



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 8, 2017 – 12:14 AM EDT

PDB ID : 5NJ9  
Title : E. coli Microcin-processing metalloprotease TldD/E with DRVY angiotensin fragment bound  
Authors : Ghilarov, D.; Serebryakova, M.; Stevenson, C.E.M.; Hearnshaw, S.J.; Volkov, D.; Maxwell, A.; Lawson, D.M.; Severinov, K.  
Deposited on : unknown  
Resolution : 1.25 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

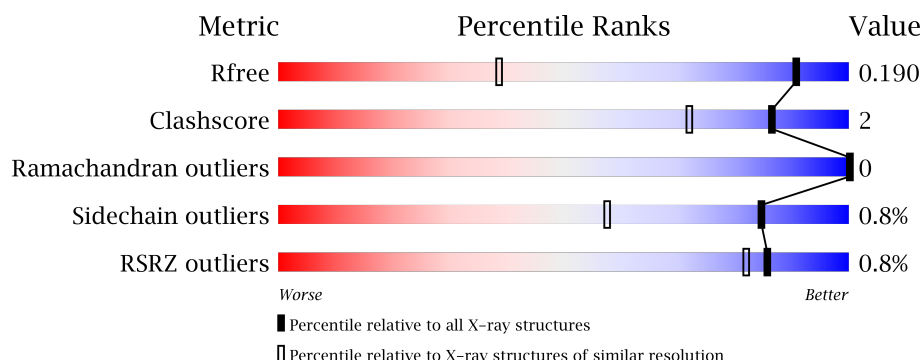
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.25 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	1690 (1.30-1.22)
Clashscore	112137	1781 (1.30-1.22)
Ramachandran outliers	110173	1716 (1.30-1.22)
Sidechain outliers	110143	1714 (1.30-1.22)
RSRZ outliers	101464	1693 (1.30-1.22)

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	495	<div> <div style="width: 100%;"></div> <div> <div style="width: 25%; background-color: red;"></div> <div style="width: 66%; background-color: green;"></div> <div style="width: 9%; background-color: yellow;"></div> <div style="width: 0%; background-color: orange;"></div> <div style="width: 0%; background-color: grey;"></div> </div> <div>91% 6% . .</div> </div>
1	C	495	<div> <div style="width: 100%;"></div> <div> <div style="width: 25%; background-color: red;"></div> <div style="width: 68%; background-color: green;"></div> <div style="width: 7%; background-color: yellow;"></div> <div style="width: 0%; background-color: orange;"></div> <div style="width: 0%; background-color: grey;"></div> </div> <div>93% . .</div> </div>
2	B	450	<div> <div style="width: 100%;"></div> <div> <div style="width: 25%; background-color: red;"></div> <div style="width: 69%; background-color: green;"></div> <div style="width: 6%; background-color: yellow;"></div> <div style="width: 0%; background-color: orange;"></div> <div style="width: 0%; background-color: grey;"></div> </div> <div>94% . .</div> </div>
2	D	450	<div> <div style="width: 100%;"></div> <div> <div style="width: 0%; background-color: red;"></div> <div style="width: 94%; background-color: green;"></div> <div style="width: 6%; background-color: yellow;"></div> <div style="width: 0%; background-color: orange;"></div> <div style="width: 0%; background-color: grey;"></div> </div> <div>94% . .</div> </div>
3	E	4	<div> <div style="width: 100%;"></div> <div> <div style="width: 25%; background-color: red;"></div> <div style="width: 75%; background-color: green;"></div> </div> <div>25% 100%</div> </div>

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Mol	Chain	Length	Quality of chain
3	F	4	<div> <div>25%</div> <div>100%</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
5	MES	B	701	-	-	-	X
5	MES	D	701	-	-	-	X
6	EDO	B	702	-	-	-	X
6	EDO	D	702	-	-	-	X

