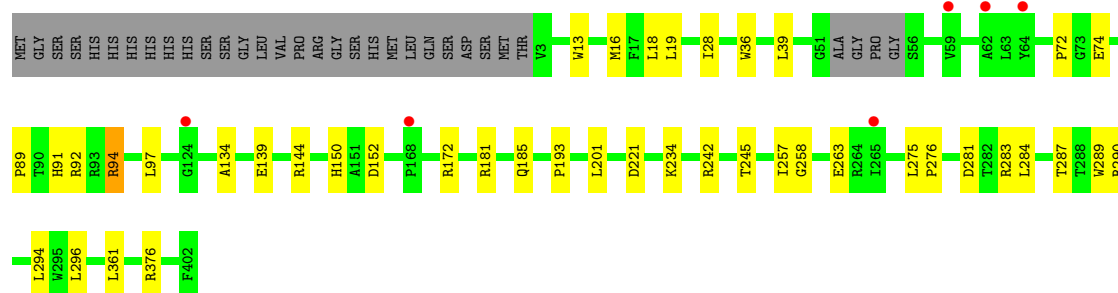


- Molecule 1: Enhanced intracellular survival protein

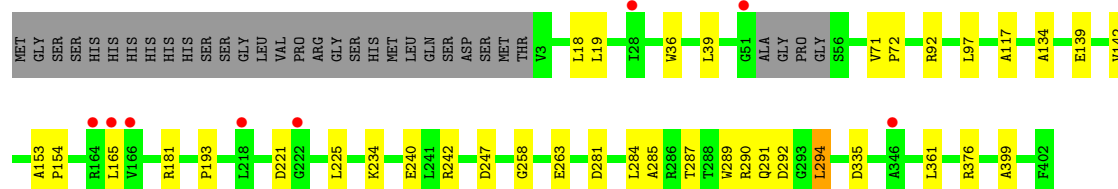
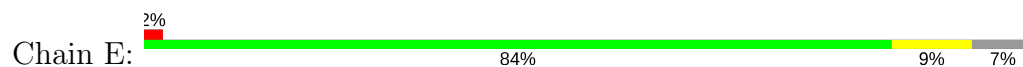


- Molecule 1: Enhanced intracellular survival protein

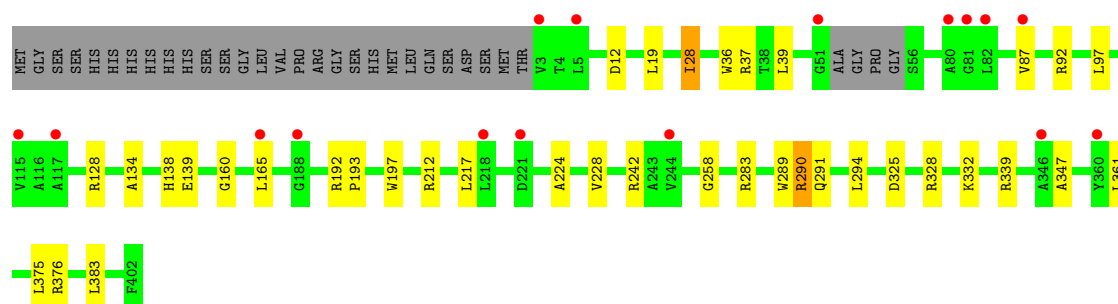
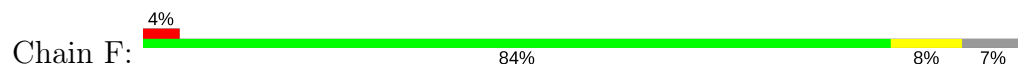




- Molecule 1: Enhanced intracellular survival protein



- Molecule 1: Enhanced intracellular survival protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	82.23Å 154.91Å 115.29Å 90.00° 104.70° 90.00°	Depositor
Resolution (Å)	40.00 – 3.50 49.57 – 3.50	Depositor EDS
% Data completeness (in resolution range)	99.9 (40.00-3.50) 99.9 (49.57-3.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.37 (at 3.48Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.244 , 0.276 0.243 , 0.276	Depositor DCC
R_{free} test set	1767 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	98.4	Xtriage
Anisotropy	0.450	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 57.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	18716	wwPDB-VP
Average B, all atoms (Å ²)	126.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.02% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: COA, TOY

