



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 21, 2016 – 08:42 PM EDT

PDB ID : 4XGV  
Title : Crystal structure of Escherichia coli Flavin trafficking protein, an FMN transferase  
Authors : Tomchick, D.R.; Brautigam, C.A.; Deka, R.K.; Norgard, M.V.  
Deposited on : 2015-01-02  
Resolution : 1.88 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 : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20027107  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0122  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20027107

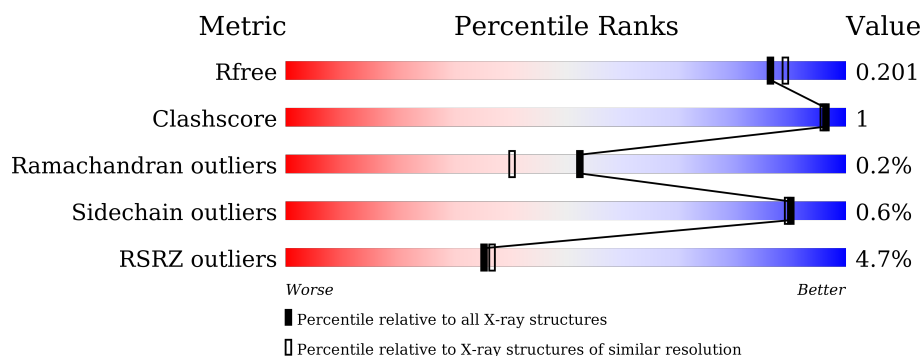
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.88 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))
$R_{free}$	91344	6965 (1.90-1.86)
Clashscore	102246	7778 (1.90-1.86)
Ramachandran outliers	100387	7691 (1.90-1.86)
Sidechain outliers	100360	7692 (1.90-1.86)
RSRZ outliers	91569	6979 (1.90-1.86)

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	340	<div> <div>4%</div> <div>86%</div> <div>9%</div> </div>
1	B	340	<div> <div>5%</div> <div>87%</div> <div>9%</div> </div>
1	C	340	<div> <div>4%</div> <div>88%</div> <div>9%</div> </div>
1	D	340	<div> <div>4%</div> <div>87%</div> <div>10%</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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NA	A	502	-	-	-	X
4	EDO	A	504	-	-	-	X
4	EDO	B	504	-	-	-	X
4	EDO	D	503	-	-	-	X
4	EDO	D	504	-	-	-	X
5	ACT	A	507	-	-	-	X

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 19989 atoms, of which 9603 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 FAD:protein FMN transferase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	309	Total	C	H	N	O	S	0	3	0
			4793	1511	2393	414	465	10			
1	B	309	Total	C	H	N	O	S	0	4	0
			4787	1510	2390	409	468	10			
1	C	309	Total	C	H	N	O	S	0	1	0
			4776	1506	2385	410	465	10			
1	D	305	Total	C	H	N	O	S	0	2	0
			4714	1485	2354	406	459	10			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP P0AB85
A	333	LEU	-	expression tag	UNP P0AB85
A	334	GLU	-	expression tag	UNP P0AB85
A	335	HIS	-	expression tag	UNP P0AB85
A	336	HIS	-	expression tag	UNP P0AB85
A	337	HIS	-	expression tag	UNP P0AB85
A	338	HIS	-	expression tag	UNP P0AB85
A	339	HIS	-	expression tag	UNP P0AB85
A	340	HIS	-	expression tag	UNP P0AB85
B	1	MET	-	initiating methionine	UNP P0AB85
B	333	LEU	-	expression tag	UNP P0AB85
B	334	GLU	-	expression tag	UNP P0AB85
B	335	HIS	-	expression tag	UNP P0AB85
B	336	HIS	-	expression tag	UNP P0AB85
B	337	HIS	-	expression tag	UNP P0AB85
B	338	HIS	-	expression tag	UNP P0AB85
B	339	HIS	-	expression tag	UNP P0AB85
B	340	HIS	-	expression tag	UNP P0AB85
C	1	MET	-	initiating methionine	UNP P0AB85
C	333	LEU	-	expression tag	UNP P0AB85
C	334	GLU	-	expression tag	UNP P0AB85

