



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 06:23 am GMT

PDB ID : 5EJ6  
Title : EcMenD-ThDP-Mn<sup>2+</sup> complex soaked with 2-ketoglutarate for 2min then soaked with isochorismate for 2 min  
Authors : Song, H.G.; Dong, C.; Chen, Y.Z.; Sun, Y.R.; Guo, Z.H.  
Deposited on : 2015-11-01  
Resolution : 2.24 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<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 : 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

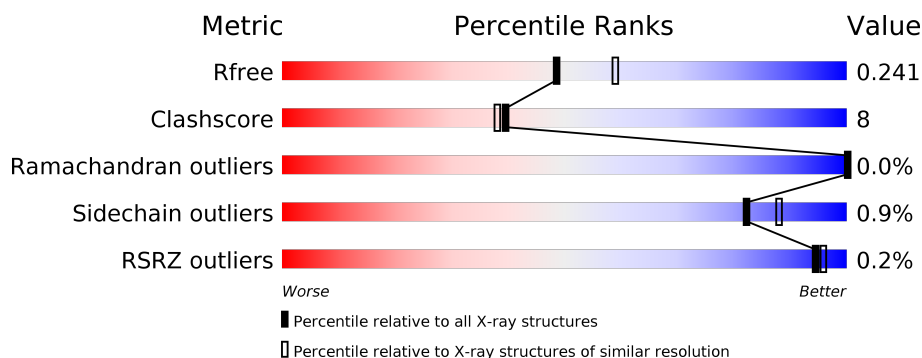
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.24 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	1804 (2.26-2.22)
Clashscore	112137	1957 (2.26-2.22)
Ramachandran outliers	110173	1916 (2.26-2.22)
Sidechain outliers	110143	1917 (2.26-2.22)
RSRZ outliers	101464	1809 (2.26-2.22)

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	556	<div> <div>86%</div> <div>14%</div> </div>
1	B	556	<div> <div>85%</div> <div>15%</div> </div>
1	C	556	<div> <div>84%</div> <div>16%</div> </div>
1	D	556	<div> <div>79%</div> <div>20%</div> </div>
1	E	556	<div> <div>83%</div> <div>17%</div> </div>
1	F	556	<div> <div>85%</div> <div>14%</div> </div>

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Mol	Chain	Length	Quality of chain
1	G	556	<div><div>%</div><div><div></div><div>84%</div><div>16%</div></div></div>
1	H	556	<div><div></div><div><div>78%</div><div>21%</div><div></div></div><div></div></div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 36789 atoms, of which 160 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 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	556	Total	C	N	O	S	0	0	0
			4325	2743	778	789	15			
1	B	556	Total	C	N	O	S	0	0	0
			4321	2741	778	787	15			
1	C	556	Total	C	N	O	S	0	0	0
			4307	2734	774	784	15			
1	D	556	Total	C	N	O	S	0	0	0
			4303	2731	773	784	15			
1	E	556	Total	C	N	O	S	0	0	0
			4325	2743	778	789	15			
1	F	556	Total	C	N	O	S	0	0	0
			4317	2739	777	786	15			
1	G	556	Total	C	N	O	S	0	0	0
			4307	2734	774	784	15			
1	H	556	Total	C	N	O	S	0	0	0
			4303	2731	773	784	15			

- Molecule 2 is (4S)-4-{3-[(4-amino-2-methylpyrimidin-5-yl)methyl]-5-(2-{[(S)-hydroxy(phosphonooxy)phosphoryl]oxy}ethyl)-4-methyl-1,3lambda 5 -thiazol-2-yl}-4-hydroxybutanoic acid (three-letter code: TD6) (formula: C<sub>16</sub>H<sub>25</sub>N<sub>4</sub>O<sub>10</sub>P<sub>2</sub>S).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
2	A	1	Total 53	C 16	H 20	N 4	O 10	P 2	S 1	0	0
2	B	1	Total 53	C 16	H 20	N 4	O 10	P 2	S 1	0	0
2	C	1	Total 53	C 16	H 20	N 4	O 10	P 2	S 1	0	0
2	D	1	Total 53	C 16	H 20	N 4	O 10	P 2	S 1	0	0
2	E	1	Total 53	C 16	H 20	N 4	O 10	P 2	S 1	0	0
2	F	1	Total 53	C 16	H 20	N 4	O 10	P 2	S 1	0	0
2	G	1	Total 53	C 16	H 20	N 4	O 10	P 2	S 1	0	0
2	H	1	Total 53	C 16	H 20	N 4	O 10	P 2	S 1	0	0

