



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 01:27 AM GMT

PDB ID : 2D0V  
Title : Crystal structure of methanol dehydrogenase from *Hyphomicrobium denitrificans*  
Authors : Nojiri, M.; Hira, D.; Yamaguchi, K.; Suzuki, S.  
Deposited on : 2005-08-09  
Resolution : 2.49 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 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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) : trunk26865

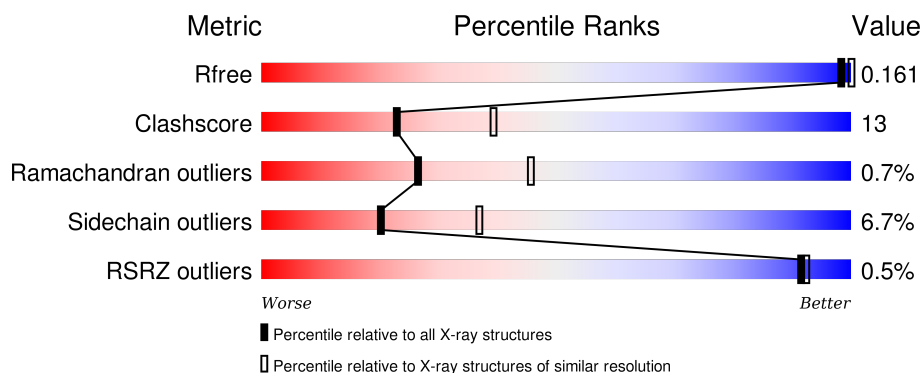
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.49 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	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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	597	<div> <div></div> <div>73% 23% .</div> </div>
1	D	597	<div> <div>%</div> <div>68% 29% .</div> </div>
1	I	597	<div> <div></div> <div>70% 26% .</div> </div>
2	B	72	<div> <div>%</div> <div>60% 31% 7% .</div> </div>
2	E	72	<div> <div>3%</div> <div>57% 35% . 6%</div> </div>

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Mol	Chain	Length	Quality of chain
2	J	72	 56% 33% 6% . .

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
3	CA	A	775	-	-	-	X
4	PQQ	A	601	-	-	-	X
4	PQQ	D	601	-	-	-	X
4	PQQ	I	601	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 16491 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 methanol dehydrogenase large subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	597	Total	C	N	O	S	0	0	0
			4668	2962	797	889	20			
1	D	597	Total	C	N	O	S	0	0	0
			4668	2962	797	889	20			
1	I	595	Total	C	N	O	S	0	0	0
			4655	2954	794	887	20			

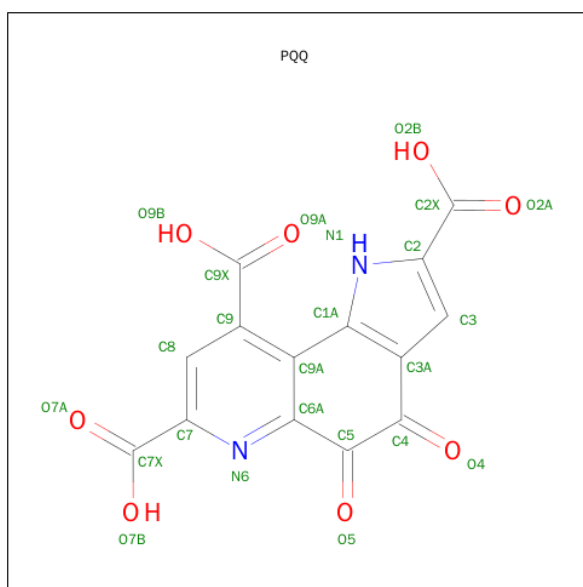
- Molecule 2 is a protein called methanol dehydrogenase small subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	70	Total	C	N	O	S	0	0	0
			572	359	105	106	2			
2	E	68	Total	C	N	O	S	0	0	0
			554	347	101	104	2			
2	J	70	Total	C	N	O	S	0	0	0
			572	359	105	106	2			

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	I	1	Total	Ca	0	0
			1	1		
3	A	1	Total	Ca	0	0
			1	1		
3	D	1	Total	Ca	0	0
			1	1		

- Molecule 4 is PYRROLOQUINOLINE QUINONE (three-letter code: PQQ) (formula: C<sub>14</sub>H<sub>6</sub>N<sub>2</sub>O<sub>8</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			24	14	2	8		
4	D	1	Total	C	N	O	0	0
			24	14	2	8		
4	I	1	Total	C	N	O	0	0
			24	14	2	8		