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Chain	Residue	Modelled	Actual	Comment	Reference
C	335	HIS	-	expression tag	UNP P0AB85
C	336	HIS	-	expression tag	UNP P0AB85
C	337	HIS	-	expression tag	UNP P0AB85
C	338	HIS	-	expression tag	UNP P0AB85
C	339	HIS	-	expression tag	UNP P0AB85
C	340	HIS	-	expression tag	UNP P0AB85
D	1	MET	-	initiating methionine	UNP P0AB85
D	333	LEU	-	expression tag	UNP P0AB85
D	334	GLU	-	expression tag	UNP P0AB85
D	335	HIS	-	expression tag	UNP P0AB85
D	336	HIS	-	expression tag	UNP P0AB85
D	337	HIS	-	expression tag	UNP P0AB85
D	338	HIS	-	expression tag	UNP P0AB85
D	339	HIS	-	expression tag	UNP P0AB85
D	340	HIS	-	expression tag	UNP P0AB85

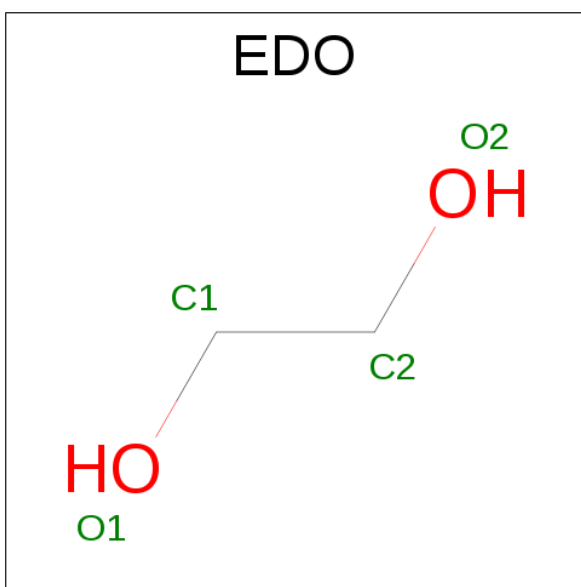
- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Ca 1 1	0	0
2	A	1	Total Ca 1 1	0	0
2	D	1	Total Ca 1 1	0	0
2	C	1	Total Ca 1 1	0	0

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

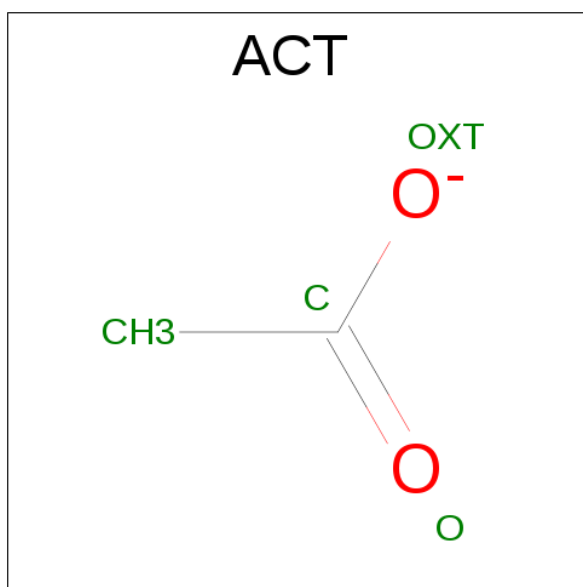
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Na 1 1	0	0
3	C	1	Total Na 1 1	0	0

- Molecule 4 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
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		
4	C	1	Total	C	H	O	0	0
			10	2	6	2		
4	D	1	Total	C	H	O	0	0
			10	2	6	2		
4	D	1	Total	C	H	O	0	0
			10	2	6	2		
4	D	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	H	O	0	0
			7	2	3	2		