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 17131 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 Metalloprotease TldD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	480	Total	C	N	O	S	0	29	0
			3833	2382	671	762	18			
1	C	480	Total	C	N	O	S	0	23	0
			3779	2351	664	747	17			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	initiating methionine	UNP P0AGG8
A	-12	GLY	-	expression tag	UNP P0AGG8
A	-11	SER	-	expression tag	UNP P0AGG8
A	-10	SER	-	expression tag	UNP P0AGG8
A	-9	HIS	-	expression tag	UNP P0AGG8
A	-8	HIS	-	expression tag	UNP P0AGG8
A	-7	HIS	-	expression tag	UNP P0AGG8
A	-6	HIS	-	expression tag	UNP P0AGG8
A	-5	HIS	-	expression tag	UNP P0AGG8
A	-4	HIS	-	expression tag	UNP P0AGG8
A	-3	SER	-	expression tag	UNP P0AGG8
A	-2	GLN	-	expression tag	UNP P0AGG8
A	-1	ASP	-	expression tag	UNP P0AGG8
A	0	PRO	-	expression tag	UNP P0AGG8
A	401	ASP	GLY	engineered mutation	UNP P0AGG8
C	-13	MET	-	initiating methionine	UNP P0AGG8
C	-12	GLY	-	expression tag	UNP P0AGG8
C	-11	SER	-	expression tag	UNP P0AGG8
C	-10	SER	-	expression tag	UNP P0AGG8
C	-9	HIS	-	expression tag	UNP P0AGG8
C	-8	HIS	-	expression tag	UNP P0AGG8
C	-7	HIS	-	expression tag	UNP P0AGG8
C	-6	HIS	-	expression tag	UNP P0AGG8
C	-5	HIS	-	expression tag	UNP P0AGG8
C	-4	HIS	-	expression tag	UNP P0AGG8

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-3	SER	-	expression tag	UNP P0AGG8
C	-2	GLN	-	expression tag	UNP P0AGG8
C	-1	ASP	-	expression tag	UNP P0AGG8
C	0	PRO	-	expression tag	UNP P0AGG8
C	401	ASP	GLY	engineered mutation	UNP P0AGG8

- Molecule 2 is a protein called Metalloprotease PmbA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	443	Total	C	N	O	S	0	26	0
			3541	2197	623	705	16			
2	D	442	Total	C	N	O	S	0	35	0
			3614	2242	633	722	17			

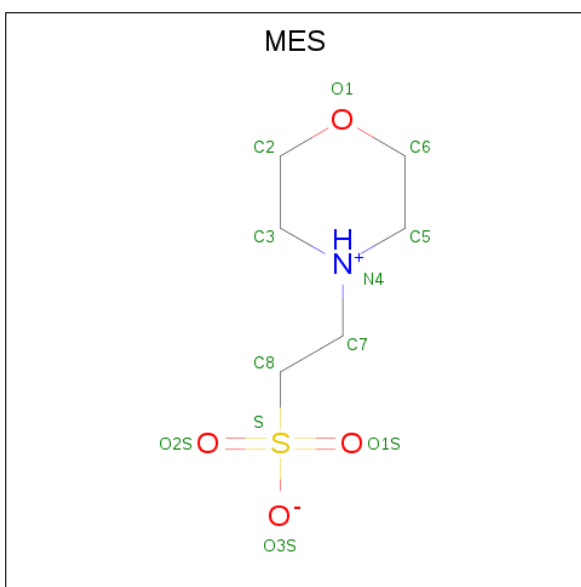
- Molecule 3 is a protein called ASP-ARG-VAL-TYR.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	4	Total	C	N	O	0	0	0
			35	23	4	8			
3	F	4	Total	C	N	O	0	0	0
			35	23	4	8			