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	G	1	Total Mn 1 1	0	0
3	D	1	Total Mn 1 1	0	0
3	E	1	Total Mn 1 1	0	0
3	H	1	Total Mn 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total 1	Mn 1	0	0
3	C	1	Total 1	Mn 1	0	0
3	A	1	Total 1	Mn 1	0	0
3	F	1	Total 1	Mn 1	0	0

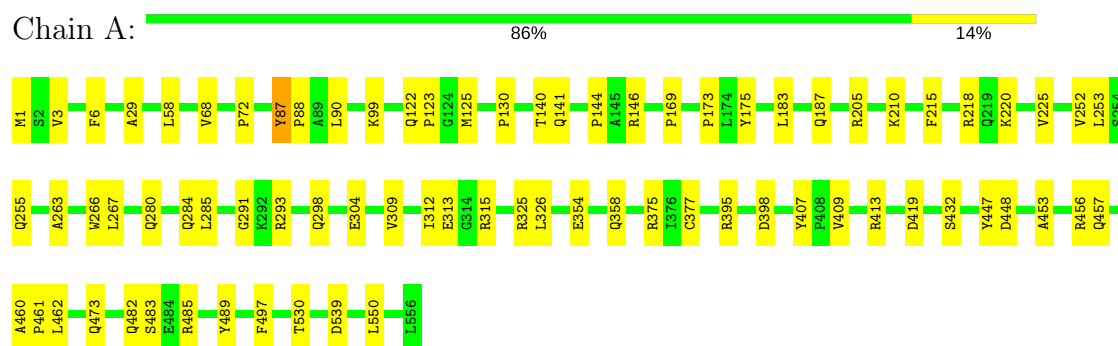
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	288	Total 288	O 288	0	0
4	B	247	Total 247	O 247	0	0
4	C	208	Total 208	O 208	0	0
4	D	201	Total 201	O 201	0	0
4	E	225	Total 225	O 225	0	0
4	F	260	Total 260	O 260	0	0
4	G	181	Total 181	O 181	0	0
4	H	239	Total 239	O 239	0	0

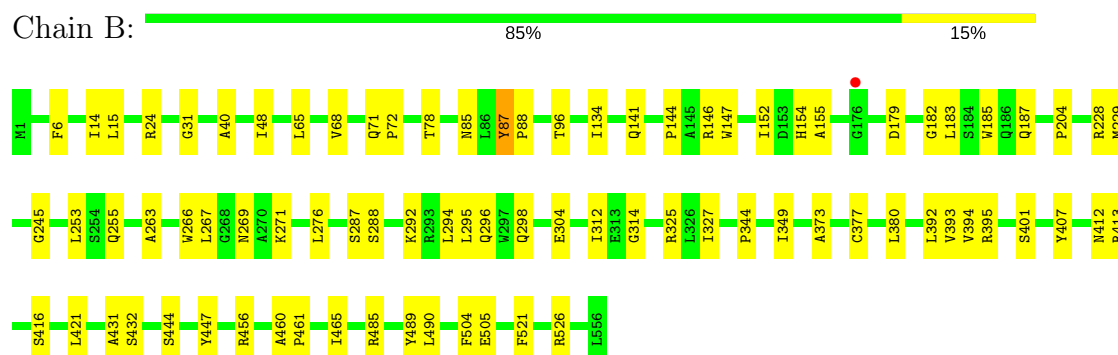
### 3 Residue-property plots

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.

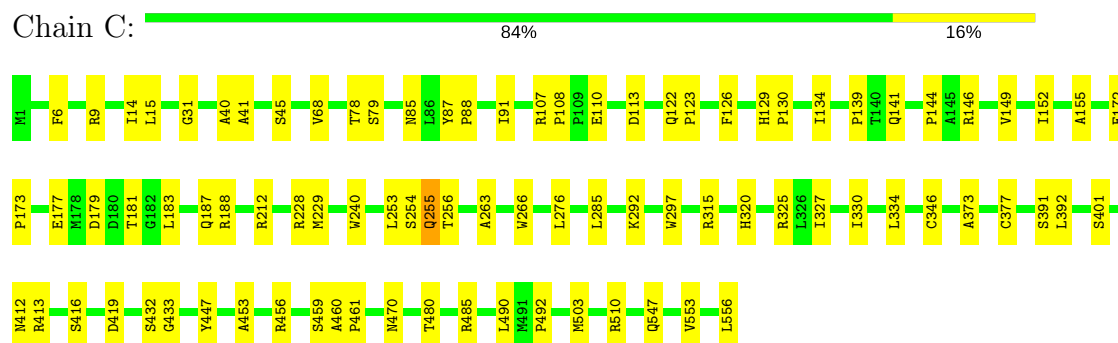
- Molecule 1: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase



