



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 31, 2017 – 09:07 AM EDT

PDB ID : 3FSY  
Title : Structure of tetrahydrodipicolinate N-succinyltransferase (Rv1201c;DapD) in complex with succinyl-CoA from Mycobacterium tuberculosis  
Authors : Schuldt, L.; Weyand, S.; Kefala, G.; Weiss, M.S.  
Deposited on : unknown  
Resolution : 1.97 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

<http://wwpdb.org/validation/2016/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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20030345  
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) : rb-20030345

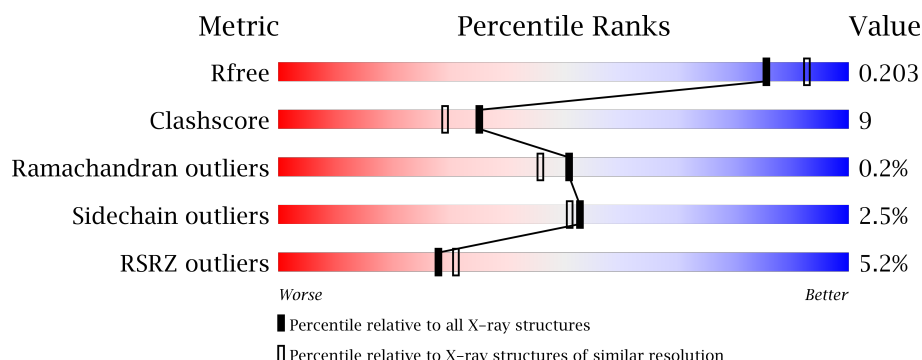
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.97 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	9293 (2.00-1.96)
Clashscore	112137	10621 (2.00-1.96)
Ramachandran outliers	110173	10502 (2.00-1.96)
Sidechain outliers	110143	10501 (2.00-1.96)
RSRZ outliers	101464	9395 (2.00-1.96)

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. 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	332	<div> <div>3%</div> <div>82% 9% 8%</div> </div>
1	B	332	<div> <div>3%</div> <div>81% 10% 8%</div> </div>
1	C	332	<div> <div>2%</div> <div>80% 9% 11%</div> </div>
1	D	332	<div> <div>4%</div> <div>80% 11% 7%</div> </div>
1	E	332	<div> <div>13%</div> <div>71% 17% 9%</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	SCA	E	331	-	-	-	X
3	MPD	B	340	-	-	-	X
3	MPD	D	340	-	-	-	X
5	NA	A	337	-	-	-	X
6	ACY	B	332	-	-	X	-
6	ACY	C	331	-	-	X	-

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 11992 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 Tetrahydronicotinate N-succinyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	304	Total	C	N	O	S	0	1	0
			2206	1370	402	426	8			
1	B	307	Total	C	N	O	S	0	3	0
			2229	1383	408	430	8			
1	C	297	Total	C	N	O	S	0	4	0
			2172	1351	397	416	8			
1	D	308	Total	C	N	O	S	0	6	0
			2247	1401	406	432	8			
1	E	301	Total	C	N	O	S	0	0	0
			2182	1355	399	420	8			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	EXPRESSION TAG	UNP O05302
A	0	ALA	-	EXPRESSION TAG	UNP O05302
A	1	VAL	-	EXPRESSION TAG	UNP O05302
A	318	GLY	-	EXPRESSION TAG	UNP O05302
A	319	VAL	-	EXPRESSION TAG	UNP O05302
A	320	PRO	-	EXPRESSION TAG	UNP O05302
A	321	ARG	-	EXPRESSION TAG	UNP O05302
A	322	GLY	-	EXPRESSION TAG	UNP O05302
A	323	LEU	-	EXPRESSION TAG	UNP O05302
A	324	GLU	-	EXPRESSION TAG	UNP O05302
A	325	HIS	-	EXPRESSION TAG	UNP O05302
A	326	HIS	-	EXPRESSION TAG	UNP O05302
A	327	HIS	-	EXPRESSION TAG	UNP O05302
A	328	HIS	-	EXPRESSION TAG	UNP O05302
A	329	HIS	-	EXPRESSION TAG	UNP O05302
A	330	HIS	-	EXPRESSION TAG	UNP O05302
B	-1	MET	-	EXPRESSION TAG	UNP O05302
B	0	ALA	-	EXPRESSION TAG	UNP O05302
B	1	VAL	-	EXPRESSION TAG	UNP O05302

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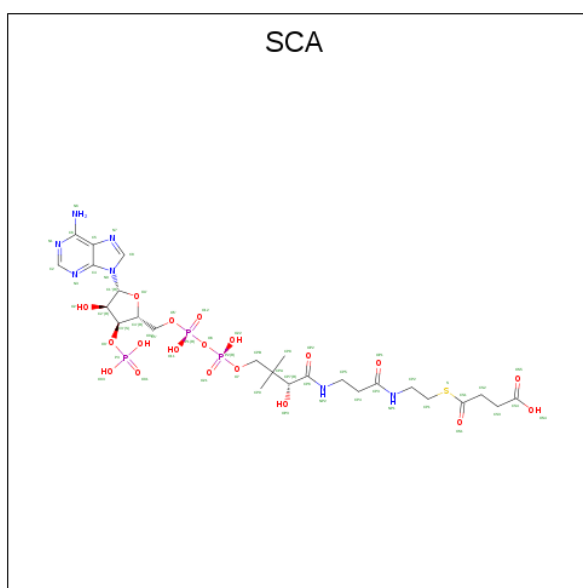
Chain	Residue	Modelled	Actual	Comment	Reference
B	318	GLY	-	EXPRESSION TAG	UNP O05302
B	319	VAL	-	EXPRESSION TAG	UNP O05302
B	320	PRO	-	EXPRESSION TAG	UNP O05302
B	321	ARG	-	EXPRESSION TAG	UNP O05302
B	322	GLY	-	EXPRESSION TAG	UNP O05302
B	323	LEU	-	EXPRESSION TAG	UNP O05302
B	324	GLU	-	EXPRESSION TAG	UNP O05302
B	325	HIS	-	EXPRESSION TAG	UNP O05302
B	326	HIS	-	EXPRESSION TAG	UNP O05302
B	327	HIS	-	EXPRESSION TAG	UNP O05302
B	328	HIS	-	EXPRESSION TAG	UNP O05302
B	329	HIS	-	EXPRESSION TAG	UNP O05302
B	330	HIS	-	EXPRESSION TAG	UNP O05302
C	-1	MET	-	EXPRESSION TAG	UNP O05302
C	0	ALA	-	EXPRESSION TAG	UNP O05302
C	1	VAL	-	EXPRESSION TAG	UNP O05302
C	318	GLY	-	EXPRESSION TAG	UNP O05302
C	319	VAL	-	EXPRESSION TAG	UNP O05302
C	320	PRO	-	EXPRESSION TAG	UNP O05302
C	321	ARG	-	EXPRESSION TAG	UNP O05302
C	322	GLY	-	EXPRESSION TAG	UNP O05302
C	323	LEU	-	EXPRESSION TAG	UNP O05302
C	324	GLU	-	EXPRESSION TAG	UNP O05302
C	325	HIS	-	EXPRESSION TAG	UNP O05302
C	326	HIS	-	EXPRESSION TAG	UNP O05302
C	327	HIS	-	EXPRESSION TAG	UNP O05302
C	328	HIS	-	EXPRESSION TAG	UNP O05302
C	329	HIS	-	EXPRESSION TAG	UNP O05302
C	330	HIS	-	EXPRESSION TAG	UNP O05302
D	-1	MET	-	EXPRESSION TAG	UNP O05302
D	0	ALA	-	EXPRESSION TAG	UNP O05302
D	1	VAL	-	EXPRESSION TAG	UNP O05302
D	318	GLY	-	EXPRESSION TAG	UNP O05302
D	319	VAL	-	EXPRESSION TAG	UNP O05302
D	320	PRO	-	EXPRESSION TAG	UNP O05302
D	321	ARG	-	EXPRESSION TAG	UNP O05302
D	322	GLY	-	EXPRESSION TAG	UNP O05302
D	323	LEU	-	EXPRESSION TAG	UNP O05302
D	324	GLU	-	EXPRESSION TAG	UNP O05302
D	325	HIS	-	EXPRESSION TAG	UNP O05302
D	326	HIS	-	EXPRESSION TAG	UNP O05302
D	327	HIS	-	EXPRESSION TAG	UNP O05302