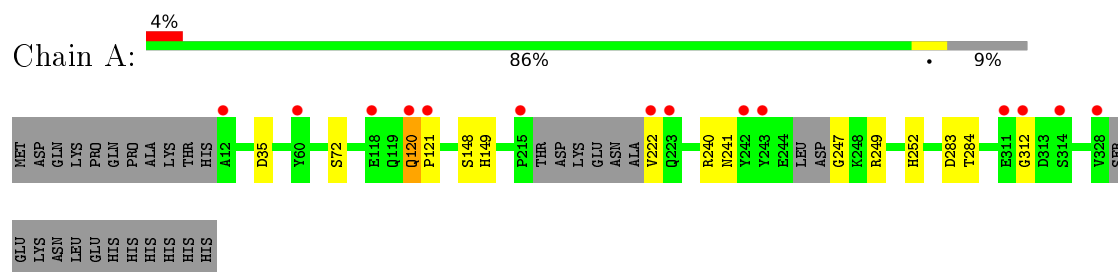
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	179	Total	O	0	0
			179	179		
6	B	194	Total	O	0	0
			194	194		
6	C	192	Total	O	0	0
			192	192		
6	D	211	Total	O	0	0
			211	211		

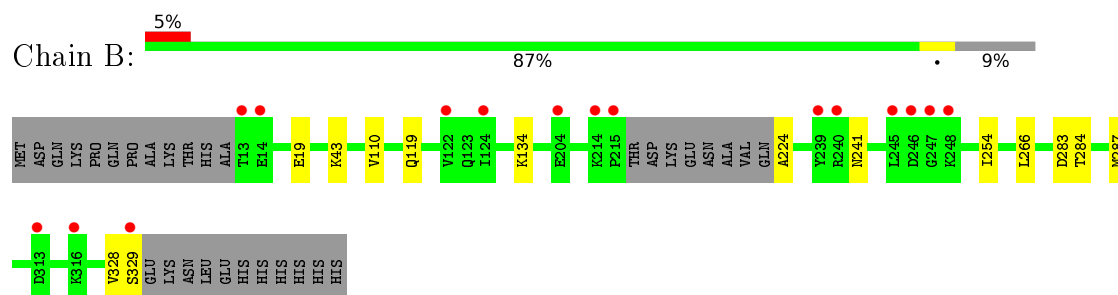
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

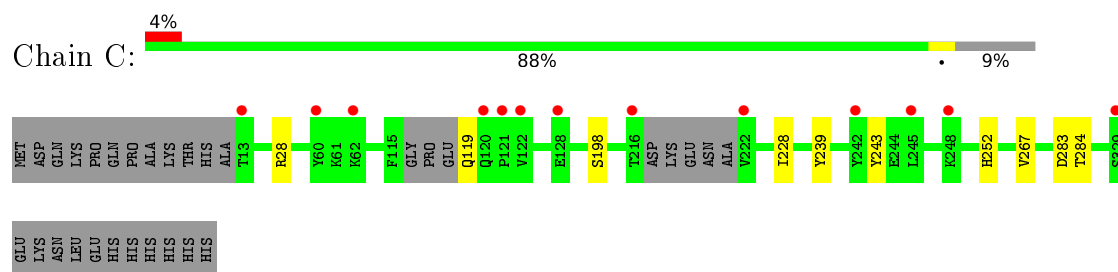
- Molecule 1: FAD:protein FMN transferase



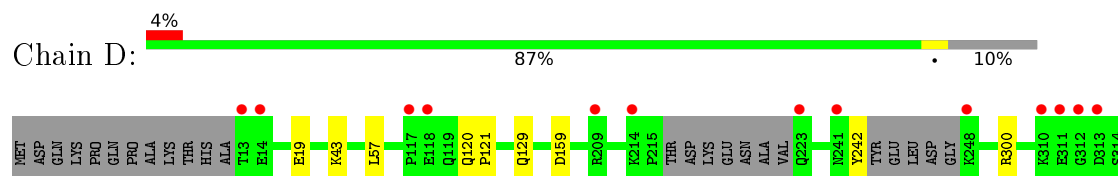
- Molecule 1: FAD:protein FMN transferase