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

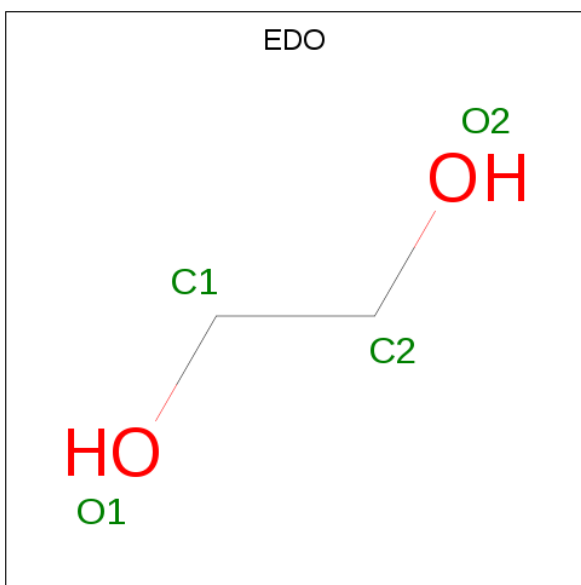
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Zn	0	0
			1	1		
4	C	1	Total	Zn	0	0
			1	1		

- Molecule 5 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C<sub>6</sub>H<sub>13</sub>NO<sub>4</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
5	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
5	C	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
5	D	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

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



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 4 2 2	0	0
6	B	1	Total C O 4 2 2	0	0
6	B	1	Total C O 8 4 4	0	1
6	B	1	Total C O 4 2 2	0	0
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
6	D	1	Total C O 4 2 2	0	0
6	D	1	Total C O 8 4 4	0	1
6	D	1	Total C O 4 2 2	0	0

- Molecule 7 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	B	1	Total Na 1 1	0	0
7	A	1	Total Na 1 1	0	0
7	D	1	Total Na 1 1	0	0
7	C	1	Total Na 1 1	0	0

- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	529	Total O 561 561	0	32
8	B	510	Total O 540 540	0	30
8	C	486	Total O 522 522	0	36
8	D	534	Total O 568 568	0	34

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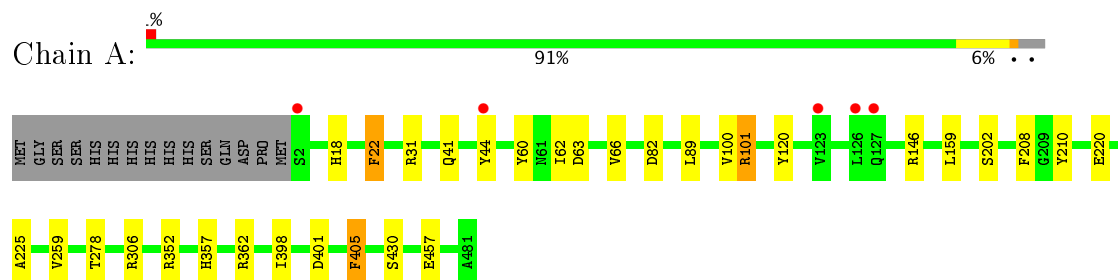
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	E	1	Total	O	0	0
			1	1		

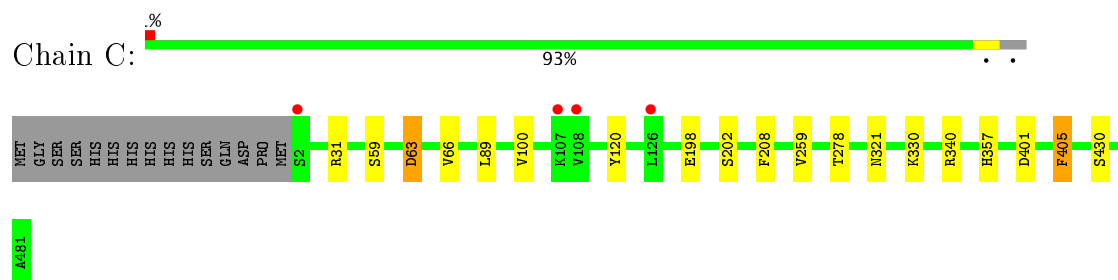
### 3 Residue-property plots [i](#)

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.