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Chain	Residue	Modelled	Actual	Comment	Reference
D	328	HIS	-	EXPRESSION TAG	UNP O05302
D	329	HIS	-	EXPRESSION TAG	UNP O05302
D	330	HIS	-	EXPRESSION TAG	UNP O05302
E	-1	MET	-	EXPRESSION TAG	UNP O05302
E	0	ALA	-	EXPRESSION TAG	UNP O05302
E	1	VAL	-	EXPRESSION TAG	UNP O05302
E	318	GLY	-	EXPRESSION TAG	UNP O05302
E	319	VAL	-	EXPRESSION TAG	UNP O05302
E	320	PRO	-	EXPRESSION TAG	UNP O05302
E	321	ARG	-	EXPRESSION TAG	UNP O05302
E	322	GLY	-	EXPRESSION TAG	UNP O05302
E	323	LEU	-	EXPRESSION TAG	UNP O05302
E	324	GLU	-	EXPRESSION TAG	UNP O05302
E	325	HIS	-	EXPRESSION TAG	UNP O05302
E	326	HIS	-	EXPRESSION TAG	UNP O05302
E	327	HIS	-	EXPRESSION TAG	UNP O05302
E	328	HIS	-	EXPRESSION TAG	UNP O05302
E	329	HIS	-	EXPRESSION TAG	UNP O05302
E	330	HIS	-	EXPRESSION TAG	UNP O05302

- Molecule 2 is SUCCINYL-COENZYME A (three-letter code: SCA) (formula:  $C_{25}H_{40}N_7O_{19}P_3S$ ).



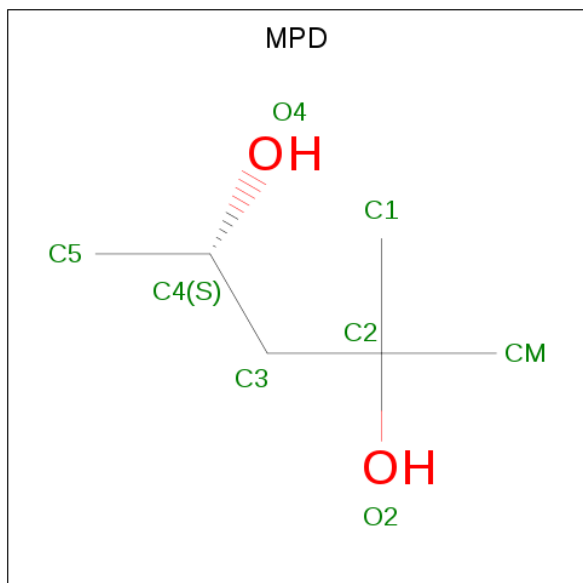
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	N	O	P		0	0
			31	10	5	13	3			
2	A	1	Total	C	N	O	P	S	0	0
			55	25	7	19	3	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
2	B	1	Total	C	N	O	P	0	0	
			31	10	5	13	3			
2	E	1	Total	C	N	O	P	S	0	0
			52	23	7	18	3	1		

- Molecule 3 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula:  $C_6H_{14}O_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			8	6	2		
3	B	1	Total	C	O	0	0
			8	6	2		
3	D	1	Total	C	O	0	0
			8	6	2		

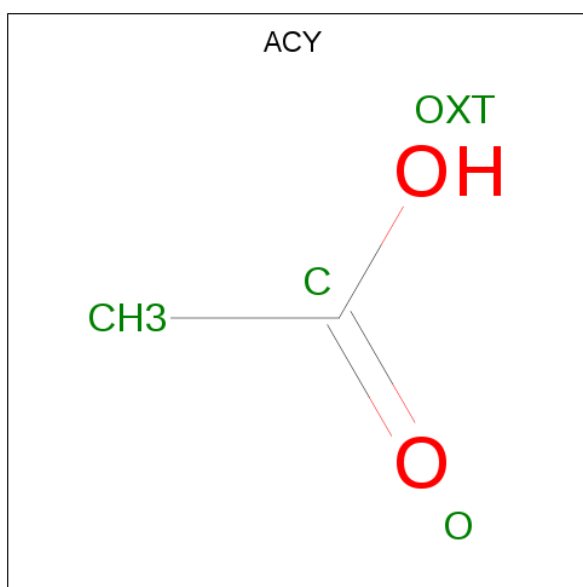
- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Mg	0	0
			1	1		
4	A	4	Total	Mg	0	0
			4	4		
4	D	2	Total	Mg	0	0
			2	2		
4	E	3	Total	Mg	0	0
			3	3		

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total Na 1 1	0	0
5	A	1	Total Na 1 1	0	0
5	D	1	Total Na 1 1	0	0
5	E	1	Total Na 1 1	0	0

- Molecule 6 is ACETIC ACID (three-letter code: ACY) (formula: C<sub>2</sub>H<sub>4</sub>O<sub>2</sub>).