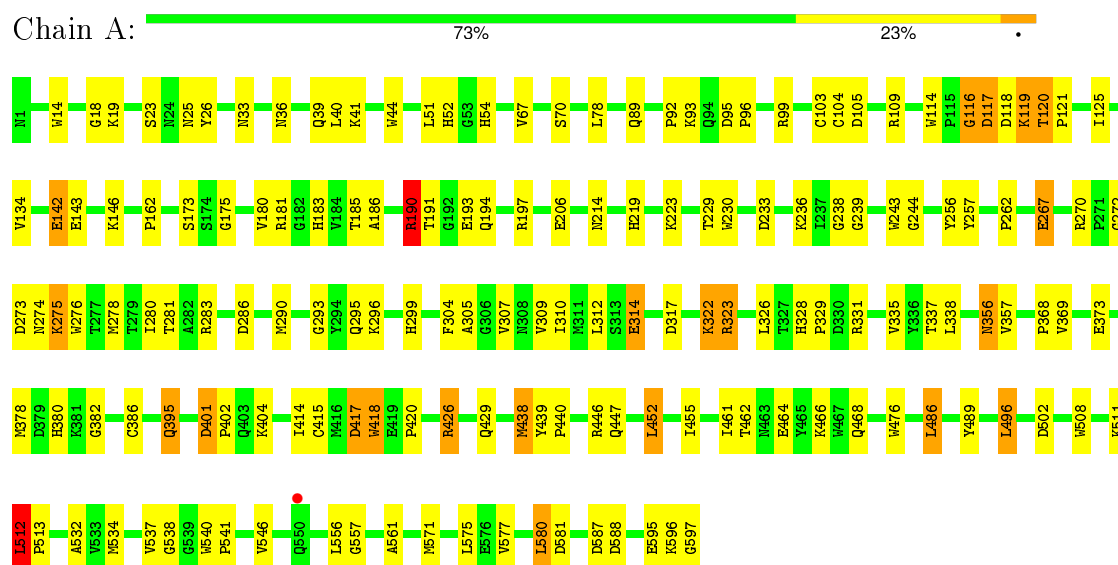
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	278	Total	O	0	0
			278	278		
5	B	31	Total	O	0	0
			31	31		
5	D	188	Total	O	0	0
			188	188		
5	E	31	Total	O	0	0
			31	31		
5	I	171	Total	O	0	0
			171	171		
5	J	28	Total	O	0	0
			28	28		

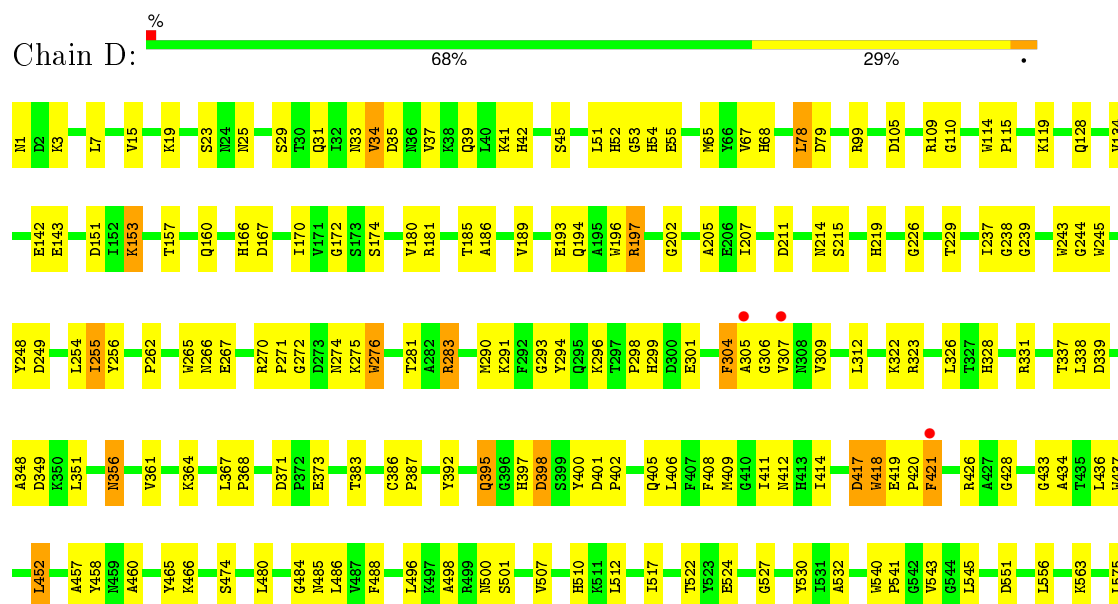
### 3 Residue-property plots

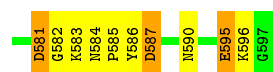
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: methanol dehydrogenase large subunit