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	0.45	1/3118 (0.0%)	0.49	0/4238
1	B	0.45	2/3118 (0.1%)	0.49	0/4238
1	C	0.45	1/3118 (0.0%)	0.49	0/4238
1	D	0.45	1/3118 (0.0%)	0.50	0/4238
1	E	0.45	1/3118 (0.0%)	0.50	0/4238
1	F	0.46	2/3118 (0.1%)	0.49	0/4238
All	All	0.45	8/18708 (0.0%)	0.49	0/25428

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	36	TRP	CD2-CE2	5.09	1.47	1.41
1	B	13	TRP	CD2-CE2	5.06	1.47	1.41
1	E	36	TRP	CD2-CE2	5.06	1.47	1.41
1	D	36	TRP	CD2-CE2	5.05	1.47	1.41
1	B	36	TRP	CD2-CE2	5.04	1.47	1.41
1	C	36	TRP	CD2-CE2	5.04	1.47	1.41
1	F	197	TRP	CD2-CE2	5.04	1.47	1.41
1	A	182	TRP	CD2-CE2	5.04	1.47	1.41

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	3050	0	3018	32	0
1	B	3050	0	3018	20	0
1	C	3050	0	3018	18	0
1	D	3050	0	3018	23	0
1	E	3050	0	3018	17	0
1	F	3050	0	3018	22	0
2	A	48	0	32	2	0
2	B	48	0	32	4	0
2	C	48	0	32	1	0
2	D	48	0	32	1	0
2	E	48	0	32	2	0
2	F	48	0	32	5	0
3	A	64	0	73	18	0
3	B	64	0	74	8	0
All	All	18716	0	18447	128	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 3.