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

- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	176	Total O 176 176	0	0
7	B	174	Total O 174 174	0	0

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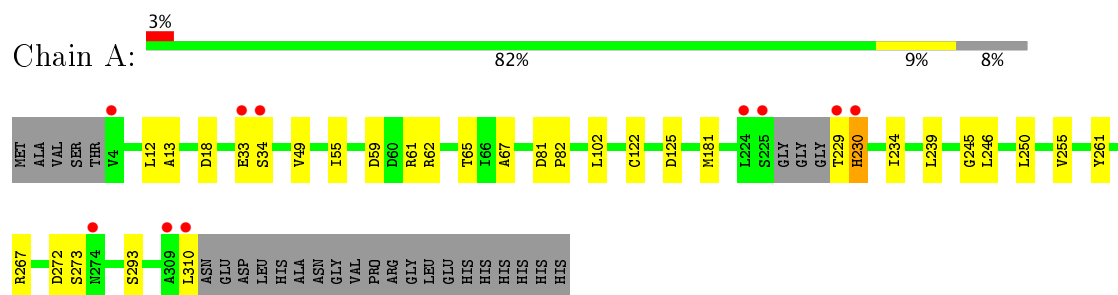
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	C	161	Total 161	O 161	0	0
7	D	203	Total 203	O 203	0	0
7	E	23	Total 23	O 23	0	0

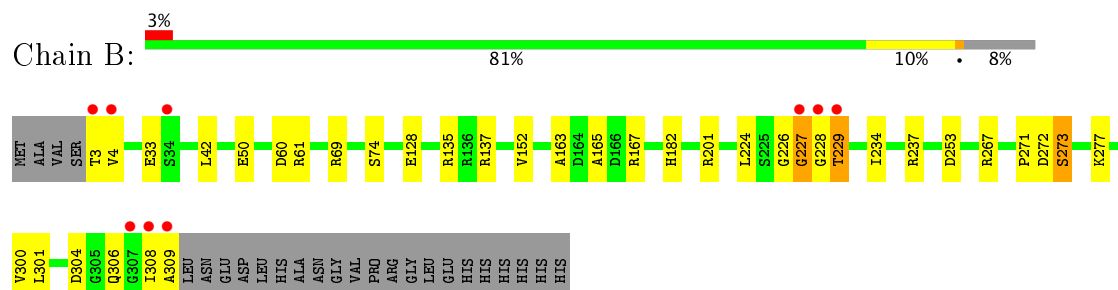
### 3 Residue-property plots [i](#)

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.

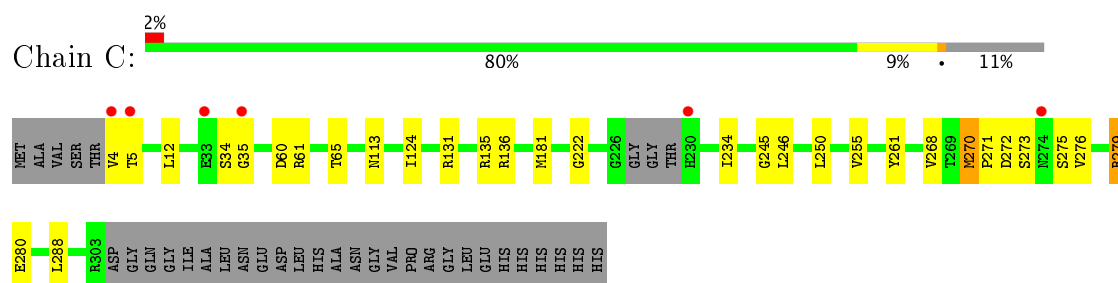
#### • Molecule 1: Tetrahydrodipicolinate N-succinyltransferase



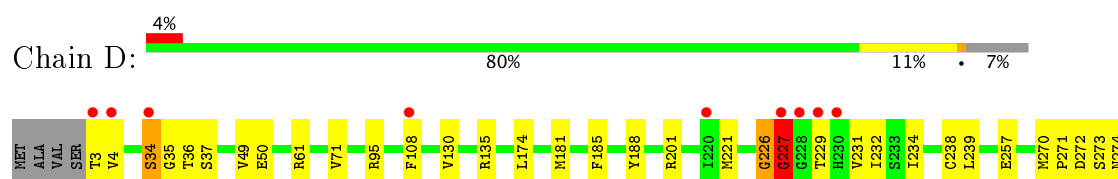
#### • Molecule 1: Tetrahydrodipicolinate N-succinyltransferase

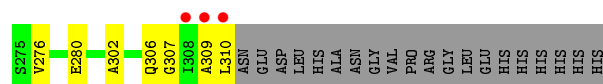


#### • Molecule 1: Tetrahydrodipicolinate N-succinyltransferase

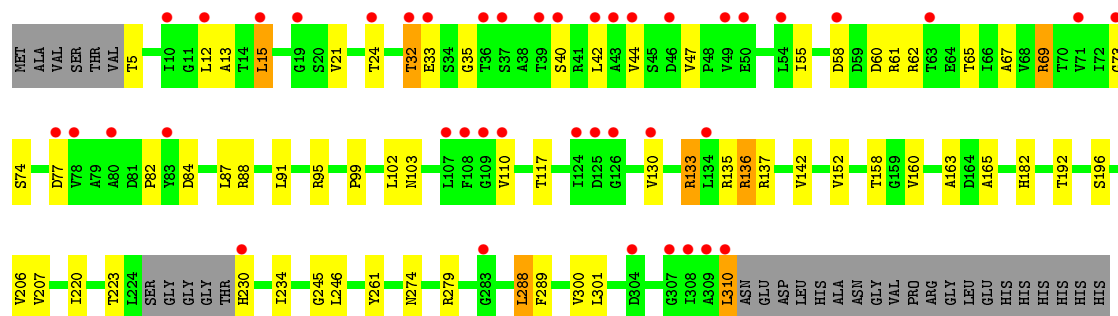


#### • Molecule 1: Tetrahydrodipicolinate N-succinyltransferase





● Molecule 1: Tetrahydrodipicolinate N-succinyltransferase



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 21 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	216.96Å 216.96Å 216.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 1.97 57.98 – 1.97	Depositor EDS
% Data completeness (in resolution range)	99.9 (30.00-1.97) 99.9 (57.98-1.97)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.28 (at 1.97Å)	Xtriage
Refinement program	REFMAC 5.4.0069	Depositor
R, $R_{free}$	0.161 , 0.200 0.163 , 0.203	Depositor DCC
$R_{free}$ test set	1488 reflections (1.27%)	DCC
Wilson B-factor (Å <sup>2</sup> )	26.2	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 45.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.017 for -l,-k,-h	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	11992	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.87% 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: ACY, NA, MG, SCA, MPD

