



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 24, 2024 – 12:15 PM JST

PDB ID : 8WM1  
Title : DHS dehydratase  
Authors : Wang, M.  
Deposited on : 2023-10-02  
Resolution : 2.74 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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  
Xtriage (Phenix) : 1.13  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.002 (Gargrove)  
Density-Fitness : 1.0.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.38.2

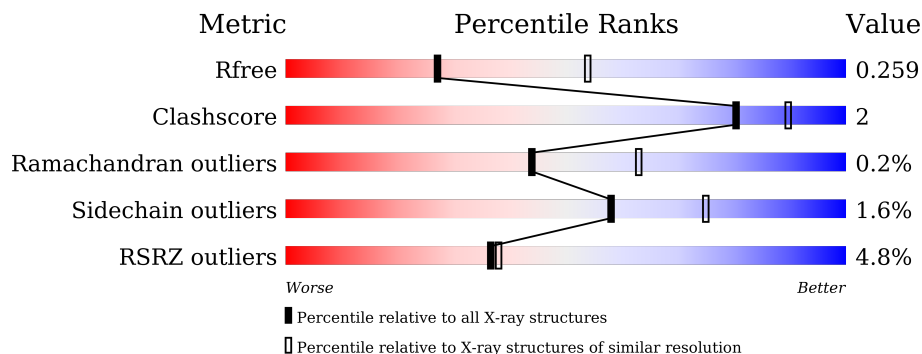
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.74 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))
$R_{free}$	164625	1649 (2.76-2.72)
Clashscore	180529	1744 (2.76-2.72)
Ramachandran outliers	177936	1710 (2.76-2.72)
Sidechain outliers	177891	1711 (2.76-2.72)
RSRZ outliers	164620	1649 (2.76-2.72)

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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. 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	484	 4% 89% 6% . .
1	B	484	 4% 89% 6% . .
1	C	484	 2% 90% 5% . .
1	D	484	 9% 89% 6% . .

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 14066 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 3-dehydroshikimate dehydratase (DHS dehydratase).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	464	Total	C	N	O	S	0	1	0
			3501	2167	632	692	10			
1	B	464	Total	C	N	O	S	0	1	0
			3501	2167	632	692	10			
1	C	464	Total	C	N	O	S	0	1	0
			3501	2167	632	692	10			
1	D	464	Total	C	N	O	S	0	0	0
			3496	2164	632	690	10			

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

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

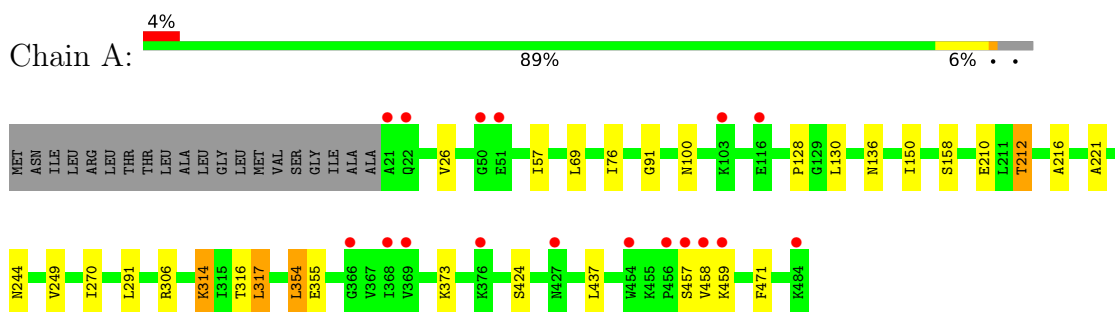
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	15	Total	O	0	0
			15	15		
3	B	13	Total	O	0	0
			13	13		
3	C	20	Total	O	0	0
			20	20		
3	D	11	Total	O	0	0
			11	11		