All (128) 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:36:TRP:CZ2	3:A:501[B]:TOY:N61	1.69	1.57
1:A:36:TRP:CE2	3:A:501[B]:TOY:N61	2.02	1.25
1:A:36:TRP:CZ2	3:A:501[B]:TOY:C61	2.45	1.00
1:A:92:ARG:HD3	1:B:258:GLY:HA2	1.65	0.79
3:B:501[B]:TOY:HN21	3:B:501[B]:TOY:HN2	0.81	0.79
1:A:36:TRP:CH2	3:A:501[B]:TOY:C61	2.66	0.78
3:B:501[B]:TOY:N32	3:B:501[B]:TOY:N21	2.21	0.77
1:A:291:GLN:HG3	1:D:283:ARG:HD2	1.68	0.75
1:A:36:TRP:CH2	3:A:501[B]:TOY:N61	2.52	0.75
1:A:36:TRP:CH2	3:A:501[B]:TOY:H611	2.25	0.70
1:A:258:GLY:HA2	1:C:92:ARG:HD3	1.73	0.69
1:B:92:ARG:HD3	1:C:258:GLY:HA2	1.80	0.63
1:D:139:GLU:HB3	1:D:289:TRP:HB3	1.80	0.63
1:E:97:LEU:HD22	2:E:500:COA:H142	1.83	0.61
1:E:258:GLY:HA2	1:F:92:ARG:HD3	1.82	0.61
1:A:36:TRP:HZ2	3:A:501[B]:TOY:N61	1.79	0.60
1:A:83:SER:HA	3:A:501[B]:TOY:O43	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:139:GLU:HB3	1:F:289:TRP:HB3	1.84	0.60
1:C:139:GLU:HB3	1:C:289:TRP:HB3	1.83	0.60
1:C:291:GLN:HG2	1:F:283:ARG:HD2	1.84	0.59
1:F:39:LEU:HD21	1:F:193:PRO:HG2	1.83	0.59
3:B:501[B]:TOY:O52	3:B:501[B]:TOY:H51	2.04	0.57
1:B:97:LEU:HD22	2:B:500:COA:H142	1.86	0.57
1:D:91:HIS:HA	1:D:94:ARG:HH21	1.70	0.56
1:C:283:ARG:HD2	1:F:291:GLN:HG2	1.88	0.56
1:B:84:PHE:H	3:B:501[B]:TOY:H632	1.70	0.56
1:A:83:SER:OG	3:A:501[B]:TOY:H632	2.06	0.55
1:A:165:LEU:HD12	1:C:89:PRO:HD2	1.88	0.55
1:D:258:GLY:HA2	1:E:92:ARG:HD3	1.87	0.55
1:F:332:LYS:HB3	1:F:339:ARG:HB2	1.89	0.54
1:A:28:ILE:HB	1:A:32:SER:HB2	1.89	0.54
1:B:134:ALA:HB1	1:B:361:LEU:HD12	1.88	0.54
1:B:290:ARG:HB2	1:E:287:THR:HB	1.90	0.54
1:B:5:LEU:HD21	1:B:103:GLU:HG2	1.90	0.53
1:A:87:VAL:H	2:A:500:COA:H133	1.74	0.53
1:A:139:GLU:HB3	1:A:289:TRP:HB3	1.90	0.52
1:B:139:GLU:HB3	1:B:289:TRP:HB3	1.92	0.52
1:A:290:ARG:HB2	1:D:287:THR:HB	1.92	0.52
1:E:258:GLY:CA	1:F:92:ARG:HD3	2.40	0.51
1:C:134:ALA:HB1	1:C:361:LEU:HD12	1.91	0.51
1:A:401:GLU:OE2	3:A:501[B]:TOY:H221	2.11	0.51
1:C:97:LEU:HD22	2:C:500:COA:H142	1.94	0.50
1:A:89:PRO:HD2	1:B:165:LEU:HD12	1.94	0.49
1:C:291:GLN:CG	1:F:283:ARG:HD2	2.41	0.49
2:E:500:COA:O9P	2:E:500:COA:H122	2.12	0.49
1:D:92:ARG:HD3	1:F:258:GLY:HA2	1.93	0.49
1:F:134:ALA:HB1	1:F:361:LEU:HD12	1.93	0.49
3:A:501[B]:TOY:O52	3:A:501[B]:TOY:O51	2.23	0.49
1:E:134:ALA:HB1	1:E:361:LEU:HD12	1.95	0.49
1:C:328:ARG:HD3	1:C:347:ALA:HB2	1.95	0.48
1:D:97:LEU:HD22	2:D:500:COA:H142	1.95	0.48
3:A:501[B]:TOY:C21	3:A:501[B]:TOY:H612	2.43	0.48
3:A:501[B]:TOY:H21	3:A:501[B]:TOY:H612	1.95	0.48
1:B:119:HIS:O	3:B:501[A]:TOY:H611	2.14	0.48
1:D:134:ALA:HB1	1:D:361:LEU:HD12	1.95	0.48
1:A:74:GLU:HG2	1:A:185:GLN:HA	1.96	0.47
1:D:234:LYS:HD2	1:D:263:GLU:HG3	1.97	0.47
3:A:501[A]:TOY:N61	3:A:501[A]:TOY:O41	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:28:ILE:HB	1:B:32:SER:HB2	1.97	0.46
3:A:501[B]:TOY:C21	3:A:501[B]:TOY:C61	2.92	0.46
1:D:72:PRO:HD3	1:D:361:LEU:HD23	1.97	0.46
1:A:149:PHE:HE2	1:A:278:LEU:HD23	1.81	0.46
1:D:172:ARG:HD2	1:D:201:LEU:HD22	1.98	0.46
1:A:134:ALA:HB1	1:A:361:LEU:HD12	1.98	0.45
1:F:87:VAL:H	2:F:500:COA:H133	1.80	0.45
2:B:500:COA:H122	2:B:500:COA:O9P	2.16	0.45
1:E:39:LEU:HD21	1:E:193:PRO:HG2	1.97	0.45