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	0.87	0/2241	0.85	1/3049 (0.0%)
1	B	0.93	1/2271 (0.0%)	0.91	2/3090 (0.1%)
1	C	0.83	0/2216	0.86	4/3014 (0.1%)
1	D	0.94	1/2301 (0.0%)	0.93	3/3131 (0.1%)
1	E	0.55	0/2214	0.74	4/3011 (0.1%)
All	All	0.84	2/11243 (0.0%)	0.86	14/15295 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	130	VAL	CB-CG1	5.65	1.64	1.52
1	B	167	ARG	CG-CD	-5.18	1.39	1.51

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	135	ARG	NE-CZ-NH1	10.96	125.78	120.30
1	B	61	ARG	NE-CZ-NH1	-8.65	115.97	120.30
1	B	61	ARG	NE-CZ-NH2	7.90	124.25	120.30
1	E	135	ARG	NE-CZ-NH2	-7.88	116.36	120.30
1	E	133	ARG	NE-CZ-NH1	7.15	123.87	120.30
1	D	61	ARG	NE-CZ-NH1	-6.47	117.06	120.30
1	E	133	ARG	NE-CZ-NH2	-6.10	117.25	120.30
1	D	227	GLY	N-CA-C	-5.87	98.44	113.10
1	C	61	ARG	NE-CZ-NH2	5.56	123.08	120.30
1	C	131	ARG	NE-CZ-NH1	5.29	122.94	120.30
1	A	18	ASP	CB-CG-OD1	5.27	123.04	118.30
1	C	131	ARG	NE-CZ-NH2	-5.26	117.67	120.30
1	D	226	GLY	N-CA-C	5.24	126.21	113.10
1	C	61	ARG	NE-CZ-NH1	-5.11	117.75	120.30

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts ⓘ

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	2206	0	2216	36	0
1	B	2229	0	2244	39	0
1	C	2172	0	2194	40	0
1	D	2247	0	2268	37	0
1	E	2182	0	2188	62	0
2	A	86	0	46	2	0
2	B	31	0	11	1	0
2	E	52	0	31	2	0
3	A	8	0	14	1	0
3	B	8	0	14	1	0
3	D	8	0	14	0	0
4	A	4	0	0	0	0
4	B	1	0	0	0	0
4	D	2	0	0	0	0
4	E	3	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	D	1	0	0	0	0
5	E	1	0	0	0	0
6	B	4	0	3	2	0
6	C	4	0	3	2	0
6	D	4	0	3	0	0
7	A	176	0	0	4	0
7	B	174	0	0	2	0
7	C	161	0	0	6	0
7	D	203	0	0	8	0
7	E	23	0	0	1	0
All	All	11992	0	11249	210	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 9.