- Molecule 1: FAD:protein FMN transferase



- Molecule 1: FAD:protein FMN transferase



F215	
S229	
GLU	
LYS	
ASN	
LEU	
GLU	
HIS	
HIS	
HIS	
HIS	
HIS	

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	56.20Å 70.64Å 85.96Å 75.70° 72.45° 69.28°	Depositor
Resolution (Å)	31.51 – 1.88 31.51 – 1.88	Depositor EDS
% Data completeness (in resolution range)	96.4 (31.51-1.88) 91.4 (31.51-1.88)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.14 (at 1.88Å)	Xtriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.163 , 0.201 0.163 , 0.201	Depositor DCC
$R_{free}$ test set	4542 reflections (5.00%)	DCC
Wilson B-factor (Å <sup>2</sup> )	21.4	Xtriage
Anisotropy	0.219	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.42 , 40.9	EDS
Estimated twinning fraction	0.017 for h,h-k,h-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 90898 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	19989	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 5.35% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: NA, CA, EDO, ACT

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	0.30	0/2457	0.50	0/3330
1	B	0.29	0/2459	0.49	0/3336
1	C	0.30	0/2439	0.49	0/3306
1	D	0.32	0/2412	0.51	0/3270
All	All	0.30	0/9767	0.50	0/13242

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	2400	2393	2386	7	0
1	B	2397	2390	2381	8	0
1	C	2391	2385	2382	5	0
1	D	2360	2354	2349	7	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	1	0	0	0	0
4	A	16	24	24	1	0
4	B	20	30	30	0	0
4	C	4	6	6	0	0
4	D	12	18	18	1	0
5	A	4	3	3	0	0
6	A	179	0	0	3	0
6	B	194	0	0	2	0
6	C	192	0	0	1	0
6	D	211	0	0	2	0
All	All	10386	9603	9579	27	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 1.

All (27) 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:222:VAL:N	6:A:604:HOH:O	2.33	0.60
1:A:148:SER:O	6:A:601:HOH:O	2.16	0.59
1:A:247:GLY:N	6:A:606:HOH:O	2.37	0.56
1:C:28:ARG:NH1	6:C:601:HOH:O	2.39	0.56
1:B:134:LYS:NZ	6:B:607:HOH:O	2.41	0.54
1:B:224:ALA:N	6:B:608:HOH:O	2.42	0.53
1:A:240:ARG:O	1:A:249:ARG:NH2	2.45	0.49
1:B:19:GLU:O	1:B:43:LYS:NZ	2.50	0.45
1:D:300:ARG:NH2	6:D:611:HOH:O	2.49	0.45
1:A:283:ASP:OD1	1:A:284:THR:N	2.50	0.45
1:D:120:GLN:HB2	1:D:121:PRO:HD2	2.00	0.44
1:D:120:GLN:HB2	1:D:121:PRO:CD	2.48	0.44
1:B:266:LEU:HD23	1:B:287:MET:HA	2.00	0.44
1:A:120:GLN:HB2	1:A:121:PRO:HD3	1.99	0.43
1:D:129:GLN:NE2	6:D:608:HOH:O	2.41	0.43
1:D:159:ASP:OD1	1:D:159:ASP:N	2.49	0.43
1:C:239:TYR:HA	1:C:267:VAL:CG1	2.49	0.43
1:B:283:ASP:OD1	1:B:284:THR:N	2.52	0.42
1:B:328:VAL:HG12	1:B:329:SER:N	2.35	0.42
1:A:252:HIS:HB2	4:A:503:EDO:H11	1.99	0.42
1:D:57:LEU:HB2	4:D:504:EDO:H11	2.02	0.42
1:C:198:SER:HB3	1:C:228:ILE:HG13	2.02	0.42
1:C:119:GLN:HG3	1:C:243:TYR:CD2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:283:ASP:OD1	1:C:284:THR:N	2.53	0.41
1:B:119:GLN:NE2	1:B:241:ASN:O	2.54	0.41
1:D:19:GLU:O	1:D:43:LYS:NZ	2.52	0.41
1:B:110:VAL:HA	1:B:254:ILE:CD1	2.51	0.41