1:E:234:LYS:HD2	1:E:263:GLU:HG3	1.98	0.45
1:D:234:LYS:HB3	1:D:263:GLU:HB2	1.99	0.45
1:F:92:ARG:HA	2:F:500:COA:O5A	2.17	0.45
1:C:82:LEU:HB2	1:C:118:LEU:HB3	1.98	0.45
1:C:149:PHE:HE2	1:C:278:LEU:HD23	1.81	0.45
1:E:281:ASP:HB3	1:E:284:LEU:HD12	1.99	0.45
1:A:79:THR:HG23	1:A:115:VAL:HG23	1.99	0.45
1:B:283:ARG:HD2	1:E:291:GLN:HG2	1.98	0.45
1:F:28:ILE:H	1:F:28:ILE:HG13	1.56	0.45
1:D:134:ALA:HB2	1:D:296:LEU:HB2	1.97	0.44
1:C:153:ALA:HA	1:C:154:PRO:HD3	1.90	0.44
1:D:181:ARG:HH22	1:D:221:ASP:HA	1.82	0.44
1:D:275:LEU:N	1:D:276:PRO:HD2	2.32	0.44
1:D:144:ARG:HB2	1:D:257:ILE:HG23	2.00	0.44
1:B:82:LEU:HB2	1:B:118:LEU:HB3	2.00	0.44
1:A:83:SER:HG	3:A:501[B]:TOY:H632	1.83	0.44
1:D:89:PRO:HD2	1:F:165:LEU:HD12	2.00	0.43
1:F:217:LEU:HB2	1:F:224:ALA:HB3	1.99	0.43
1:B:234:LYS:HD2	1:B:263:GLU:HG3	1.99	0.43
1:E:139:GLU:HB3	1:E:289:TRP:HB3	2.01	0.43
1:C:270:HIS:HB2	1:C:271:PRO:HD2	2.01	0.43
1:F:328:ARG:HD3	1:F:347:ALA:HB2	2.01	0.43
1:A:192:ARG:HG3	1:A:196:LEU:HB2	2.01	0.43
1:A:119:HIS:O	3:A:501[A]:TOY:H611	2.18	0.43
1:D:74:GLU:HG2	1:D:185:GLN:HA	2.00	0.43
2:F:500:COA:H122	2:F:500:COA:O9P	2.18	0.43
1:A:164:ARG:HH11	1:C:57:GLU:HG3	1.83	0.43
1:E:225:LEU:HB2	1:E:240:GLU:HB3	2.02	0.42
1:F:212:ARG:HD3	1:F:228:VAL:HB	2.02	0.42
1:F:375:LEU:HD11	1:F:383:LEU:HD21	1.99	0.42
1:B:128:ARG:NH1	2:B:500:COA:H1B	2.34	0.42
1:C:167:ARG:HA	1:C:168:PRO:HD3	1.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:71:VAL:HB	1:E:72:PRO:HD2	2.01	0.42
1:A:226:TYR:CE1	1:A:259:LEU:HD21	2.55	0.42
1:B:134:ALA:HB2	1:B:296:LEU:HB2	2.02	0.42
1:A:142:VAL:HG22	1:A:285:ALA:HA	2.02	0.42
1:A:83:SER:CA	3:A:501[B]:TOY:O43	2.67	0.42
1:B:224:ALA:HB2	1:B:241:LEU:HD23	2.02	0.42
1:D:13:TRP:HA	1:D:16:MET:HE3	2.01	0.41
1:C:192:ARG:HG3	1:C:196:LEU:HB3	2.02	0.41
1:B:192:ARG:HG3	1:B:196:LEU:HB2	2.01	0.41
1:D:94:ARG:HH12	1:F:160:GLY:HA2	1.85	0.41
1:E:153:ALA:HA	1:E:154:PRO:HD3	1.96	0.41
1:E:181:ARG:HH22	1:E:221:ASP:HA	1.85	0.41
1:D:281:ASP:HB3	1:D:284:LEU:HD12	2.02	0.41
1:D:39:LEU:HD21	1:D:193:PRO:HG2	2.03	0.41
1:E:117:ALA:HB1	1:E:294:LEU:HD21	2.03	0.41
1:B:24:PHE:CE2	3:B:501[A]:TOY:H312	2.55	0.41
2:F:500:COA:N8P	2:F:500:COA:H132	2.08	0.41
1:B:332:LYS:HB3	1:B:339:ARG:HB2	2.03	0.41
1:F:138:HIS:HD1	1:F:290:ARG:HE	1.68	0.41
1:A:234:LYS:HD2	1:A:263:GLU:HG3	2.03	0.41
1:F:192:ARG:HA	1:F:193:PRO:HD3	1.86	0.41
1:F:97:LEU:HB2	2:F:500:COA:H142	2.02	0.41
1:C:234:LYS:HD2	1:C:263:GLU:HG3	2.03	0.41
2:A:500:COA:H122	2:A:500:COA:O9P	2.20	0.40
3:B:501[A]:TOY:N61	3:B:501[A]:TOY:O41	2.54	0.40
1:E:142:VAL:HG22	1:E:285:ALA:HA	2.03	0.40
1:A:82:LEU:HB2	1:A:118:LEU:HB3	2.02	0.40
1:D:150:HIS:HD2	1:D:152:ASP:H	1.69	0.40
2:B:500:COA:S1P	3:B:501[A]:TOY:N61	2.95	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	392/428 (92%)	379 (97%)	13 (3%)	0	100	100
1	B	392/428 (92%)	379 (97%)	13 (3%)	0	100	100
1	C	392/428 (92%)	380 (97%)	12 (3%)	0	100	100
1	D	392/428 (92%)	378 (96%)	13 (3%)	1 (0%)	44	80
1	E	392/428 (92%)	378 (96%)	13 (3%)	1 (0%)	44	80
1	F	392/428 (92%)	377 (96%)	14 (4%)	1 (0%)	44	80
All	All	2352/2568 (92%)	2271 (97%)	78 (3%)	3 (0%)	55	88