All (210) 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:C:12:LEU:HD11	1:C:65[B]:THR:CG2	1.60	1.30
1:D:4:VAL:HG13	1:D:34:SER:CB	1.74	1.18
1:E:32:THR:HG22	1:E:33:GLU:O	1.42	1.16
1:C:12:LEU:CD1	1:C:65[B]:THR:CG2	2.25	1.14
1:D:4:VAL:CG1	1:D:34:SER:HB3	1.76	1.14
1:C:12:LEU:HD11	1:C:65[B]:THR:HG21	1.25	1.12
1:E:60:ASP:HB2	1:E:137:ARG:NH2	1.65	1.10
1:C:234:ILE:HD11	1:C:246:LEU:CD2	1.81	1.09
1:E:288:LEU:HD12	1:E:289:PHE:N	1.71	1.05
1:D:4:VAL:O	1:D:4:VAL:HG12	1.50	1.02
1:A:234:ILE:HD11	1:A:246:LEU:CD2	1.90	0.99
1:D:221:MET:HG3	1:D:232[B]:ILE:CD1	1.91	0.99
1:D:221:MET:HG3	1:D:232[B]:ILE:HD13	1.43	0.98
1:C:135:ARG:HD2	7:C:415:HOH:O	1.66	0.95
1:D:4:VAL:CG1	1:D:4:VAL:O	2.14	0.95
1:D:4:VAL:HG13	1:D:34:SER:HB3	0.94	0.93
1:D:108[B]:PHE:CE1	7:D:489:HOH:O	2.21	0.92
1:E:234:ILE:HD11	1:E:246:LEU:CD2	2.00	0.92
1:E:32:THR:CG2	1:E:33:GLU:O	2.17	0.91
1:C:35:GLY:HA3	7:C:546:HOH:O	1.71	0.90
1:E:288:LEU:HD12	1:E:288:LEU:C	1.90	0.89
1:A:234:ILE:HD11	1:A:246:LEU:HD21	1.56	0.88
1:A:229:THR:O	1:A:229:THR:HG22	1.76	0.84
1:C:272:ASP:O	1:C:273:SER:HB2	1.78	0.82
1:C:234:ILE:HD11	1:C:246:LEU:HD21	1.61	0.82
1:C:12:LEU:CD1	1:C:65[B]:THR:HG23	2.09	0.82
6:B:332:ACY:H1	7:B:493:HOH:O	1.79	0.81
1:B:308:ILE:O	1:B:309:ALA:CB	2.27	0.80
1:D:108[B]:PHE:CZ	7:D:489:HOH:O	2.32	0.80
1:D:276:VAL:CG2	1:D:280:GLU:CD	2.50	0.80
1:B:267[B]:ARG:NH2	1:B:277:LYS:HE3	1.96	0.79
1:B:272:ASP:O	1:B:273:SER:CB	2.33	0.77
1:C:4:VAL:CG1	1:C:5:THR:H	1.99	0.76
1:E:300:VAL:C	1:E:301:LEU:HD12	2.06	0.76
1:C:12:LEU:HD11	1:C:65[B]:THR:HG22	1.64	0.75
1:C:12:LEU:HD13	1:C:65[B]:THR:HG23	1.69	0.75
1:D:276:VAL:HG23	1:D:280:GLU:OE2	1.88	0.74
1:C:12:LEU:HD13	1:C:65[B]:THR:CG2	2.15	0.74
1:E:310:LEU:HD12	1:E:310:LEU:N	2.03	0.74
1:D:226:GLY:C	1:D:227:GLY:O	2.25	0.73
1:E:55:ILE:HD11	1:E:67:ALA:HB2	1.69	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:301:LEU:HD12	1:E:301:LEU:N	2.05	0.72
1:E:60:ASP:CB	1:E:137:ARG:NH2	2.48	0.72
1:C:276[A]:VAL:CG1	1:C:280:GLU:CD	2.59	0.71
6:C:331:ACY:H1	7:C:493:HOH:O	1.90	0.71
1:D:238:CYS:O	1:D:239:LEU:HD23	1.91	0.71
1:B:301:LEU:N	1:B:301:LEU:HD12	2.05	0.70
1:D:108[B]:PHE:HE1	7:D:489:HOH:O	1.67	0.69
1:A:230:HIS:ND1	1:A:230:HIS:N	2.41	0.69
1:B:272:ASP:O	1:B:273:SER:HB2	1.92	0.69
1:C:12:LEU:CD1	1:C:65[B]:THR:HG22	2.19	0.68
1:A:49:VAL:HG13	7:A:508:HOH:O	1.92	0.68
1:D:309:ALA:HB2	7:D:595:HOH:O	1.93	0.68
1:C:4:VAL:HG13	1:C:5:THR:H	1.59	0.68
1:B:267[B]:ARG:HH21	1:B:277:LYS:HE3	1.58	0.67
1:A:239:LEU:HD23	1:B:224:LEU:CG	2.25	0.67
1:C:4:VAL:CG1	1:C:5:THR:N	2.59	0.66
1:D:276:VAL:HG23	1:D:280:GLU:CD	2.17	0.66
1:D:276:VAL:CG2	1:D:280:GLU:OE2	2.44	0.65
1:A:229:THR:O	1:A:229:THR:CG2	2.45	0.65
1:D:221:MET:HG3	1:D:232[B]:ILE:HD12	1.79	0.65
1:A:239:LEU:CD2	1:B:224:LEU:HG	2.27	0.64
1:C:234:ILE:HD11	1:C:246:LEU:HD23	1.74	0.63
1:B:271:PRO:HD2	1:B:308:ILE:CD1	2.29	0.63
1:E:60:ASP:OD2	1:E:137:ARG:NE	2.32	0.62
1:E:35:GLY:O	1:E:73:GLY:HA3	2.00	0.62
1:C:60:ASP:OD1	1:C:136[B]:ARG:NH2	2.32	0.62
1:E:310:LEU:HD12	1:E:310:LEU:H	1.64	0.62
1:E:301:LEU:CD1	1:E:301:LEU:N	2.62	0.61
1:E:32:THR:CG2	1:E:33:GLU:N	2.62	0.61
1:A:267:ARG:HD2	7:A:571:HOH:O	2.00	0.61
1:C:181:MET:HE2	7:C:549:HOH:O	2.00	0.61
2:B:331:SCA:O21	2:B:331:SCA:O11	2.18	0.61
1:C:181:MET:CE	7:C:549:HOH:O	2.47	0.61
1:A:272:ASP:O	1:A:273:SER:OG	2.16	0.61
1:B:308:ILE:O	1:B:309:ALA:HB2	2.00	0.61
1:D:3:THR:HG22	1:D:3:THR:O	2.01	0.61
1:E:60:ASP:HB2	1:E:137:ARG:HH21	1.64	0.60
2:E:331:SCA:H4'	2:E:331:SCA:O31	2.02	0.60
1:E:288:LEU:C	1:E:288:LEU:CD1	2.65	0.59
1:B:308:ILE:O	1:B:309:ALA:HB3	2.01	0.59
1:D:272:ASP:O	1:D:273:SER:CB	2.50	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:271:PRO:CD	1:B:308:ILE:CD1	2.81	0.58
1:E:234:ILE:HD11	1:E:246:LEU:HD23	1.80	0.58
1:A:239:LEU:HD23	1:B:224:LEU:HG	1.83	0.58
1:C:276[A]:VAL:HG13	1:C:280:GLU:CD	2.22	0.58
1:E:152:VAL:HG21	1:E:165:ALA:HB1	1.85	0.58
1:B:227:GLY:HA2	7:B:525:HOH:O	2.03	0.58
1:C:4:VAL:O	1:C:34:SER:HB3	2.04	0.57
1:E:84:ASP:O	1:E:88:ARG:HG3	2.05	0.57
1:B:50:GLU:H	1:B:50:GLU:CD	2.08	0.56
1:E:95:ARG:NH1	1:E:158:THR:O	2.23	0.56
1:A:12:LEU:HG	1:A:65[A]:THR:CG2	2.35	0.56
1:D:50:GLU:H	1:D:50:GLU:CD	2.09	0.56
1:B:271:PRO:HD2	1:B:308:ILE:HD12	1.86	0.56
1:A:239:LEU:CD2	1:B:224:LEU:HD21	2.37	0.55
1:E:130:VAL:HG22	1:E:133:ARG:NH2	2.20	0.54
1:A:239:LEU:HD23	1:B:224:LEU:HD11	1.89	0.54
1:E:55:ILE:HD11	1:E:67:ALA:CB	2.35	0.54
1:E:62:ARG:HG2	1:E:62:ARG:NH1	2.22	0.54
1:E:87:LEU:O	1:E:91:LEU:HG	2.08	0.54
1:E:133:ARG:O	1:E:136:ARG:HD3	2.09	0.53
1:A:81:ASP:HB2	1:A:82:PRO:CD	2.38	0.53
1:E:234:ILE:HD11	1:E:246:LEU:HD21	1.87	0.53
1:E:223:THR:HB	1:E:230:HIS:O	2.08	0.53
1:C:4:VAL:HG12	1:C:5:THR:N	2.24	0.53
1:A:181:MET:HE3	7:A:585:HOH:O	2.09	0.53
1:C:234:ILE:HD12	1:C:250:LEU:HD12	1.91	0.52
1:B:42:LEU:HD21	1:B:69:ARG:HB2	1.92	0.52