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	306/340 (90%)	299 (98%)	5 (2%)	2 (1%)	26	13
1	B	309/340 (91%)	304 (98%)	5 (2%)	0	100	100
1	C	304/340 (89%)	299 (98%)	5 (2%)	0	100	100
1	D	301/340 (88%)	296 (98%)	5 (2%)	0	100	100
All	All	1220/1360 (90%)	1198 (98%)	20 (2%)	2 (0%)	52	40

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	120	GLN
1	A	312	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	262/288 (91%)	258 (98%)	4 (2%)	72	66
1	B	264/288 (92%)	264 (100%)	0	100	100
1	C	262/288 (91%)	261 (100%)	1 (0%)	93	93
1	D	259/288 (90%)	258 (100%)	1 (0%)	93	93
All	All	1047/1152 (91%)	1041 (99%)	6 (1%)	90	89

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	35	ASP
1	A	72	SER
1	A	149	HIS
1	A	241	ASN
1	C	252	HIS
1	D	242	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 20 ligands modelled in this entry, 6 are monoatomic - leaving 14 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	$\# Z  > 2$
4	EDO	A	503	-	3,3,3	0.52	0	2,2,2	0.12	0
4	EDO	A	504	-	3,3,3	0.47	0	2,2,2	0.43	0
4	EDO	A	505	-	3,3,3	0.50	0	2,2,2	0.29	0
4	EDO	A	506	-	3,3,3	0.42	0	2,2,2	0.41	0
5	ACT	A	507	-	0,3,3	0.00	-	0,3,3	0.00	-
4	EDO	B	502	-	3,3,3	0.43	0	2,2,2	0.35	0
4	EDO	B	503	-	3,3,3	0.44	0	2,2,2	0.48	0
4	EDO	B	504	-	3,3,3	0.48	0	2,2,2	0.27	0
4	EDO	B	505	-	3,3,3	0.42	0	2,2,2	0.38	0
4	EDO	B	506	-	3,3,3	0.40	0	2,2,2	0.51	0
4	EDO	C	503	-	3,3,3	0.45	0	2,2,2	0.41	0
4	EDO	D	502	-	3,3,3	0.46	0	2,2,2	0.40	0
4	EDO	D	503	-	3,3,3	0.39	0	2,2,2	0.46	0
4	EDO	D	504	-	3,3,3	0.39	0	2,2,2	0.31	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
4	EDO	A	503	-	-	0/1/1/1	0/0/0/0
4	EDO	A	504	-	-	0/1/1/1	0/0/0/0
4	EDO	A	505	-	-	0/1/1/1	0/0/0/0
4	EDO	A	506	-	-	0/1/1/1	0/0/0/0
5	ACT	A	507	-	-	0/0/0/0	0/0/0/0
4	EDO	B	502	-	-	0/1/1/1	0/0/0/0
4	EDO	B	503	-	-	0/1/1/1	0/0/0/0
4	EDO	B	504	-	-	0/1/1/1	0/0/0/0
4	EDO	B	505	-	-	0/1/1/1	0/0/0/0
4	EDO	B	506	-	-	0/1/1/1	0/0/0/0
4	EDO	C	503	-	-	0/1/1/1	0/0/0/0
4	EDO	D	502	-	-	0/1/1/1	0/0/0/0
4	EDO	D	503	-	-	0/1/1/1	0/0/0/0
4	EDO	D	504	-	-	0/1/1/1	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	503	EDO	1	0
4	D	504	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	309/340 (90%)	-0.10	14 (4%) 37 39	14, 25, 63, 97	0
1	B	309/340 (90%)	-0.08	16 (5%) 31 33	15, 25, 63, 86	0