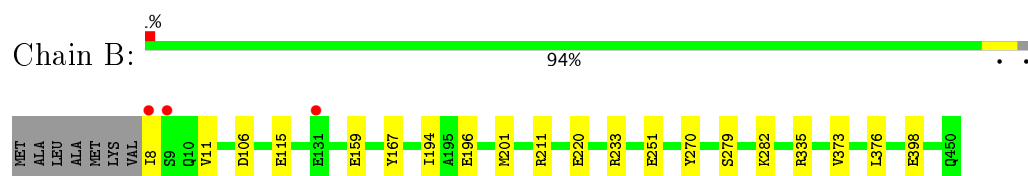
- Molecule 1: Metalloprotease TldD



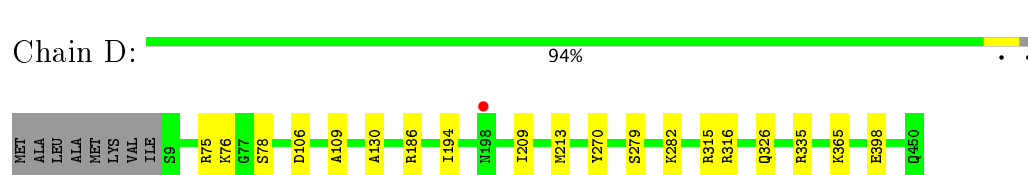
- Molecule 1: Metalloprotease TldD



- Molecule 2: Metalloprotease PmbA



- Molecule 2: Metalloprotease PmbA



- Molecule 3: ASP-ARG-VAL-TYR





- Molecule 3: ASP-ARG-VAL-TYR

Chain F:  25%  100%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	64.63Å 173.53Å 82.86Å 90.00° 90.03° 90.00°	Depositor
Resolution (Å)	74.77 – 1.25 74.77 – 1.25	Depositor EDS
% Data completeness (in resolution range)	99.8 (74.77-1.25) 99.8 (74.77-1.25)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.54 (at 1.25Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, $R_{free}$	0.149 , 0.182 0.159 , 0.190	Depositor DCC
$R_{free}$ test set	25030 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	10.2	Xtriage
Anisotropy	0.134	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 27.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.427 for h,-k,-l	Xtriage
Reported twinning fraction	0.610 for H, K, L 0.390 for -h,-k,l	Depositor
Outliers	0 of 500650 reflections	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	17131	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.14% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NA, ZN, EDO, MES

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	0.56	0/3886	0.83	6/5252 (0.1%)
1	C	0.55	0/3832	0.81	2/5180 (0.0%)
2	B	0.56	0/3601	0.74	1/4871 (0.0%)
2	D	0.56	0/3678	0.74	1/4973 (0.0%)
3	E	0.78	0/35	0.86	0/45
3	F	0.58	0/35	0.61	0/45
All	All	0.56	0/15067	0.78	10/20366 (0.0%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	63[A]	ASP	CB-CG-OD1	6.52	124.17	118.30
1	C	63[B]	ASP	CB-CG-OD1	6.52	124.17	118.30
1	A	146	ARG	NE-CZ-NH1	6.11	123.35	120.30
2	B	211	ARG	NE-CZ-NH1	5.76	123.18	120.30
1	A	362	ARG	NE-CZ-NH1	5.71	123.15	120.30
1	A	306	ARG	NE-CZ-NH2	-5.59	117.50	120.30
2	D	75	ARG	NE-CZ-NH2	-5.44	117.58	120.30
1	A	22	PHE	CB-CG-CD1	5.43	124.60	120.80
1	A	63	ASP	CB-CG-OD1	5.39	123.16	118.30
1	A	352	ARG	NE-CZ-NH2	-5.18	117.71	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	3833	0	3778	24	0
1	C	3779	0	3735	17	0
2	B	3541	0	3458	16	0
2	D	3614	0	3523	19	0
3	E	35	0	27	0	0
3	F	35	0	27	0	0
4	A	1	0	0	0	0
4	C	1	0	0	0	0
5	A	12	0	13	0	0
5	B	12	0	13	1	0
5	C	12	0	13	0	0
5	D	12	0	13	0	0
6	A	4	0	6	0	0
6	B	20	0	30	0	0
6	C	4	0	6	1	0
6	D	20	0	30	1	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
7	C	1	0	0	0	0
7	D	1	0	0	0	0
8	A	561	0	0	7	0
8	B	540	0	0	9	0
8	C	522	0	0	7	0
8	D	568	0	0	12	0
8	E	1	0	0	0	0
All	All	17131	0	14672	74	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 2.