1:E:58:ASP:OD2	1:E:61:ARG:HD3	2.09	0.52
1:A:255:VAL:HG13	1:B:224:LEU:HD11	1.92	0.52
1:B:271:PRO:CD	1:B:308:ILE:HD11	2.40	0.52
1:B:237:ARG:NH2	1:B:253:ASP:OD2	2.42	0.51
1:E:42:LEU:HD11	1:E:69:ARG:HB3	1.91	0.51
1:A:239:LEU:HD23	1:B:224:LEU:CD1	2.41	0.51
1:E:245:GLY:HA3	1:E:261:TYR:CD1	2.46	0.51
1:D:3:THR:O	1:D:4:VAL:HB	2.12	0.50
1:C:234:ILE:CD1	1:C:246:LEU:HD21	2.37	0.50
1:A:234:ILE:HD12	1:A:250:LEU:HD12	1.94	0.50
1:E:62:ARG:HH11	1:E:62:ARG:HG2	1.77	0.49
1:A:239:LEU:CD2	1:B:224:LEU:CG	2.88	0.49
1:E:117:THR:HG22	1:E:142:VAL:HG22	1.94	0.49
1:A:234:ILE:HD11	1:A:246:LEU:HD22	1.86	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:35:GLY:O	1:E:73:GLY:CA	2.60	0.49
1:E:152:VAL:HG21	1:E:165:ALA:CB	2.43	0.49
1:E:69:ARG:O	1:E:69:ARG:HG3	2.13	0.49
1:B:227:GLY:O	1:B:229:THR:N	2.46	0.49
1:E:12:LEU:HG	1:E:65:THR:CG2	2.43	0.49
1:A:239:LEU:HD21	1:B:224:LEU:HG	1.94	0.49
1:B:304:ASP:OD1	1:B:306:GLN:N	2.36	0.49
1:D:181:MET:HE3	7:D:556:HOH:O	2.11	0.49
1:A:33:GLU:HG2	1:A:34:SER:N	2.28	0.48
1:E:310:LEU:CD1	1:E:310:LEU:N	2.74	0.48
1:B:300:VAL:C	1:B:301:LEU:HD12	2.34	0.48
1:B:33:GLU:CD	1:B:33:GLU:H	2.16	0.48
1:C:234:ILE:CD1	1:C:246:LEU:CD2	2.74	0.47
1:D:95:ARG:HD3	1:D:174:LEU:O	2.15	0.47
1:E:60:ASP:CB	1:E:137:ARG:HH21	2.25	0.47
1:E:32:THR:HG22	1:E:33:GLU:N	2.30	0.47
1:D:221:MET:CG	1:D:232[B]:ILE:CD1	2.80	0.47
1:E:13:ALA:O	1:E:65:THR:HA	2.15	0.47
1:A:310:LEU:N	1:A:310:LEU:HD22	2.29	0.47
1:A:59:ASP:O	1:A:62:ARG:HD3	2.15	0.47
1:D:49:VAL:HG23	1:D:50:GLU:OE2	2.15	0.47
1:E:60:ASP:HB2	1:E:137:ARG:HH22	1.71	0.47
1:C:234:ILE:HD11	1:C:246:LEU:HD22	1.89	0.46
1:D:181:MET:CE	7:D:556:HOH:O	2.62	0.46
1:C:181:MET:HE3	7:C:549:HOH:O	2.14	0.46
1:E:44:VAL:HA	1:E:47:VAL:HG23	1.97	0.46
1:B:152:VAL:HG21	1:B:165:ALA:HB1	1.97	0.46
1:C:222:GLY:HA2	6:C:331:ACY:H3	1.97	0.46
1:B:226:GLY:HA2	1:D:306:GLN:HG3	1.97	0.46
1:C:272:ASP:O	1:C:273:SER:CB	2.53	0.46
1:A:239:LEU:CD2	1:B:224:LEU:CD2	2.94	0.46
1:E:152:VAL:CG2	1:E:165:ALA:HB1	2.46	0.45
1:E:192:THR:HG21	1:E:196:SER:HB2	1.98	0.45
2:A:331:SCA:H4'	2:A:331:SCA:O32	2.16	0.45
1:C:255:VAL:HB	1:C:288:LEU:HD12	1.99	0.45
1:C:270:MET:HB3	1:C:271:PRO:HD2	1.99	0.45
1:D:35:GLY:HA3	7:D:604:HOH:O	2.16	0.45
1:D:270:MET:HB3	1:D:271:PRO:CD	2.47	0.45
1:E:206:VAL:HG11	1:E:220:ILE:HG21	1.99	0.45
1:D:37:SER:HA	1:D:71:VAL:O	2.17	0.44
1:E:99:PRO:HG2	1:E:207:VAL:HG22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:276[A]:VAL:CG1	1:C:280:GLU:HB2	2.47	0.44
1:B:4:VAL:HG11	1:B:74:SER:HB2	1.98	0.44
1:D:272:ASP:O	1:D:273:SER:HB3	2.18	0.44
3:A:340:MPD:HM3	1:B:128:GLU:HG3	1.99	0.44
1:E:152:VAL:HG22	7:E:402:HOH:O	2.18	0.44
1:A:181:MET:CE	7:A:585:HOH:O	2.64	0.44
1:A:61:ARG:HG2	1:A:122:CYS:SG	2.58	0.44
1:B:60:ASP:OD2	1:B:137:ARG:NH2	2.46	0.44
1:E:15:LEU:N	1:E:15:LEU:CD1	2.80	0.44
1:E:288:LEU:CD1	1:E:289:PHE:N	2.62	0.44
1:E:77:ASP:O	1:E:103:ASN:HB3	2.18	0.44
1:A:293:SER:N	2:A:331:SCA:N1	2.63	0.44
3:B:340:MPD:H4	3:B:340:MPD:HM2	1.86	0.44
1:E:102:LEU:C	1:E:102:LEU:HD12	2.38	0.43
1:A:12:LEU:HD11	1:A:65[A]:THR:HG22	2.00	0.43
1:D:108[B]:PHE:HE2	1:D:188:TYR:HH	1.66	0.43
1:E:69:ARG:HE	1:E:69:ARG:HB2	1.38	0.43
1:E:163:ALA:HB1	1:E:182:HIS:CE1	2.53	0.43
2:E:331:SCA:O31	2:E:331:SCA:C4'	2.63	0.43
1:A:12:LEU:CD1	1:A:65[A]:THR:HG22	2.49	0.43
1:C:113:ASN:ND2	1:C:124:ILE:HD11	2.33	0.43
1:E:60:ASP:CG	1:E:137:ARG:HH21	2.22	0.43
1:E:21:VAL:HB	1:E:82:PRO:HB2	2.01	0.42
1:C:245:GLY:HA3	1:C:261:TYR:CD1	2.53	0.42
1:D:36:THR:N	7:D:604:HOH:O	2.15	0.42
1:D:185:PHE:HB3	1:D:201:ARG:HG2	2.01	0.42
1:D:221:MET:CG	1:D:232[B]:ILE:HD12	2.49	0.42
1:E:245:GLY:HA3	1:E:261:TYR:CE1	2.55	0.42
1:A:13:ALA:O	1:A:65[A]:THR:HA	2.20	0.42
1:A:245:GLY:HA3	1:A:261:TYR:CD1	2.55	0.41
1:B:163:ALA:HB1	1:B:182:HIS:CE1	2.54	0.41
1:A:272:ASP:OD1	1:A:272:ASP:C	2.58	0.41
1:C:270:MET:CB	1:C:271:PRO:CD	2.98	0.41
1:C:268:VAL:O	1:C:275:SER:HA	2.20	0.41
1:B:201:ARG:HE	6:B:332:ACY:C	2.32	0.41
1:E:12:LEU:O	1:E:24:THR:HA	2.20	0.41
1:E:61:ARG:O	1:E:62:ARG:HB2	2.19	0.41
1:B:301:LEU:CD1	1:B:301:LEU:N	2.78	0.41
1:E:95:ARG:NH1	1:E:160:VAL:HG23	2.35	0.41
1:C:276[A]:VAL:HG13	1:C:280:GLU:OE2	2.21	0.41
1:B:152:VAL:CG2	1:B:165:ALA:HB1	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:279:ARG:HD2	1:C:279:ARG:HH11	1.76	0.40
1:A:55:ILE:HD11	1:A:67:ALA:HB2	2.03	0.40
1:E:99:PRO:HB2	1:E:207:VAL:CG2	2.51	0.40
1:A:102:LEU:HD12	1:A:102:LEU:C	2.42	0.40
1:D:302:ALA:CB	1:D:307:GLY:H	2.34	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	301/332 (91%)	295 (98%)	6 (2%)	0	100	100
1	B	308/332 (93%)	298 (97%)	8 (3%)	2 (1%)	28	20
1	C	297/332 (90%)	293 (99%)	4 (1%)	0	100	100
1	D	312/332 (94%)	303 (97%)	8 (3%)	1 (0%)	44	38
1	E	297/332 (90%)	292 (98%)	5 (2%)	0	100	100
All	All	1515/1660 (91%)	1481 (98%)	31 (2%)	3 (0%)	51	46