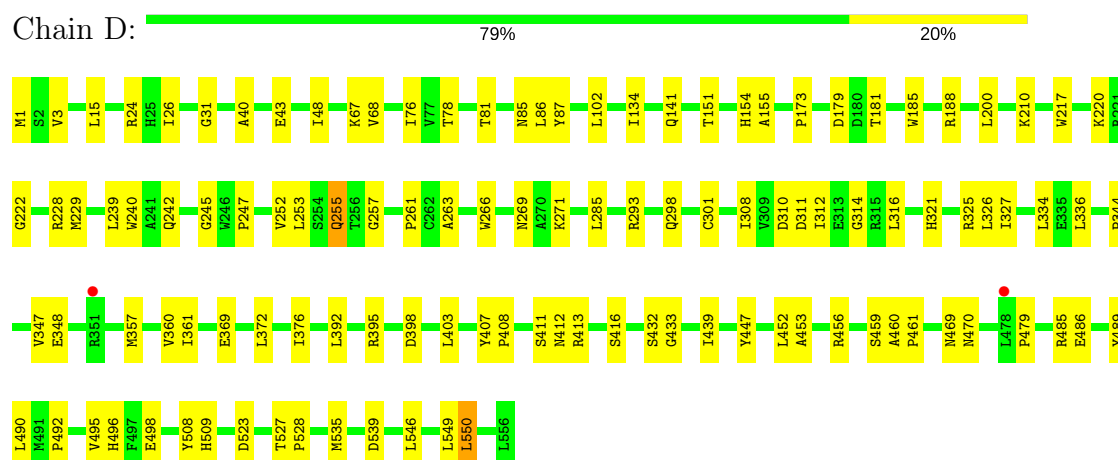
- Molecule 1: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase



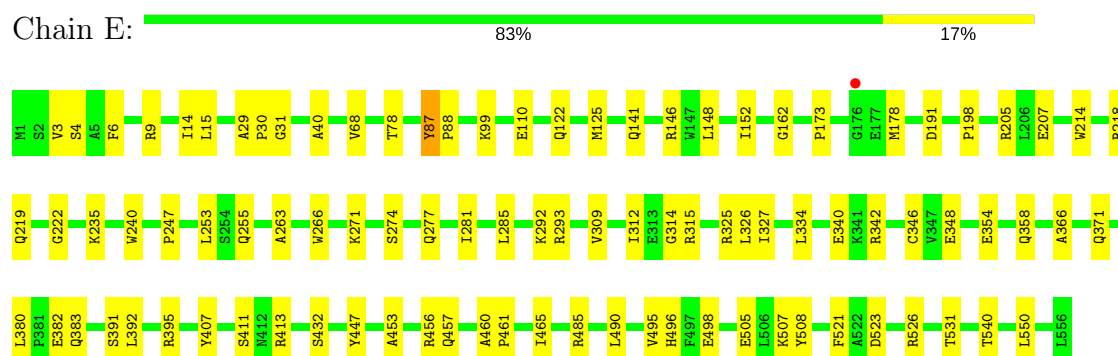
- Molecule 1: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase



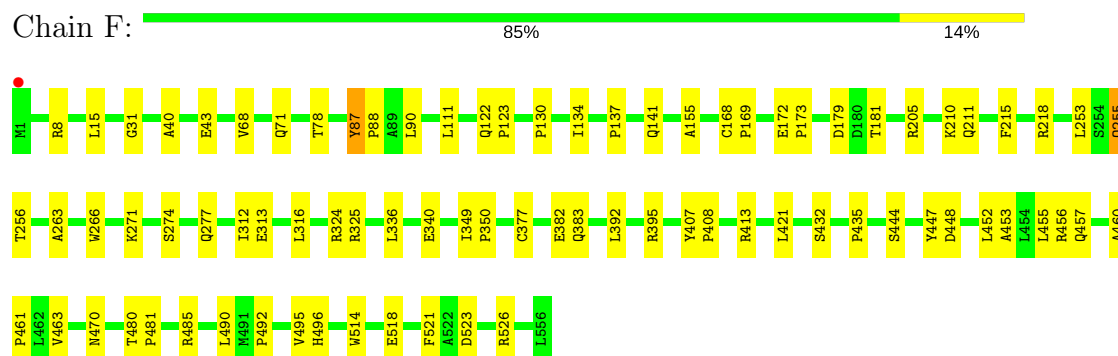
• Molecule 1: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase