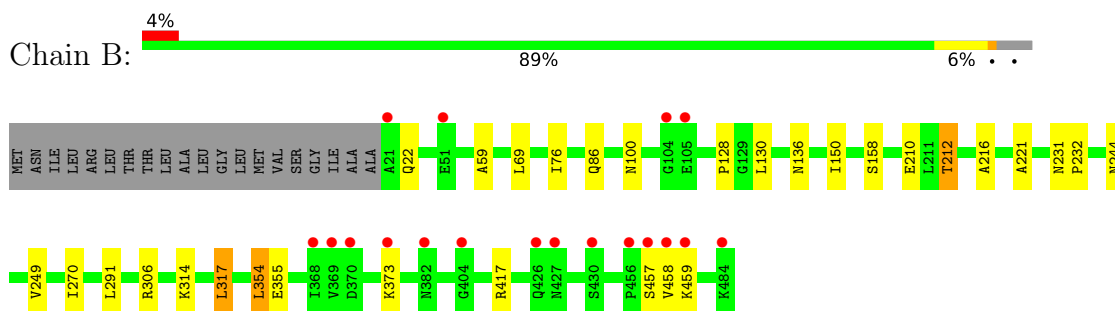
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

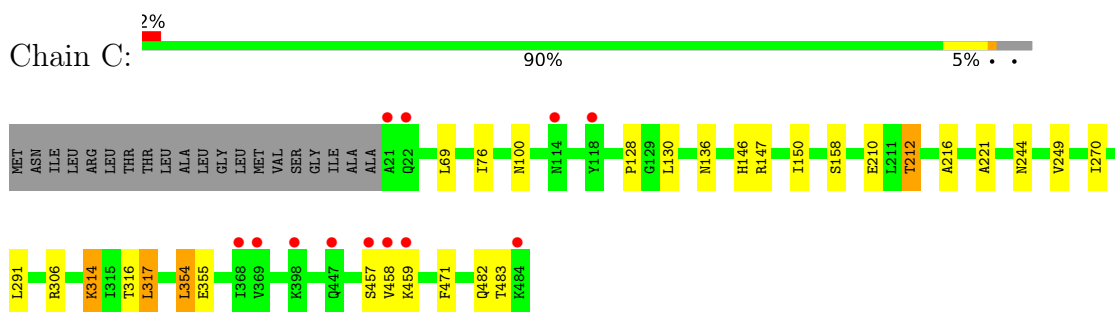
- Molecule 1: 3-dehydroshikimate dehydratase (DHS dehydratase)



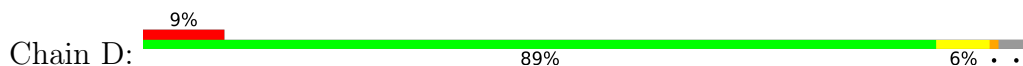
- Molecule 1: 3-dehydroshikimate dehydratase (DHS dehydratase)

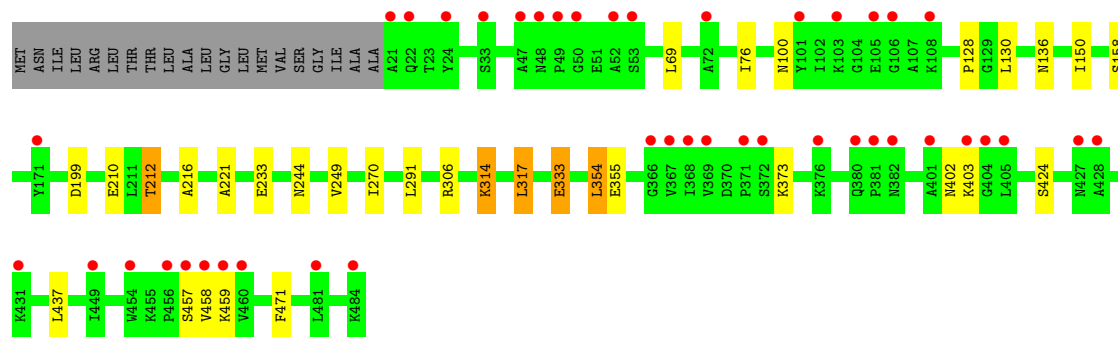


- Molecule 1: 3-dehydroshikimate dehydratase (DHS dehydratase)



- Molecule 1: 3-dehydroshikimate dehydratase (DHS dehydratase)





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	143.56Å 97.67Å 132.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.28 – 2.74 46.28 – 2.74	Depositor EDS
% Data completeness (in resolution range)	99.8 (46.28-2.74) 99.8 (46.28-2.74)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.95 (at 2.73Å)	Xtrriage
Refinement program	REFMAC 5.8.0267	Depositor
R, $R_{free}$	0.224 , 0.255 0.227 , 0.259	Depositor DCC
$R_{free}$ test set	2532 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	25.8	Xtrriage
Anisotropy	0.184	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 34.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	14066	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 33.41 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 8.0366e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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: 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	0.44	0/3561	0.66	0/4831
1	B	0.44	0/3561	0.66	0/4831
1	C	0.44	0/3561	0.67	0/4831
1	D	0.42	0/3553	0.65	0/4820
All	All	0.43	0/14236	0.66	0/19313