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	227	GLY
1	B	228	GLY
1	D	227	GLY

### 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	231/251 (92%)	229 (99%)	2 (1%)	82	85
1	B	233/251 (93%)	228 (98%)	5 (2%)	59	59
1	C	229/251 (91%)	227 (99%)	2 (1%)	82	85
1	D	237/251 (94%)	228 (96%)	9 (4%)	38	32
1	E	227/251 (90%)	215 (95%)	12 (5%)	26	19
All	All	1157/1255 (92%)	1127 (97%)	30 (3%)	53	49

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	125	ASP
1	A	230	HIS
1	B	3	THR
1	B	135	ARG
1	B	229	THR
1	B	234	ILE
1	B	273	SER
1	C	270	MET
1	C	279	ARG
1	D	34	SER
1	D	135	ARG
1	D	229	THR
1	D	231	VAL
1	D	234[A]	ILE
1	D	234[B]	ILE
1	D	257	GLU
1	D	274	ASN
1	D	310	LEU
1	E	5	THR
1	E	15	LEU
1	E	32	THR
1	E	40	SER
1	E	69	ARG
1	E	74	SER
1	E	110	VAL
1	E	136	ARG
1	E	274	ASN
1	E	279	ARG

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Mol	Chain	Res	Type
1	E	288	LEU
1	E	310	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	274	ASN
1	B	230	HIS
1	D	230	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 14 are monoatomic - leaving 10 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	$\# Z  > 2$
2	SCA	A	331	-	29,33,57	1.06	2 (6%)	31,52,84	1.72	4 (12%)
2	SCA	A	332	-	47,57,57	1.41	5 (10%)	55,84,84	2.14	13 (23%)
3	MPD	A	340	-	7,7,7	0.26	0	9,10,10	0.49	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	SCA	B	331	-	29,33,57	1.14	3 (10%)	31,52,84	1.64	4 (12%)
6	ACY	B	332	-	1,3,3	3.19	1 (100%)	0,3,3	0.00	-
3	MPD	B	340	-	7,7,7	0.34	0	9,10,10	0.72	0
6	ACY	C	331	-	1,3,3	2.35	1 (100%)	0,3,3	0.00	-
6	ACY	D	331	-	1,3,3	1.93	0	0,3,3	0.00	-
3	MPD	D	340	-	7,7,7	0.40	0	9,10,10	0.71	0
2	SCA	E	331	-	44,53,57	1.08	5 (11%)	48,78,84	1.45	3 (6%)

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	SCA	A	331	-	-	0/17/37/72	0/3/3/3
2	SCA	A	332	-	-	0/50/72/72	0/3/3/3
3	MPD	A	340	-	-	0/5/5/5	0/0/0/0
2	SCA	B	331	-	-	0/17/37/72	0/3/3/3
6	ACY	B	332	-	-	0/0/0/0	0/0/0/0
3	MPD	B	340	-	-	0/5/5/5	0/0/0/0
6	ACY	C	331	-	-	0/0/0/0	0/0/0/0
6	ACY	D	331	-	-	0/0/0/0	0/0/0/0
3	MPD	D	340	-	-	0/5/5/5	0/0/0/0
2	SCA	E	331	-	-	0/44/64/72	0/3/3/3

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	332	SCA	CS1-S	-4.17	1.67	1.76
2	A	331	SCA	P3-O3'	2.07	1.63	1.59
2	E	331	SCA	P3-O3'	2.25	1.63	1.59
2	E	331	SCA	C2-N3	2.25	1.35	1.32
2	E	331	SCA	O4'-C1'	2.27	1.44	1.41
2	B	331	SCA	P3-O3'	2.31	1.63	1.59
6	C	331	ACY	CH3-C	2.35	1.51	1.48
2	E	331	SCA	CS3-CS4	2.53	1.52	1.48
2	B	331	SCA	C2-N3	2.56	1.36	1.32
2	A	331	SCA	C5-C4	3.00	1.47	1.40
2	A	332	SCA	O4'-C1'	3.08	1.45	1.41
2	E	331	SCA	C5-C4	3.16	1.47	1.40
6	B	332	ACY	CH3-C	3.19	1.52	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	332	SCA	C5-C4	3.25	1.47	1.40
2	B	331	SCA	C5-C4	3.29	1.47	1.40
2	A	332	SCA	CS2-CS1	3.81	1.55	1.50
2	A	332	SCA	P3-O3'	4.21	1.66	1.59

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	332	SCA	OS1-CS1-S	-7.38	115.12	122.84
2	A	331	SCA	N3-C2-N1	-6.79	122.94	128.86
2	E	331	SCA	N3-C2-N1	-6.74	122.99	128.86
2	A	332	SCA	N3-C2-N1	-6.45	123.24	128.86
2	B	331	SCA	N3-C2-N1	-6.07	123.58	128.86
2	B	331	SCA	C4-C5-N7	-3.59	105.94	109.41
2	E	331	SCA	C4-C5-N7	-2.92	106.59	109.41
2	A	332	SCA	C1'-N9-C4	-2.29	122.68	126.64
2	A	332	SCA	CP5-CP4-CP3	-2.23	108.64	112.22
2	B	331	SCA	C1'-N9-C4	-2.05	123.10	126.64
2	A	332	SCA	CP5-NP2-CP6	-2.04	118.78	122.59
2	A	332	SCA	CP1-S-CS1	2.07	108.73	101.90
2	A	332	SCA	C2-N1-C6	2.11	122.47	118.77
2	A	332	SCA	O22-P2-O21	2.34	124.41	112.28
2	A	331	SCA	C2-N1-C6	2.35	122.88	118.77
2	E	331	SCA	C2-N1-C6	2.38	122.94	118.77
2	A	331	SCA	O22-P2-O21	2.44	120.06	110.50
2	A	331	SCA	N6-C6-N1	2.54	123.80	118.77
2	A	332	SCA	OS1-CS1-CS2	2.59	126.21	123.95
2	B	331	SCA	O22-P2-O21	2.83	121.56	110.50
2	A	332	SCA	N6-C6-N1	2.83	124.38	118.77
2	A	332	SCA	CP9-CPA-CP7	4.17	116.05	108.82
2	A	332	SCA	CS2-CS1-S	5.28	118.60	113.28
2	A	332	SCA	CS3-CS2-CS1	5.32	120.41	112.41