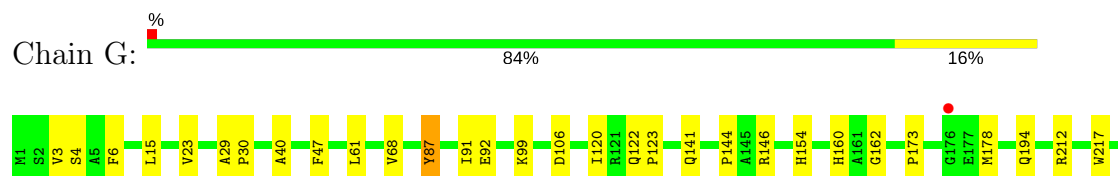
• Molecule 1: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase



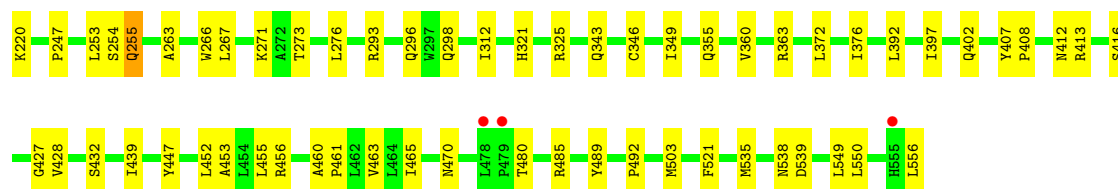
• Molecule 1: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase



• Molecule 1: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase

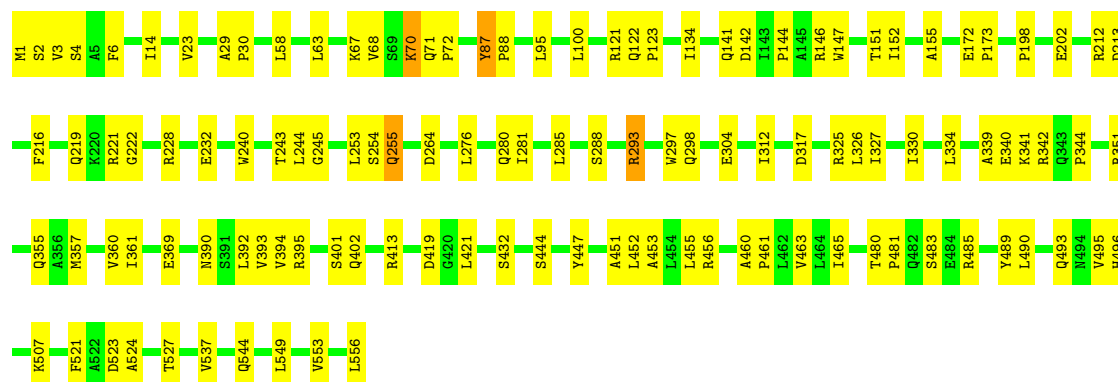






- Molecule 1: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase

Chain H: 78% 21% .



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.48Å 90.51Å 171.64Å 83.02° 75.85° 64.33°	Depositor
Resolution (Å)	34.89 – 2.24 37.45 – 2.24	Depositor EDS
% Data completeness (in resolution range)	93.7 (34.89-2.24) 93.0 (37.45-2.24)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.44 (at 2.24Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, $R_{free}$	0.194 , 0.241 0.194 , 0.241	Depositor DCC
$R_{free}$ test set	10853 reflections (5.08%)	DCC
Wilson B-factor (Å <sup>2</sup> )	14.8	Xtriage
Anisotropy	0.275	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 18.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.38$ , $\langle L^2 \rangle = 0.20$	Xtriage
Estimated twinning fraction	0.108 for -h,-k,-h+l	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	36789	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.11% 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: MN, TD6