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	28	ILE
1	E	399	ALA
1	F	28	ILE

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	309/335 (92%)	300 (97%)	9 (3%)	48	78
1	B	309/335 (92%)	296 (96%)	13 (4%)	34	70
1	C	309/335 (92%)	300 (97%)	9 (3%)	48	78
1	D	309/335 (92%)	301 (97%)	8 (3%)	51	80
1	E	309/335 (92%)	299 (97%)	10 (3%)	44	76
1	F	309/335 (92%)	300 (97%)	9 (3%)	48	78
All	All	1854/2010 (92%)	1796 (97%)	58 (3%)	45	78

All (58) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	LEU
1	A	28	ILE

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Mol	Chain	Res	Type
1	A	165	LEU
1	A	205	LYS
1	A	242	ARG
1	A	290	ARG
1	A	294	LEU
1	A	349	ILE
1	A	376	ARG
1	B	18	LEU
1	B	19	LEU
1	B	28	ILE
1	B	136	THR
1	B	165	LEU
1	B	242	ARG
1	B	290	ARG
1	B	292	ASP
1	B	294	LEU
1	B	308	ARG
1	B	321	LEU
1	B	376	ARG
1	B	383	LEU
1	C	19	LEU
1	C	165	LEU
1	C	196	LEU
1	C	242	ARG
1	C	290	ARG
1	C	292	ASP
1	C	294	LEU
1	C	339	ARG
1	C	349	ILE
1	D	18	LEU
1	D	19	LEU
1	D	94	ARG
1	D	242	ARG
1	D	245	THR
1	D	290	ARG
1	D	294	LEU
1	D	376	ARG
1	E	18	LEU
1	E	19	LEU
1	E	165	LEU
1	E	242	ARG
1	E	247	ASP

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Mol	Chain	Res	Type
1	E	290	ARG
1	E	292	ASP
1	E	294	LEU
1	E	335	ASP
1	E	376	ARG
1	F	12	ASP
1	F	19	LEU
1	F	37	ARG
1	F	128	ARG
1	F	242	ARG
1	F	290	ARG
1	F	294	LEU
1	F	325	ASP
1	F	376	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	91	HIS
1	A	150	HIS
1	A	270	HIS
1	B	91	HIS
1	B	270	HIS
1	C	91	HIS
1	C	150	HIS
1	C	270	HIS
1	C	381	GLN
1	D	91	HIS
1	D	150	HIS
1	E	91	HIS
1	E	150	HIS
1	F	91	HIS
1	F	270	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