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	331	SCA	2	0
3	A	340	MPD	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	331	SCA	1	0
6	B	332	ACY	2	0
3	B	340	MPD	1	0
6	C	331	ACY	2	0
2	E	331	SCA	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

### 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, 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	304/332 (91%)	0.13	10 (3%) 47 50	26, 32, 43, 59	0
1	B	307/332 (92%)	0.10	9 (2%) 52 55	26, 32, 46, 69	0
1	C	297/332 (89%)	-0.18	6 (2%) 65 68	27, 32, 43, 60	0
1	D	308/332 (92%)	0.16	12 (3%) 40 43	26, 32, 46, 75	0
1	E	301/332 (90%)	0.74	42 (13%) 3 4	27, 33, 45, 69	0
All	All	1517/1660 (91%)	0.19	79 (5%) 28 31	26, 32, 45, 75	0

All (79) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	3	THR	8.2
1	C	4	VAL	6.9
1	D	228	GLY	6.0
1	D	3	THR	5.4
1	D	4	VAL	5.4
1	D	310	LEU	5.4
1	E	309	ALA	5.3
1	D	309	ALA	5.2
1	B	4	VAL	5.1
1	D	227	GLY	5.0
1	D	34	SER	4.8
1	E	307	GLY	4.8
1	E	308	ILE	4.7
1	A	229	THR	4.6
1	E	80	ALA	4.5
1	E	46	ASP	4.5
1	D	308	ILE	4.3
1	A	4	VAL	4.1
1	E	50	GLU	4.0
1	B	228	GLY	3.9

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Mol	Chain	Res	Type	RSRZ
1	B	309	ALA	3.7
1	E	230	HIS	3.7
1	E	130	VAL	3.7
1	B	307	GLY	3.6
1	A	309	ALA	3.6
1	E	310	LEU	3.5
1	C	230	HIS	3.4
1	E	19	GLY	3.2
1	B	308	ILE	3.2
1	E	43	ALA	3.1
1	B	227	GLY	3.1
1	E	10	ILE	3.0
1	E	108	PHE	2.9
1	A	225	SER	2.9
1	E	42	LEU	2.9
1	D	108[A]	PHE	2.9
1	E	44	VAL	2.8
1	E	71	VAL	2.8
1	A	230	HIS	2.7
1	E	49	VAL	2.7
1	E	77	ASP	2.7
1	D	229	THR	2.7
1	E	58	ASP	2.7
1	E	83	TYR	2.7
1	E	73	GLY	2.7
1	A	274	ASN	2.7
1	E	24	THR	2.7
1	D	230	HIS	2.6
1	E	36	THR	2.6
1	E	78	VAL	2.6
1	E	37	SER	2.5
1	C	5	THR	2.5
1	A	310	LEU	2.5
1	E	12	LEU	2.5
1	C	35	GLY	2.5
1	E	110	VAL	2.5
1	E	32	THR	2.5
1	E	107	LEU	2.4
1	B	229	THR	2.4
1	E	33	GLU	2.4
1	E	40	SER	2.3
1	E	63	THR	2.3

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Mol	Chain	Res	Type	RSRZ
1	E	126	GLY	2.3
1	E	124	ILE	2.3
1	E	283	GLY	2.3
1	E	134	LEU	2.3
1	A	33	GLU	2.2
1	A	34	SER	2.2
1	E	109	GLY	2.2
1	E	304	ASP	2.2
1	A	224	LEU	2.1
1	E	125	ASP	2.1
1	C	274	ASN	2.1
1	D	220	ILE	2.1
1	C	33	GLU	2.1
1	E	54	LEU	2.1
1	B	34	SER	2.0
1	E	15	LEU	2.0
1	E	39	THR	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, 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	MPD	B	340	8/8	0.93	0.18	11.28	28,43,51,52	0
2	SCA	E	331	52/55	0.93	0.25	4.80	38,57,68,73	0
3	MPD	D	340	8/8	0.93	0.15	4.29	30,46,52,54	0
5	NA	A	337	1/1	0.93	0.17	3.81	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	SCA	A	332	55/55	0.96	0.18	1.89	28,39,46,54	0
2	SCA	A	331	31/55	0.84	0.16	1.46	26,41,53,55	31
2	SCA	B	331	31/55	0.86	0.14	1.06	23,38,50,55	31
6	ACY	B	332	4/4	0.95	0.15	0.81	28,32,34,34	0
3	MPD	A	340	8/8	0.91	0.14	0.49	33,40,49,51	0
6	ACY	C	331	4/4	0.97	0.12	0.13	33,35,37,37	0
6	ACY	D	331	4/4	0.95	0.10	-1.36	31,34,36,36	0
4	MG	A	334	1/1	0.97	0.10	-2.36	29,29,29,29	0
4	MG	A	333	1/1	0.98	0.04	-6.96	23,23,23,23	0
4	MG	E	333	1/1	1.00	0.02	-	45,45,45,45	1
4	MG	A	335	1/1	0.89	0.11	-	50,50,50,50	0
4	MG	D	332	1/1	0.98	0.06	-	21,21,21,21	1
5	NA	D	334	1/1	0.99	0.06	-	39,39,39,39	1
5	NA	E	335	1/1	0.95	0.25	-	29,29,29,29	1
4	MG	E	332	1/1	0.93	0.03	-	52,52,52,52	1
4	MG	E	334	1/1	0.99	0.06	-	38,38,38,38	1
4	MG	A	336	1/1	0.93	0.06	-	45,45,45,45	0
4	MG	B	333	1/1	0.96	0.08	-	48,48,48,48	0
4	MG	D	333	1/1	0.99	0.15	-	51,51,51,51	1
5	NA	B	334	1/1	0.94	0.11	-	39,39,39,39	1

## 6.5 Other polymers

There are no such residues in this entry.