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	3501	0	3438	18	0
1	B	3501	0	3438	16	0
1	C	3501	0	3438	17	0
1	D	3496	0	3434	18	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	15	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	13	0	0	0	0
3	C	20	0	0	1	0
3	D	11	0	0	0	0
All	All	14066	0	13748	68	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 (68) 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:233:GLU:HB2	1:D:333:GLU:HG2	1.70	0.73
1:A:136:ASN:HD22	1:A:158:SER:H	1.37	0.72
1:D:136:ASN:HD22	1:D:158:SER:H	1.38	0.72
1:C:136:ASN:HD22	1:C:158:SER:H	1.39	0.71
1:B:136:ASN:HD22	1:B:158:SER:H	1.39	0.68
1:C:483:THR:HG22	3:C:620:HOH:O	1.98	0.62
1:D:76:ILE:HD11	1:D:130:LEU:HD22	1.85	0.59
1:C:306:ARG:NH1	1:C:355:GLU:OE2	2.38	0.56
1:B:306:ARG:NH1	1:B:355:GLU:OE2	2.39	0.56
1:A:76:ILE:HD11	1:A:130:LEU:HD22	1.87	0.55
1:A:306:ARG:NH1	1:A:355:GLU:OE2	2.40	0.55
1:D:306:ARG:NH1	1:D:355:GLU:OE2	2.39	0.55
1:C:210:GLU:OE2	1:C:212:THR:HG21	2.09	0.53
1:A:210:GLU:OE2	1:A:212:THR:HG21	2.10	0.52
1:C:76:ILE:HD11	1:C:130:LEU:HD22	1.90	0.51
1:C:270:ILE:HB	1:C:291:LEU:HD23	1.92	0.51
1:B:210:GLU:OE2	1:B:212:THR:HG21	2.10	0.51
1:D:210:GLU:OE2	1:D:212:THR:HG21	2.11	0.51
1:D:314:LYS:HE3	1:D:471:PHE:HB3	1.92	0.51
1:B:76:ILE:HD11	1:B:130:LEU:HD22	1.92	0.51
1:A:270:ILE:HB	1:A:291:LEU:HD23	1.93	0.50
1:B:270:ILE:HB	1:B:291:LEU:HD23	1.94	0.49
1:D:270:ILE:HB	1:D:291:LEU:HD23	1.94	0.49
1:A:291:LEU:HD12	1:A:317:LEU:HD22	1.94	0.48
1:D:291:LEU:HD12	1:D:317:LEU:HD22	1.94	0.48
1:A:314:LYS:HE3	1:A:471:PHE:HB3	1.96	0.48
1:C:291:LEU:HD12	1:C:317:LEU:HD22	1.95	0.47
1:B:291:LEU:HD12	1:B:317:LEU:HD22	1.96	0.47
1:A:76:ILE:CD1	1:A:130:LEU:HD22	2.45	0.47
1:C:314:LYS:HE3	1:C:471:PHE:HB3	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:91:GLY:HA2	1:B:417:ARG:HD2	1.97	0.46
1:D:402:ASN:O	1:D:403:LYS:HG2	2.17	0.45
1:A:221:ALA:HA	1:A:249:VAL:O	2.17	0.45
1:D:221:ALA:HA	1:D:249:VAL:O	2.18	0.44
1:B:221:ALA:HA	1:B:249:VAL:O	2.18	0.44
1:C:221:ALA:HA	1:C:249:VAL:O	2.18	0.44
1:B:76:ILE:CD1	1:B:130:LEU:HD22	2.47	0.43
1:A:424:SER:HB3	1:A:437:LEU:HD11	2.00	0.43
1:C:76:ILE:CD1	1:C:130:LEU:HD22	2.48	0.43
1:B:354:LEU:C	1:B:354:LEU:HD23	2.39	0.43
1:D:424:SER:HB3	1:D:437:LEU:HD11	2.01	0.43
1:D:354:LEU:C	1:D:354:LEU:HD23	2.39	0.43
1:A:458:VAL:HG12	1:A:459:LYS:H	1.84	0.42
1:D:458:VAL:HG12	1:D:459:LYS:H	1.84	0.42
1:A:354:LEU:C	1:A:354:LEU:HD23	2.39	0.42
1:D:76:ILE:CD1	1:D:130:LEU:HD22	2.48	0.42
1:B:69:LEU:O	1:B:100:ASN:HB2	2.19	0.42
1:D:69:LEU:O	1:D:100:ASN:HB2	2.20	0.42
1:C:146:HIS:CE1	1:C:147:ARG:HG3	2.55	0.42
1:A:69:LEU:O	1:A:100:ASN:HB2	2.20	0.41
1:D:128:PRO:HA	1:D:150:ILE:O	2.21	0.41
1:A:128:PRO:HA	1:A:150:ILE:O	2.20	0.41
1:B:216:ALA:HA	1:B:244:ASN:O	2.20	0.41
1:A:26:VAL:HB	1:A:57:ILE:HA	2.03	0.41
1:C:69:LEU:O	1:C:100:ASN:HB2	2.20	0.41
1:C:216:ALA:HA	1:C:244:ASN:O	2.21	0.41
1:C:316:THR:C	1:C:317:LEU:HD23	2.41	0.41
1:C:354:LEU:C	1:C:354:LEU:HD23	2.41	0.41
1:B:59:ALA:HB2	1:B:86:GLN:OE1	2.22	0.40
1:C:458:VAL:HG12	1:C:459:LYS:H	1.86	0.40
1:A:316:THR:C	1:A:317:LEU:HD23	2.42	0.40
1:C:128:PRO:HA	1:C:150:ILE:O	2.22	0.40
1:A:216:ALA:HA	1:A:244:ASN:O	2.21	0.40
1:B:231:ASN:HA	1:B:232:PRO:HD2	1.94	0.40
1:D:216:ALA:HA	1:D:244:ASN:O	2.21	0.40
1:B:128:PRO:HA	1:B:150:ILE:O	2.21	0.40
1:B:458:VAL:HG12	1:B:459:LYS:H	1.86	0.40
1:D:402:ASN:O	1:D:403:LYS:CG	2.69	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	463/484 (96%)	441 (95%)	21 (4%)	1 (0%)	44	63
1	B	463/484 (96%)	444 (96%)	18 (4%)	1 (0%)	44	63
1	C	463/484 (96%)	442 (96%)	20 (4%)	1 (0%)	44	63
1	D	462/484 (96%)	440 (95%)	21 (4%)	1 (0%)	44	63
All	All	1851/1936 (96%)	1767 (96%)	80 (4%)	4 (0%)	44	63