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	0.43	0/4433	0.58	0/6047
1	B	0.42	0/4429	0.58	0/6042
1	C	0.41	0/4415	0.58	0/6025
1	D	0.38	0/4411	0.56	0/6021
1	E	0.42	0/4433	0.57	0/6047
1	F	0.43	0/4425	0.58	0/6037
1	G	0.39	0/4415	0.56	0/6025
1	H	0.40	0/4411	0.57	0/6021
All	All	0.41	0/35372	0.57	0/48265

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4325	0	4287	63	0
1	B	4321	0	4283	57	0
1	C	4307	0	4262	71	0
1	D	4303	0	4251	89	0
1	E	4325	0	4287	71	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	4317	0	4277	57	0
1	G	4307	0	4262	68	0
1	H	4303	0	4251	104	0
2	A	33	20	21	4	0
2	B	33	20	21	4	0
2	C	33	20	21	5	0
2	D	33	20	21	4	0
2	E	33	20	21	5	0
2	F	33	20	21	6	0
2	G	33	20	21	5	0
2	H	33	20	21	6	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
4	A	288	0	0	21	0
4	B	247	0	0	12	0
4	C	208	0	0	13	0
4	D	201	0	0	16	0
4	E	225	0	0	12	0
4	F	260	0	0	12	0
4	G	181	0	0	20	0
4	H	239	0	0	32	0
All	All	36629	160	34328	580	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 580 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:D:360:VAL:HG22	1:D:549:LEU:HD13	1.44	0.96
1:H:312:ILE:O	1:H:325:ARG:NH2	2.00	0.95
1:A:482:GLN:O	4:A:701:HOH:O	1.85	0.94
1:D:452:LEU:O	4:D:701:HOH:O	1.86	0.92
1:B:312:ILE:O	1:B:325:ARG:NH1	2.03	0.91

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	554/556 (100%)	541 (98%)	13 (2%)	0	100	100
1	B	554/556 (100%)	543 (98%)	11 (2%)	0	100	100
1	C	554/556 (100%)	543 (98%)	10 (2%)	1 (0%)	51	58
1	D	554/556 (100%)	544 (98%)	10 (2%)	0	100	100
1	E	554/556 (100%)	542 (98%)	12 (2%)	0	100	100
1	F	554/556 (100%)	544 (98%)	10 (2%)	0	100	100
1	G	554/556 (100%)	542 (98%)	12 (2%)	0	100	100
1	H	554/556 (100%)	542 (98%)	12 (2%)	0	100	100
All	All	4432/4448 (100%)	4341 (98%)	90 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	391	SER

### 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	451/452 (100%)	446 (99%)	5 (1%)	78	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	450/452 (100%)	447 (99%)	3 (1%)	87	91
1	C	447/452 (99%)	444 (99%)	3 (1%)	87	91
1	D	446/452 (99%)	441 (99%)	5 (1%)	78	85
1	E	451/452 (100%)	448 (99%)	3 (1%)	87	91
1	F	449/452 (99%)	445 (99%)	4 (1%)	82	88
1	G	447/452 (99%)	442 (99%)	5 (1%)	78	85
1	H	446/452 (99%)	441 (99%)	5 (1%)	78	85
All	All	3587/3616 (99%)	3554 (99%)	33 (1%)	82	88

5 of 33 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	447	TYR
1	E	447	TYR
1	H	255	GLN
1	D	550	LEU
1	E	87	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	255	GLN
1	F	277	GLN
1	G	298	GLN
1	H	71	GLN
1	H	355	GLN

### 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 [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 8 are monoatomic - leaving 8 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	TD6	A	601	3	25,34,34	1.35	3 (12%)	28,50,50	1.96	7 (25%)
2	TD6	B	601	3	25,34,34	1.31	3 (12%)	28,50,50	1.98	7 (25%)
2	TD6	C	601	3	25,34,34	1.40	5 (20%)	28,50,50	1.78	8 (28%)
2	TD6	D	601	3	25,34,34	1.30	3 (12%)	28,50,50	1.69	7 (25%)
2	TD6	E	601	3	25,34,34	1.36	3 (12%)	28,50,50	1.95	9 (32%)
2	TD6	F	601	3	25,34,34	1.34	3 (12%)	28,50,50	1.95	8 (28%)
2	TD6	G	601	3	25,34,34	1.29	3 (12%)	28,50,50	1.76	6 (21%)
2	TD6	H	601	3	25,34,34	1.26	5 (20%)	28,50,50	1.96	7 (25%)