All (74) 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)
2:D:316[A]:ARG:HD2	8:D:814:HOH:O	1.35	1.25
1:A:82[A]:ASP:OD2	8:A:602:HOH:O	1.54	1.21

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:340[B]:ARG:NH2	8:C:603:HOH:O	1.77	1.18
1:A:41[B]:GLN:NE2	8:A:603:HOH:O	1.76	1.16
2:D:398[B]:GLU:OE1	8:D:802:HOH:O	1.64	1.13
1:A:101[A]:ARG:HG2	1:A:101[A]:ARG:HH11	1.05	1.08
1:C:202[B]:SER:OG	8:C:979[B]:HOH:O	1.79	1.00
1:C:340[B]:ARG:CZ	8:C:603:HOH:O	2.11	0.92
1:A:101[A]:ARG:HG2	1:A:101[A]:ARG:NH1	1.73	0.91
2:D:316[B]:ARG:HG3	8:D:814:HOH:O	1.71	0.90
2:B:196:GLU:HG2	2:B:201:MET:HG2	1.54	0.89
2:D:76[B]:LYS:HE2	8:D:809:HOH:O	1.75	0.85
1:A:457[A]:GLU:OE1	8:A:604:HOH:O	1.95	0.84
2:D:106[B]:ASP:OD1	8:D:803:HOH:O	1.95	0.83
2:D:316[A]:ARG:CD	8:D:814:HOH:O	2.04	0.82
1:A:202[B]:SER:OG	8:A:1013[B]:HOH:O	1.97	0.82
2:B:115[A]:GLU:OE2	8:B:802[A]:HOH:O	2.00	0.80
2:D:316[B]:ARG:CG	8:D:814:HOH:O	2.31	0.74
1:A:101[A]:ARG:CG	1:A:101[A]:ARG:HH11	1.90	0.71
2:B:106[B]:ASP:OD1	8:B:803:HOH:O	2.10	0.69
2:D:109:ALA:O	8:D:804:HOH:O	2.14	0.66
2:B:8:ILE:HA	2:B:11[B]:VAL:HG12	1.77	0.66
1:C:63[A]:ASP:OD1	8:C:601:HOH:O	0.65	0.65
2:B:398[A]:GLU:OE2	8:B:805:HOH:O	2.14	0.65
1:A:66[B]:VAL:HG21	1:A:89:LEU:HD21	1.78	0.65
5:B:701:MES:O3S	8:B:804:HOH:O	2.13	0.65
1:C:340[B]:ARG:NE	6:C:503:EDO:O2	2.30	0.65
1:A:398[B]:ILE:HD13	8:B:830:HOH:O	1.97	0.64
2:B:398[B]:GLU:OE1	8:B:806:HOH:O	2.15	0.63
2:B:335:ARG:NH1	8:B:808:HOH:O	2.32	0.61
2:B:11[A]:VAL:HG22	2:B:167:TYR:CE2	2.35	0.61
1:C:340[B]:ARG:HG2	1:C:340[B]:ARG:HH11	1.66	0.61
1:C:66[A]:VAL:HG21	1:C:89:LEU:HD21	1.84	0.58
1:A:457[A]:GLU:CD	8:A:604:HOH:O	2.39	0.56
1:A:82[A]:ASP:CG	8:A:602:HOH:O	2.17	0.56
1:A:66[B]:VAL:HG21	1:A:89:LEU:CD2	2.35	0.55
2:D:186[B]:ARG:HE	2:D:209:ILE:HD11	1.71	0.55
2:B:233[B]:ARG:NH2	8:B:809:HOH:O	2.38	0.54
2:D:213[A]:MET:O	8:D:805[A]:HOH:O	2.18	0.54
1:A:278:THR:HG22	2:B:194[A]:ILE:HD12	1.88	0.54
1:C:278:THR:HG22	2:D:194[B]:ILE:HD12	1.90	0.54
1:C:357:HIS:HD2	8:C:1011:HOH:O	1.91	0.52
2:B:8:ILE:CA	2:B:11[B]:VAL:HG12	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:259[B]:VAL:HG23	1:A:405:PHE:HD2	1.76	0.51