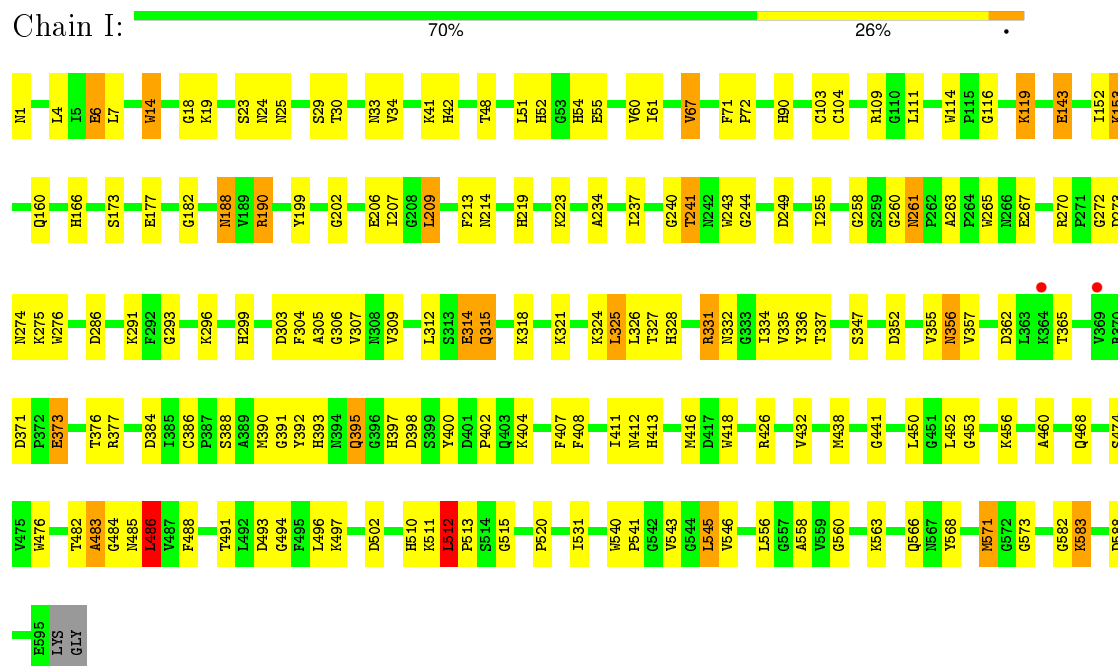


- Molecule 1: methanol dehydrogenase large subunit

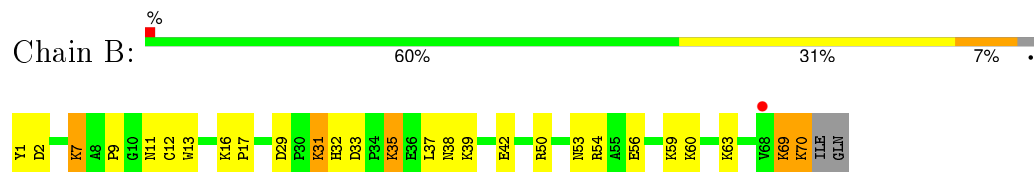




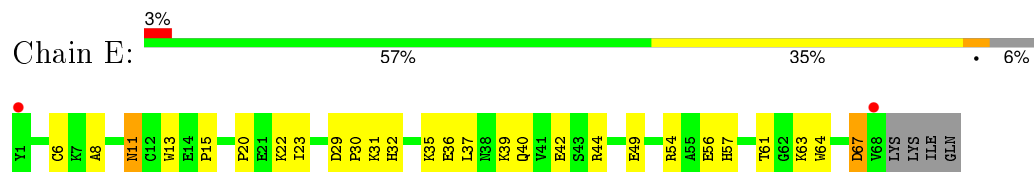
• Molecule 1: methanol dehydrogenase large subunit