1	C	309/340 (90%)	-0.07	13 (4%) 40 42	15, 27, 59, 96	0
1	D	305/340 (89%)	-0.20	15 (4%) 33 35	13, 22, 63, 101	0
All	All	1232/1360 (90%)	-0.11	58 (4%) 35 37	13, 25, 63, 101	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	222	VAL	8.7
1	D	13	THR	6.2
1	C	60	TYR	5.4
1	A	120	GLN	5.0
1	A	215	PRO	4.8
1	A	121	PRO	4.6
1	B	204	GLU	4.5
1	A	60	TYR	4.4
1	C	122	VAL	4.4
1	B	215	PRO	4.3
1	C	13	THR	4.3
1	A	312	GLY	4.3
1	D	313	ASP	4.2
1	A	222	VAL	4.2
1	C	62	LYS	4.0
1	B	13	THR	3.9
1	A	243	TYR	3.8
1	C	242	TYR	3.7
1	D	214	LYS	3.6
1	B	245	LEU	3.6
1	B	247	GLY	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	246	ASP	3.4
1	B	14	GLU	3.4
1	B	240	ARG	3.4
1	D	312	GLY	3.4
1	D	311	GLU	3.4
1	D	223	GLN	3.1
1	B	248	LYS	3.1
1	D	248	LYS	3.0
1	D	117	PRO	3.0
1	B	124	ILE	3.0
1	C	216	THR	3.0
1	C	329	SER	2.9
1	D	118	GLU	2.9
1	A	311	GLU	2.9
1	A	12	ALA	2.7
1	C	128	GLU	2.7
1	B	239	TYR	2.7
1	A	242	TYR	2.4
1	C	120	GLN	2.4
1	B	313	ASP	2.3
1	A	314	SER	2.3
1	D	14	GLU	2.3
1	A	223	GLN	2.3
1	B	214	LYS	2.3
1	B	316	LYS	2.2
1	C	245	LEU	2.2
1	D	329	SER	2.2
1	D	209	ARG	2.1
1	B	329	SER	2.1
1	B	122	VAL	2.1
1	C	248	LYS	2.1
1	D	241	ASN	2.0
1	A	328	VAL	2.0
1	D	315	PHE	2.0
1	C	121	PRO	2.0
1	D	310	LYS	2.0
1	A	118	GLU	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
4	EDO	D	504	4/4	0.73	0.22	7.60	49,68,76,82	0
4	EDO	A	504	4/4	0.92	0.13	3.19	32,38,40,49	0
3	NA	A	502	1/1	0.93	0.22	3.05	36,36,36,36	0
4	EDO	D	503	4/4	0.92	0.18	2.76	33,39,47,48	0
5	ACT	A	507	4/4	0.87	0.19	2.65	39,46,47,50	0
4	EDO	B	504	4/4	0.81	0.18	2.26	35,42,50,50	0
4	EDO	B	506	4/4	0.89	0.13	1.43	28,38,45,47	0
3	NA	C	502	1/1	0.94	0.15	0.78	31,31,31,31	0
4	EDO	A	503	4/4	0.86	0.14	0.58	33,44,54,65	0
4	EDO	B	505	4/4	0.89	0.12	0.56	45,54,58,61	0
4	EDO	C	503	4/4	0.94	0.10	0.40	19,30,39,46	0
4	EDO	B	503	4/4	0.96	0.12	0.30	20,32,44,53	0
4	EDO	B	502	4/4	0.96	0.10	0.14	21,30,46,55	0
4	EDO	D	502	4/4	0.94	0.10	-0.21	24,29,30,30	0
4	EDO	A	505	4/4	0.94	0.08	-2.12	32,39,40,40	0
2	CA	A	501	1/1	0.99	0.04	-3.18	20,20,20,20	0
2	CA	B	501	1/1	0.99	0.02	-3.60	22,22,22,22	0
2	CA	D	501	1/1	1.00	0.05	-4.13	20,20,20,20	0
2	CA	C	501	1/1	0.99	0.03	-4.73	26,26,26,26	0
4	EDO	A	506	4/4	0.84	0.20	-	42,50,56,58	0

### 6.5 Other polymers ⓘ

There are no such residues in this entry.