2:B:220:GLU:HG2	6:D:704[B]:EDO:C1	2.41	0.50
1:A:44:TYR:CD2	1:A:62:ILE:HD12	2.48	0.48
1:C:66[A]:VAL:HG21	1:C:89:LEU:CD2	2.43	0.48
2:D:316[A]:ARG:CG	8:D:814:HOH:O	2.53	0.47
1:C:401:ASP:O	1:C:430:SER:HA	2.14	0.47
1:A:401:ASP:O	1:A:430[B]:SER:HA	2.14	0.47
2:D:130[B]:ALA:HB2	2:D:213[B]:MET:HG3	1.97	0.47
1:A:401:ASP:O	1:A:430[A]:SER:HA	2.14	0.46
2:D:316[A]:ARG:HG3	8:D:814:HOH:O	2.15	0.46
1:A:60:TYR:CE2	1:A:62:ILE:HD11	2.51	0.46
2:B:159:GLU:HG3	2:B:194[B]:ILE:HD11	1.98	0.46
2:D:279:SER:HA	2:D:282:LYS:HD3	1.98	0.45
1:A:44:TYR:CD2	1:A:62:ILE:CD1	2.99	0.45
1:A:31:ARG:HB3	1:A:100[A]:VAL:HG23	1.99	0.45
1:C:340[B]:ARG:HG2	1:C:340[B]:ARG:NH1	2.31	0.44
2:D:315:ARG:O	2:D:316[B]:ARG:NE	2.45	0.43
1:A:220:GLU:HG3	1:A:225:ALA:HB2	1.99	0.43
2:D:335:ARG:NH1	8:D:817:HOH:O	2.51	0.43
1:C:330[A]:LYS:HE2	8:C:913[A]:HOH:O	2.19	0.43
1:A:18:HIS:CD2	1:A:22:PHE:CZ	3.07	0.42
1:C:31:ARG:HB3	1:C:100[A]:VAL:HG23	2.01	0.42
2:B:279:SER:HA	2:B:282:LYS:HD3	2.01	0.42
1:C:259[B]:VAL:HG23	1:C:405:PHE:HD2	1.85	0.41
1:C:321:ASN:HB3	8:C:907[A]:HOH:O	2.20	0.41
1:A:357:HIS:HD2	8:A:1048:HOH:O	2.01	0.41
2:B:251[A]:GLU:OE2	8:B:807:HOH:O	2.22	0.41
2:B:373:VAL:HG11	2:B:376:LEU:HD21	2.02	0.41
1:C:59:SER:HA	2:D:78:SER:O	2.22	0.40
1:A:159:LEU:HG	1:A:210:TYR:CE1	2.56	0.40
2:D:316[A]:ARG:HD3	2:D:326:GLN:OE1	2.22	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	508/495 (103%)	493 (97%)	15 (3%)	0	100	100
1	C	502/495 (101%)	489 (97%)	13 (3%)	0	100	100
2	B	468/450 (104%)	460 (98%)	8 (2%)	0	100	100
2	D	477/450 (106%)	469 (98%)	8 (2%)	0	100	100
3	E	2/4 (50%)	2 (100%)	0	0	100	100
3	F	2/4 (50%)	2 (100%)	0	0	100	100
All	All	1959/1898 (103%)	1915 (98%)	44 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	409/396 (103%)	404 (99%)	5 (1%)	75	40
1	C	401/396 (101%)	397 (99%)	4 (1%)	80	47
2	B	375/360 (104%)	374 (100%)	1 (0%)	94	80
2	D	385/360 (107%)	383 (100%)	2 (0%)	91	69
3	E	3/4 (75%)	3 (100%)	0	100	100
3	F	3/4 (75%)	3 (100%)	0	100	100
All	All	1576/1520 (104%)	1564 (99%)	12 (1%)	85	57