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	TD6	A	601	3	-	0/19/26/26	0/2/2/2
2	TD6	B	601	3	-	0/19/26/26	0/2/2/2
2	TD6	C	601	3	-	0/19/26/26	0/2/2/2
2	TD6	D	601	3	-	0/19/26/26	0/2/2/2
2	TD6	E	601	3	-	0/19/26/26	0/2/2/2
2	TD6	F	601	3	-	0/19/26/26	0/2/2/2
2	TD6	G	601	3	-	0/19/26/26	0/2/2/2
2	TD6	H	601	3	-	0/19/26/26	0/2/2/2

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	601	TD6	C7'-C5'	2.00	1.55	1.51
2	H	601	TD6	C4'-N3'	2.02	1.38	1.35
2	E	601	TD6	C7'-C5'	2.09	1.55	1.51
2	C	601	TD6	C7'-C5'	2.10	1.55	1.51
2	B	601	TD6	C6-C7	2.11	1.58	1.50

The worst 5 of 59 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	601	TD6	CM4-C4-C5	-4.01	119.53	127.29
2	E	601	TD6	CM4-C4-C5	-3.98	119.58	127.29
2	B	601	TD6	CM4-C4-C5	-3.89	119.77	127.29
2	F	601	TD6	CM4-C4-C5	-3.63	120.27	127.29
2	B	601	TD6	C5'-C6'-N1'	-3.62	117.74	123.87

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 39 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	TD6	4	0
2	B	601	TD6	4	0
2	C	601	TD6	5	0
2	D	601	TD6	4	0
2	E	601	TD6	5	0
2	F	601	TD6	6	0
2	G	601	TD6	5	0
2	H	601	TD6	6	0

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.



## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	556/556 (100%)	-0.86	0 100 100	6, 12, 25, 51	0
1	B	556/556 (100%)	-0.84	1 (0%) 94 96	6, 14, 25, 47	0
1	C	556/556 (100%)	-0.80	0 100 100	8, 15, 27, 44	0
1	D	556/556 (100%)	-0.65	2 (0%) 92 93	9, 19, 35, 48	0
1	E	556/556 (100%)	-0.82	1 (0%) 94 96	6, 14, 26, 47	0
1	F	556/556 (100%)	-0.84	1 (0%) 94 96	7, 12, 26, 46	0
1	G	556/556 (100%)	-0.64	4 (0%) 87 87	7, 19, 34, 48	0
1	H	556/556 (100%)	-0.80	0 100 100	9, 15, 28, 40	0
All	All	4448/4448 (100%)	-0.78	9 (0%) 94 96	6, 15, 29, 51	0

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	176	GLY	3.4
1	B	176	GLY	3.3
1	G	176	GLY	3.0
1	G	479	PRO	2.6
1	D	478	LEU	2.5

### 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

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
2	TD6	D	601	33/33	0.97	0.10	0.47	12,18,35,43	0
3	MN	A	602	1/1	1.00	0.08	0.44	14,14,14,14	0
2	TD6	A	601	33/33	0.98	0.09	0.21	7,12,21,36	0
2	TD6	F	601	33/33	0.98	0.08	0.18	7,14,25,37	0
3	MN	F	602	1/1	1.00	0.08	0.14	14,14,14,14	0
2	TD6	G	601	33/33	0.98	0.09	0.11	13,19,31,46	0
2	TD6	B	601	33/33	0.98	0.08	0.08	7,13,23,28	0
2	TD6	E	601	33/33	0.98	0.08	-0.15	6,13,32,44	0
2	TD6	C	601	33/33	0.98	0.08	-0.65	9,15,28,35	0
2	TD6	H	601	33/33	0.98	0.07	-1.14	8,15,21,28	0
3	MN	B	602	1/1	1.00	0.06	-1.55	14,14,14,14	0
3	MN	G	602	1/1	1.00	0.05	-2.26	14,14,14,14	0
3	MN	H	602	1/1	1.00	0.04	-2.52	14,14,14,14	0
3	MN	E	602	1/1	0.99	0.06	-3.35	14,14,14,14	0
3	MN	D	602	1/1	0.99	0.05	-3.71	14,14,14,14	0
3	MN	C	602	1/1	1.00	0.02	-5.77	14,14,14,14	0

## 6.5 Other polymers

There are no such residues in this entry.