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	354	LEU
1	B	354	LEU
1	C	354	LEU
1	D	354	LEU

### 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	371/385 (96%)	366 (99%)	5 (1%)	65	80
1	B	371/385 (96%)	365 (98%)	6 (2%)	58	75
1	C	371/385 (96%)	366 (99%)	5 (1%)	65	80
1	D	370/385 (96%)	363 (98%)	7 (2%)	52	71
All	All	1483/1540 (96%)	1460 (98%)	23 (2%)	58	75

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	212	THR
1	A	314	LYS
1	A	317	LEU
1	A	373	LYS
1	A	457	SER
1	B	22	GLN
1	B	212	THR
1	B	314	LYS
1	B	317	LEU
1	B	373	LYS
1	B	457	SER
1	C	212	THR
1	C	314	LYS
1	C	317	LEU
1	C	457	SER
1	C	482	GLN
1	D	199	ASP
1	D	212	THR
1	D	314	LYS
1	D	317	LEU
1	D	333	GLU
1	D	373	LYS
1	D	457	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	136	ASN
1	A	146	HIS
1	A	155	ASN
1	A	169	ASN
1	A	374	GLN
1	B	136	ASN
1	B	146	HIS
1	B	155	ASN
1	B	374	GLN
1	C	136	ASN
1	C	146	HIS
1	C	155	ASN
1	C	374	GLN
1	D	136	ASN

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Mol	Chain	Res	Type
1	D	146	HIS
1	D	155	ASN
1	D	169	ASN
1	D	374	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 oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