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	101[A]	ARG
1	A	101[B]	ARG
1	A	120	TYR
1	A	208	PHE

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	405	PHE
2	B	270	TYR
1	C	120	TYR
1	C	198	GLU
1	C	208	PHE
1	C	405	PHE
2	D	270	TYR
2	D	365	LYS

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	357	HIS
2	B	356	GLN
2	D	379	GLN

### 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 22 ligands modelled in this entry, 6 are monoatomic - leaving 16 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
5	MES	A	502	-	12,12,12	0.70	0	14,16,16	0.74	1 (7%)
6	EDO	A	503	-	3,3,3	0.77	0	2,2,2	0.20	0
5	MES	B	701	-	12,12,12	0.76	0	14,16,16	0.60	0
6	EDO	B	702	-	3,3,3	0.61	0	2,2,2	0.16	0
6	EDO	B	703[A]	-	3,3,3	0.41	0	2,2,2	0.50	0
6	EDO	B	703[B]	-	3,3,3	0.62	0	2,2,2	0.26	0
6	EDO	B	704	-	3,3,3	0.49	0	2,2,2	0.54	0
6	EDO	B	705	-	3,3,3	0.53	0	2,2,2	0.34	0
5	MES	C	502	-	12,12,12	0.85	0	14,16,16	0.55	0
6	EDO	C	503	-	3,3,3	0.74	0	2,2,2	0.39	0
5	MES	D	701	-	12,12,12	0.68	0	14,16,16	0.59	0
6	EDO	D	702	-	3,3,3	0.49	0	2,2,2	0.45	0
6	EDO	D	703	-	3,3,3	0.36	0	2,2,2	0.52	0
6	EDO	D	704[A]	-	3,3,3	0.41	0	2,2,2	0.32	0
6	EDO	D	704[B]	-	3,3,3	0.21	0	2,2,2	0.54	0
6	EDO	D	705	-	3,3,3	0.52	0	2,2,2	0.45	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	MES	A	502	-	-	0/6/14/14	0/1/1/1
6	EDO	A	503	-	-	0/1/1/1	0/0/0/0
5	MES	B	701	-	-	0/6/14/14	0/1/1/1
6	EDO	B	702	-	-	0/1/1/1	0/0/0/0
6	EDO	B	703[A]	-	-	0/1/1/1	0/0/0/0
6	EDO	B	703[B]	-	-	0/1/1/1	0/0/0/0
6	EDO	B	704	-	-	0/1/1/1	0/0/0/0
6	EDO	B	705	-	-	0/1/1/1	0/0/0/0
5	MES	C	502	-	-	0/6/14/14	0/1/1/1
6	EDO	C	503	-	-	0/1/1/1	0/0/0/0
5	MES	D	701	-	-	0/6/14/14	0/1/1/1
6	EDO	D	702	-	-	0/1/1/1	0/0/0/0
6	EDO	D	703	-	-	0/1/1/1	0/0/0/0
6	EDO	D	704[A]	-	-	0/1/1/1	0/0/0/0
6	EDO	D	704[B]	-	-	0/1/1/1	0/0/0/0
6	EDO	D	705	-	-	0/1/1/1	0/0/0/0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
5	A	502	MES	C7-N4-C3	2.33	117.23	111.26