10 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	COA	A	500	-	43,50,50	0.90	1 (2%)	48,75,75	3.17	8 (16%)
3	TOY	A	501[A]	-	34,34,34	0.48	0	40,50,50	1.05	4 (10%)
3	TOY	A	501[B]	-	34,34,34	0.59	0	40,50,50	1.25	6 (15%)
2	COA	B	500	-	43,50,50	0.85	1 (2%)	48,75,75	3.17	8 (16%)
3	TOY	B	501[A]	-	34,34,34	0.51	0	40,50,50	1.05	4 (10%)
3	TOY	B	501[B]	-	34,34,34	0.60	0	40,50,50	1.50	5 (12%)
2	COA	C	500	-	43,50,50	0.86	1 (2%)	48,75,75	3.11	8 (16%)
2	COA	D	500	-	43,50,50	0.86	1 (2%)	48,75,75	3.15	8 (16%)
2	COA	E	500	-	43,50,50	0.86	1 (2%)	48,75,75	3.22	8 (16%)
2	COA	F	500	-	43,50,50	0.91	1 (2%)	48,75,75	3.25	7 (14%)

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	COA	A	500	-	-	0/44/64/64	0/3/3/3
3	TOY	A	501[A]	-	-	0/12/68/68	0/3/3/3
3	TOY	A	501[B]	-	-	0/12/68/68	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	COA	B	500	-	-	0/44/64/64	0/3/3/3
3	TOY	B	501[A]	-	-	0/12/68/68	0/3/3/3
3	TOY	B	501[B]	-	-	1/12/68/68	0/3/3/3
2	COA	C	500	-	-	0/44/64/64	0/3/3/3
2	COA	D	500	-	-	0/44/64/64	0/3/3/3
2	COA	E	500	-	-	0/44/64/64	0/3/3/3
2	COA	F	500	-	-	0/44/64/64	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	500	COA	C5A-C4A	3.26	1.47	1.40
2	C	500	COA	C5A-C4A	3.26	1.47	1.40
2	A	500	COA	C5A-C4A	3.28	1.47	1.40
2	F	500	COA	C5A-C4A	3.28	1.47	1.40
2	D	500	COA	C5A-C4A	3.28	1.47	1.40
2	E	500	COA	C5A-C4A	3.29	1.47	1.40