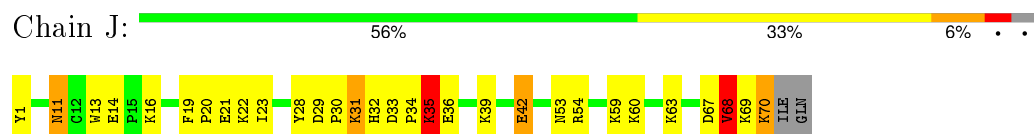
• Molecule 2: methanol dehydrogenase small subunit



• Molecule 2: methanol dehydrogenase small subunit



• Molecule 2: methanol dehydrogenase small subunit



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	291.32Å 64.00Å 109.94Å 90.00° 105.74° 90.00°	Depositor
Resolution (Å)	44.60 – 2.49 44.60 – 2.49	Depositor EDS
% Data completeness (in resolution range)	99.6 (44.60-2.49) 95.4 (44.60-2.49)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.64 (at 2.48Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.149 , 0.247 0.162 , 0.161	Depositor DCC
$R_{free}$ test set	6603 reflections (11.23%)	DCC
Wilson B-factor (Å <sup>2</sup> )	31.6	Xtriage
Anisotropy	0.561	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 39.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 65421 reflections (0.002%)	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	16491	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.32% 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: PQQ, CA

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	1.30	12/4803 (0.2%)	1.17	21/6534 (0.3%)
1	D	1.28	12/4803 (0.2%)	1.16	22/6534 (0.3%)
1	I	1.26	10/4790 (0.2%)	1.14	20/6518 (0.3%)
2	B	1.36	4/589 (0.7%)	1.18	6/789 (0.8%)
2	E	1.26	1/571 (0.2%)	1.10	1/767 (0.1%)
2	J	1.33	2/589 (0.3%)	1.06	1/789 (0.1%)
All	All	1.28	41/16145 (0.3%)	1.15	71/21931 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	1	1

The worst 5 of 41 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	143	GLU	CG-CD	8.78	1.65	1.51
1	I	314	GLU	CG-CD	8.68	1.65	1.51
2	J	42	GLU	CG-CD	8.17	1.64	1.51
1	D	39	GLN	CG-CD	7.89	1.69	1.51
1	I	143	GLU	CD-OE2	6.88	1.33	1.25

The worst 5 of 71 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	190	ARG	NE-CZ-NH2	-13.46	113.57	120.30
1	A	190	ARG	NE-CZ-NH1	11.79	126.20	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	446	ARG	NE-CZ-NH1	-9.81	115.39	120.30
1	D	167	ASP	CB-CG-OD1	9.02	126.42	118.30
1	A	275	LYS	C-N-CA	8.58	143.15	121.70

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	276	TRP	CA

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	190	ARG	Sidechain

## 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	4668	0	4426	112	0
1	D	4668	0	4426	107	0
1	I	4655	0	4410	140	0
2	B	572	0	553	19	0
2	E	554	0	527	23	0
2	J	572	0	553	24	0
3	A	1	0	0	0	0
3	D	1	0	0	0	0
3	I	1	0	0	0	0
4	A	24	0	3	5	0
4	D	24	0	3	5	0
4	I	24	0	3	4	0
5	A	278	0	0	15	0
5	B	31	0	0	2	0
5	D	188	0	0	10	0
5	E	31	0	0	3	0
5	I	171	0	0	13	0
5	J	28	0	0	1	0
All	All	16491	0	14904	413	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 13.

The worst 5 of 413 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:447:GLN:HG3	5:A:903:HOH:O	1.63	0.97
1:I:314:GLU:HG2	5:I:942:HOH:O	1.74	0.87
1:D:211:ASP:HB3	5:D:793:HOH:O	1.74	0.86
1:I:540:TRP:CZ3	4:I:601:PQQ:O4	2.32	0.83
1:A:51:LEU:O	1:A:52:HIS:HB2	1.78	0.83

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	595/597 (100%)	561 (94%)	32 (5%)	2 (0%)	46	68
1	D	595/597 (100%)	537 (90%)	53 (9%)	5 (1%)	24	41
1	I	593/597 (99%)	546 (92%)	43 (7%)	4 (1%)	26	46
2	B	68/72 (94%)	63 (93%)	5 (7%)	0	100	100
2	E	66/72 (92%)	60 (91%)	5 (8%)	1 (2%)	13	22
2	J	68/72 (94%)	60 (88%)	6 (9%)	2 (3%)	6	8
All	All	1985/2007 (99%)	1827 (92%)	144 (7%)	14 (1%)	26	46