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	701	MES	1	0
6	C	503	EDO	1	0
6	D	704[B]	EDO	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 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	480/495 (96%)	-0.50	5 (1%) 82 78	6, 11, 20, 34	0
1	C	480/495 (96%)	-0.45	4 (0%) 86 82	7, 12, 23, 37	0
2	B	443/450 (98%)	-0.52	3 (0%) 87 83	7, 11, 20, 41	0
2	D	442/450 (98%)	-0.52	1 (0%) 94 92	7, 11, 20, 51	0
3	E	4/4 (100%)	1.10	1 (25%) 1 1	9, 12, 16, 18	4 (100%)
3	F	4/4 (100%)	1.48	1 (25%) 1 1	9, 11, 14, 19	4 (100%)
All	All	1853/1898 (97%)	-0.49	15 (0%) 86 82	6, 11, 21, 51	8 (0%)

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	8	ILE	5.8
3	F	601	ASP	4.7
1	A	2	SER	4.2
1	C	2	SER	3.5
1	A	123	VAL	3.5
1	C	108	VAL	3.4
3	E	601	ASP	3.3
1	A	126	LEU	3.2
1	C	107	LYS	2.8
2	D	198	ASN	2.8
1	C	126	LEU	2.4
1	A	44	TYR	2.4
2	B	131[A]	GLU	2.4
2	B	9	SER	2.1
1	A	127	GLN	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 6.3 Carbohydrates ⓘ

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
5	MES	B	701	12/12	0.89	0.16	6.04	8,12,14,15	12
5	MES	D	701	12/12	0.92	0.13	5.77	6,12,13,14	12
6	EDO	B	702	4/4	0.95	0.10	3.80	13,14,15,17	0
6	EDO	D	702	4/4	0.95	0.12	3.10	15,16,16,18	0
6	EDO	D	703	4/4	0.95	0.08	1.21	13,13,15,17	0
5	MES	C	502	12/12	0.93	0.14	0.86	16,19,22,27	0
6	EDO	A	503	4/4	0.96	0.07	0.77	15,18,23,24	0
6	EDO	B	703[B]	4/4	0.95	0.07	0.66	8,15,16,17	4
6	EDO	B	703[A]	4/4	0.95	0.07	0.56	9,13,15,15	4
6	EDO	C	503	4/4	0.92	0.08	0.18	17,20,21,23	0
5	MES	A	502	12/12	0.99	0.05	-0.43	11,13,14,14	0
4	ZN	C	501	1/1	1.00	0.04	-0.68	9,9,9,9	0
4	ZN	A	501	1/1	1.00	0.03	-1.21	7,7,7,7	0
6	EDO	D	704[A]	4/4	0.93	0.12	-	10,14,22,31	4
6	EDO	D	704[B]	4/4	0.93	0.12	-	12,14,22,27	4
7	NA	C	504	1/1	0.99	0.10	-	17,17,17,17	0
7	NA	D	706	1/1	0.98	0.08	-	23,23,23,23	0
6	EDO	B	704	4/4	0.93	0.14	-	15,18,18,24	0
7	NA	A	504	1/1	0.99	0.07	-	16,16,16,16	0
6	EDO	B	705	4/4	0.90	0.11	-	24,24,26,28	0
6	EDO	D	705	4/4	0.95	0.10	-	20,25,31,38	0
7	NA	B	706	1/1	0.97	0.18	-	19,19,19,19	0

## 6.5 Other polymers

There are no such residues in this entry.