All (66) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	500	COA	CDP-CBP-CAP	-12.48	87.18	108.82
2	E	500	COA	CEP-CBP-CAP	-12.11	87.82	108.82
2	A	500	COA	CDP-CBP-CAP	-11.74	88.46	108.82
2	C	500	COA	CEP-CBP-CAP	-11.16	89.47	108.82
2	B	500	COA	CEP-CBP-CAP	-11.03	89.69	108.82
2	E	500	COA	CDP-CBP-CAP	-10.77	90.15	108.82
2	D	500	COA	CEP-CBP-CAP	-10.75	90.18	108.82
2	B	500	COA	CDP-CBP-CAP	-10.70	90.27	108.82
2	D	500	COA	CDP-CBP-CAP	-10.21	91.12	108.82
2	C	500	COA	CDP-CBP-CAP	-8.91	93.37	108.82
2	A	500	COA	CEP-CBP-CAP	-8.31	94.42	108.82
2	F	500	COA	CEP-CBP-CAP	-6.76	97.10	108.82
2	D	500	COA	N3A-C2A-N1A	-6.28	123.39	128.86
2	F	500	COA	N3A-C2A-N1A	-6.27	123.40	128.86
2	C	500	COA	N3A-C2A-N1A	-6.26	123.41	128.86
2	E	500	COA	N3A-C2A-N1A	-6.24	123.42	128.86
2	A	500	COA	N3A-C2A-N1A	-6.24	123.42	128.86
2	B	500	COA	N3A-C2A-N1A	-6.22	123.44	128.86
3	A	501[B]	TOY	C61-C51-C41	-3.04	107.51	113.22
2	B	500	COA	C4A-C5A-N7A	-2.98	106.53	109.41
2	F	500	COA	C4A-C5A-N7A	-2.97	106.54	109.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	500	COA	C4A-C5A-N7A	-2.93	106.58	109.41
2	D	500	COA	C4A-C5A-N7A	-2.92	106.59	109.41
2	A	500	COA	C4A-C5A-N7A	-2.91	106.59	109.41
2	E	500	COA	C4A-C5A-N7A	-2.91	106.60	109.41
3	A	501[B]	TOY	C13-O62-C62	-2.86	111.03	118.00
3	B	501[A]	TOY	C11-O11-C42	-2.81	111.14	118.00
3	A	501[A]	TOY	C11-O11-C42	-2.80	111.18	118.00
3	A	501[B]	TOY	O43-C43-C33	-2.50	106.06	110.31
3	B	501[B]	TOY	C13-O62-C62	-2.47	111.98	118.00
3	B	501[A]	TOY	C13-O62-C62	-2.45	112.03	118.00
3	B	501[B]	TOY	C53-C43-C33	-2.39	107.69	110.35
3	A	501[A]	TOY	C61-C51-C41	-2.37	108.77	113.22
3	A	501[A]	TOY	C13-O62-C62	-2.36	112.25	118.00
3	B	501[A]	TOY	C61-C51-C41	-2.21	109.07	113.22
3	A	501[B]	TOY	C13-O53-C53	-2.19	109.60	113.72
3	B	501[A]	TOY	C11-O51-C51	2.09	117.65	113.72
3	A	501[A]	TOY	C11-O51-C51	2.21	117.87	113.72
2	A	500	COA	C3B-C2B-C1B	2.43	105.41	99.95
2	C	500	COA	C3B-C2B-C1B	2.47	105.50	99.95
3	B	501[B]	TOY	C13-C23-C33	2.49	113.74	110.40
2	D	500	COA	C3B-C2B-C1B	2.52	105.61	99.95
2	E	500	COA	C3B-C2B-C1B	2.52	105.61	99.95
3	A	501[B]	TOY	O51-C11-C21	2.54	115.97	110.25
2	F	500	COA	C3B-C2B-C1B	2.57	105.73	99.95
2	B	500	COA	C3B-C2B-C1B	2.68	105.97	99.95
3	A	501[B]	TOY	O11-C42-C52	3.14	114.74	107.19
2	C	500	COA	CEP-CBP-CDP	3.19	115.96	109.19
2	D	500	COA	CEP-CBP-CDP	3.72	117.09	109.19
3	B	501[B]	TOY	C62-C52-C42	4.19	117.75	109.01
2	A	500	COA	CEP-CBP-CCP	4.38	114.80	108.37
2	A	500	COA	CEP-CBP-CDP	4.63	119.02	109.19
2	B	500	COA	CEP-CBP-CDP	4.77	119.31	109.19
3	B	501[B]	TOY	O11-C11-C21	5.25	117.99	108.21
2	E	500	COA	CEP-CBP-CDP	5.44	120.75	109.19
2	F	500	COA	CEP-CBP-CDP	5.50	120.86	109.19
2	E	500	COA	CEP-CBP-CCP	5.53	116.49	108.37
2	B	500	COA	CEP-CBP-CCP	5.99	117.17	108.37
2	D	500	COA	CEP-CBP-CCP	7.81	119.83	108.37
2	C	500	COA	CDP-CBP-CCP	8.96	121.52	108.37
2	C	500	COA	CEP-CBP-CCP	9.46	122.26	108.37
2	E	500	COA	CDP-CBP-CCP	9.74	122.68	108.37
2	D	500	COA	CDP-CBP-CCP	9.95	122.98	108.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	500	COA	CDP-CBP-CCP	10.26	123.44	108.37
2	A	500	COA	CDP-CBP-CCP	12.13	126.18	108.37
2	F	500	COA	CDP-CBP-CCP	13.56	128.28	108.37

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	501[B]	TOY	C42-O11-C11-C21

There are no ring outliers.