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	266	ASN
2	E	67	ASP
1	I	261	ASN

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Mol	Chain	Res	Type
1	I	331	ARG
1	D	587	ASP

### 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	487/487 (100%)	457 (94%)	30 (6%)	23	41
1	D	487/487 (100%)	461 (95%)	26 (5%)	28	50
1	I	486/487 (100%)	457 (94%)	29 (6%)	24	43
2	B	60/62 (97%)	50 (83%)	10 (17%)	3	5
2	E	58/62 (94%)	53 (91%)	5 (9%)	13	24
2	J	60/62 (97%)	50 (83%)	10 (17%)	3	5
All	All	1638/1647 (100%)	1528 (93%)	110 (7%)	20	37

5 of 110 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	322	LYS
1	D	496	LEU
2	J	31	LYS
1	D	364	LYS
1	D	418	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	194	GLN
1	D	299	HIS
1	I	395	GLN
1	D	219	HIS
1	D	356	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 6 ligands modelled in this entry, 3 are monoatomic - leaving 3 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	PQQ	A	601	3	16,26,26	4.28	7 (43%)	17,40,40	3.25	11 (64%)
4	PQQ	D	601	3	16,26,26	4.56	8 (50%)	17,40,40	2.43	5 (29%)
4	PQQ	I	601	3	16,26,26	3.74	7 (43%)	17,40,40	2.80	11 (64%)

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	PQQ	A	601	3	-	0/0/28/28	0/3/3/3
4	PQQ	D	601	3	-	0/0/28/28	0/3/3/3
4	PQQ	I	601	3	-	0/0/28/28	0/3/3/3

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	601	PQQ	C3-C3A	2.10	1.44	1.40
4	I	601	PQQ	C3-C3A	2.21	1.44	1.40
4	D	601	PQQ	C3A-C4	2.57	1.53	1.48
4	D	601	PQQ	C6A-N6	2.65	1.39	1.34
4	A	601	PQQ	C7-N6	2.69	1.38	1.34

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	601	PQQ	C9A-C6A-N6	-4.59	116.71	123.35
4	I	601	PQQ	O4-C4-C5	-4.51	112.39	119.29
4	I	601	PQQ	C9A-C6A-N6	-3.62	118.11	123.35
4	I	601	PQQ	C6A-C5-C4	-3.28	115.17	119.16
4	A	601	PQQ	C3A-C3-C2	-2.84	104.05	105.98

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	601	PQQ	5	0
4	D	601	PQQ	5	0
4	I	601	PQQ	4	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 [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	597/597 (100%)	-0.60	1 (0%) 95 96	17, 28, 39, 55	0
1	D	597/597 (100%)	-0.39	3 (0%) 91 92	18, 32, 45, 61	0
1	I	595/597 (99%)	-0.31	2 (0%) 94 95	20, 34, 48, 57	0
2	B	70/72 (97%)	-0.31	1 (1%) 78 80	26, 36, 48, 54	0
2	E	68/72 (94%)	0.18	2 (2%) 55 60	35, 49, 58, 68	0
2	J	70/72 (97%)	0.15	0 100 100	34, 47, 59, 68	0
All	All	1997/2007 (99%)	-0.39	9 (0%) 91 92	17, 32, 49, 68	0

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	68	VAL	4.0
1	D	307	VAL	2.6
1	D	421	PHE	2.3
2	B	68	VAL	2.2
1	D	305	ALA	2.2

### 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
4	PQQ	D	601	24/24	0.74	0.38	4.80	69,77,78,78	0
4	PQQ	A	601	24/24	0.78	0.35	4.51	59,68,69,69	0
4	PQQ	I	601	24/24	0.76	0.33	3.02	67,75,75,76	0
3	CA	A	775	1/1	0.92	0.17	2.46	55,55,55,55	1
3	CA	D	775	1/1	0.99	0.13	-0.90	49,49,49,49	1
3	CA	I	775	1/1	0.96	0.12	-1.07	49,49,49,49	1

## 6.5 Other polymers [i](#)

There are no such residues in this entry.