### 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	464/484 (95%)	0.09	17 (3%) 45 46	9, 27, 56, 105	1 (0%)
1	B	464/484 (95%)	-0.01	18 (3%) 44 45	9, 24, 51, 75	1 (0%)
1	C	464/484 (95%)	0.03	12 (2%) 57 57	11, 25, 53, 82	1 (0%)
1	D	464/484 (95%)	0.55	43 (9%) 16 18	12, 36, 75, 121	0
All	All	1856/1936 (95%)	0.16	90 (4%) 36 38	9, 27, 60, 121	3 (0%)

All (90) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	21	ALA	8.2
1	B	21	ALA	7.1
1	A	21	ALA	6.8
1	D	369	VAL	6.2
1	C	21	ALA	6.0
1	A	458	VAL	5.2
1	B	369	VAL	5.2
1	D	458	VAL	5.2
1	B	105	GLU	4.8
1	A	369	VAL	4.7
1	D	456	PRO	4.5
1	D	381	PRO	4.4
1	D	457	SER	4.4
1	B	457	SER	4.1
1	D	405	LEU	4.0
1	A	456	PRO	3.9
1	D	49	PRO	3.9
1	C	369	VAL	3.8
1	A	459	LYS	3.8
1	D	484	LYS	3.8
1	D	368	ILE	3.7

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	457	SER	3.6
1	C	458	VAL	3.4
1	D	403	LYS	3.4
1	A	368	ILE	3.3
1	C	457	SER	3.2
1	A	484	LYS	3.2
1	D	48	ASN	3.1
1	D	376	LYS	3.1
1	D	372	SER	3.1
1	A	376	LYS	3.1
1	C	484	LYS	3.1
1	D	431	LYS	3.1
1	D	371	PRO	3.0
1	D	24	TYR	3.0
1	D	459	LYS	3.0
1	A	22	GLN	2.9
1	C	22	GLN	2.9
1	C	447	GLN	2.9
1	B	427	ASN	2.9
1	C	114	ASN	2.8
1	A	366	GLY	2.8
1	C	459	LYS	2.8
1	D	47	ALA	2.8
1	D	367	VAL	2.7
1	A	427	ASN	2.7
1	A	50	GLY	2.7
1	D	404	GLY	2.7
1	B	370	ASP	2.7
1	A	454	TRP	2.7
1	B	104	GLY	2.7
1	B	484	LYS	2.6
1	D	33	SER	2.6
1	D	105	GLU	2.5
1	C	398	LYS	2.5
1	B	430	SER	2.5
1	D	366	GLY	2.5
1	D	382	ASN	2.4
1	D	103	LYS	2.4
1	B	426	GLN	2.4
1	D	449	ILE	2.4
1	B	458	VAL	2.3
1	D	380	GLN	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	460	VAL	2.3
1	B	368	ILE	2.3
1	D	108	LYS	2.3
1	D	454	TRP	2.3
1	D	401	ALA	2.3
1	D	50	GLY	2.3
1	A	116	GLU	2.3
1	D	106	GLY	2.3
1	D	481	LEU	2.3
1	A	51	GLU	2.2
1	B	404	GLY	2.2
1	D	72	ALA	2.2
1	D	53	SER	2.2
1	B	382	ASN	2.1
1	D	427	ASN	2.1
1	B	51	GLU	2.1
1	B	456	PRO	2.1
1	B	373	LYS	2.1
1	C	368	ILE	2.1
1	D	22	GLN	2.1
1	B	459	LYS	2.1
1	D	171	TYR	2.0
1	A	103	LYS	2.0
1	C	118	TYR	2.0
1	D	52	ALA	2.0
1	D	101	TYR	2.0
1	D	428	ALA	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 monosaccharides 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. 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	B-factors(Å <sup>2</sup> )	Q<0.9
2	CA	D	501	1/1	0.96	0.04	34,34,34,34	0
2	CA	B	501	1/1	0.97	0.04	20,20,20,20	0
2	CA	A	501	1/1	0.97	0.04	27,27,27,27	0
2	CA	B	502	1/1	0.98	0.02	24,24,24,24	0
2	CA	D	502	1/1	0.98	0.03	43,43,43,43	0
2	CA	C	502	1/1	0.99	0.03	26,26,26,26	0
2	CA	A	502	1/1	0.99	0.03	20,20,20,20	0
2	CA	C	501	1/1	0.99	0.02	21,21,21,21	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.