10 monomers are involved in 40 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	500	COA	2	0
3	A	501[A]	TOY	2	0
3	A	501[B]	TOY	16	0
2	B	500	COA	4	0
3	B	501[A]	TOY	4	0
3	B	501[B]	TOY	4	0
2	C	500	COA	1	0
2	D	500	COA	1	0
2	E	500	COA	2	0
2	F	500	COA	5	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

6.1 Protein, DNA and RNA chains

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	396/428 (92%)	-0.11	4 (1%) 82 75	84, 115, 138, 166	0
1	B	396/428 (92%)	-0.05	1 (0%) 93 90	79, 103, 139, 155	0
1	C	396/428 (92%)	0.26	15 (3%) 41 35	91, 134, 165, 174	0
1	D	396/428 (92%)	0.08	6 (1%) 74 66	88, 122, 153, 168	0
1	E	396/428 (92%)	0.09	8 (2%) 65 57	93, 132, 157, 180	0
1	F	396/428 (92%)	0.18	16 (4%) 39 32	106, 144, 166, 181	0
All	All	2376/2568 (92%)	0.07	50 (2%) 64 55	79, 126, 160, 181	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	218	LEU	4.3
1	F	51	GLY	4.2
1	A	158	LEU	3.6
1	F	81	GLY	3.5
1	C	346	ALA	3.5
1	E	346	ALA	3.5
1	F	360	TYR	3.4
1	C	48	VAL	3.4
1	C	3	VAL	3.2
1	A	123	GLY	3.2
1	C	5	LEU	3.1
1	F	117	ALA	3.0
1	C	4	THR	2.9
1	F	82	LEU	2.9
1	C	164	ARG	2.9
1	D	59	VAL	2.7
1	E	164	ARG	2.7
1	E	28	ILE	2.7
1	F	3	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	347	ALA	2.6
1	C	49	ARG	2.6
1	F	346	ALA	2.6
1	F	221	ASP	2.6
1	F	115	VAL	2.5
1	A	51	GLY	2.5
1	C	165	LEU	2.5
1	D	168	PRO	2.4
1	F	188	GLY	2.4
1	E	218	LEU	2.3
1	C	218	LEU	2.3
1	A	160	GLY	2.3
1	C	61	MET	2.3
1	D	124	GLY	2.3
1	E	51	GLY	2.2
1	F	5	LEU	2.2
1	F	165	LEU	2.2
1	E	165	LEU	2.2
1	D	62	ALA	2.1
1	F	87	VAL	2.1
1	E	222	GLY	2.1
1	C	244	VAL	2.1
1	C	6	CYS	2.1
1	B	316	GLU	2.1
1	F	244	VAL	2.1
1	D	265	ILE	2.0
1	F	80	ALA	2.0
1	E	166	VAL	2.0
1	C	159	GLY	2.0
1	C	175	PHE	2.0
1	D	64	TYR	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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	LLDF	B-factors(Å ²)	Q<0.9
2	COA	E	500	48/48	0.57	0.51	2.00	172,181,192,193	0
2	COA	A	500	48/48	0.64	0.44	1.22	156,167,177,179	0
2	COA	B	500	48/48	0.73	0.43	1.17	154,172,188,189	0
2	COA	F	500	48/48	0.58	0.45	0.98	189,198,217,218	0
2	COA	D	500	48/48	0.71	0.40	0.65	188,196,210,210	0
3	TOY	B	501[B]	32/32	0.74	0.36	0.61	127,139,147,147	32
3	TOY	B	501[A]	32/32	0.74	0.36	0.40	113,123,126,126	32
3	TOY	A	501[B]	32/32	0.75	0.34	0.11	138,147,149,150	32
2	COA	C	500	48/48	0.77	0.40	0.04	187,196,200,200	0
3	TOY	A	501[A]	32/32	0.75	0.34	0.02	123,132,135,136	32

6.5 Other polymers [i](#)

There are no such residues in this entry.