wwPDB X-ray Structure Validation Summary Report (i)

Feb 1, 2016 – 02:09 AM GMT

PDB ID	:	2FVM
Title	:	Crystal structure of dihydropyrimidinase from Saccharomyces kluyveri in complex with the reaction product N-carbamyl-beta-alanine
Authors	:	Dobritzsch, D.; Lohkamp, B.
Deposited on	:	2006-01-31
Resolution	:	2.45 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
A user guide is available at
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

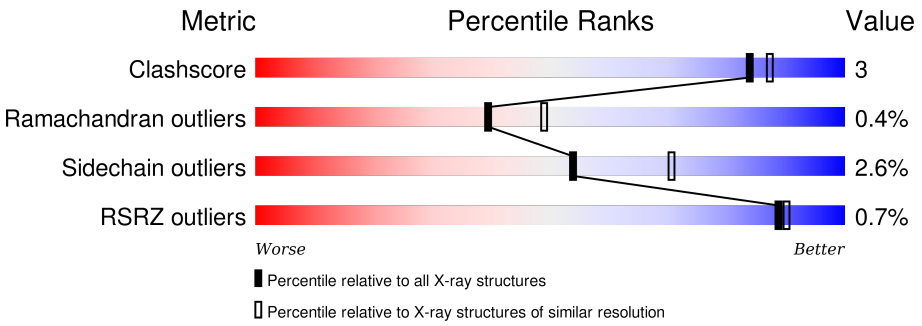
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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))
Clashscore	102246	1030 (2.48-2.44)
Ramachandran outliers	100387	1024 (2.48-2.44)
Sidechain outliers	100360	1024 (2.48-2.44)
RSRZ outliers	91569	4787 (2.50-2.42)

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 >=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 <=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	559	% 87% 8% 5%
1	B	559	% 86% 9% 5%
1	C	559	% 86% 8% • 5%
1	D	559	% 86% 9% • 5%

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	URP	A	604	-	-	-	X
3	URP	B	604	-	-	-	X

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 17433 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 dihydropyrimidinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	532	4155	2638	680	810	27	0	1	0
1	B	532	4155	2638	680	810	27	0	1	0
1	C	531	4145	2632	677	809	27	0	1	0
1	D	532	4157	2639	680	811	27	0	1	0

There are 76 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	167	KCX	LYS	MODIFIED RESIDUE	UNP Q9P903
A	543	PRO	-	EXPRESSION TAG	UNP Q9P903
A	544	GLY	-	EXPRESSION TAG	UNP Q9P903
A	545	ASP	-	EXPRESSION TAG	UNP Q9P903
A	546	ASP	-	EXPRESSION TAG	UNP Q9P903
A	547	ASP	-	EXPRESSION TAG	UNP Q9P903
A	548	ASP	-	EXPRESSION TAG	UNP Q9P903
A	549	LYS	-	EXPRESSION TAG	UNP Q9P903
A	550	HIS	-	EXPRESSION TAG	UNP Q9P903
A	551	HIS	-	EXPRESSION TAG	UNP Q9P903
A	552	HIS	-	EXPRESSION TAG	UNP Q9P903
A	553	HIS	-	EXPRESSION TAG	UNP Q9P903
A	554	HIS	-	EXPRESSION TAG	UNP Q9P903
A	555	HIS	-	EXPRESSION TAG	UNP Q9P903
A	556	HIS	-	EXPRESSION TAG	UNP Q9P903
A	557	HIS	-	EXPRESSION TAG	UNP Q9P903
A	558	SER	-	EXPRESSION TAG	UNP Q9P903
A	559	GLY	-	EXPRESSION TAG	UNP Q9P903
A	560	ASP	-	EXPRESSION TAG	UNP Q9P903
B	167	KCX	LYS	MODIFIED RESIDUE	UNP Q9P903
B	543	PRO	-	EXPRESSION TAG	UNP Q9P903

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Chain	Residue	Modelled	Actual	Comment	Reference
B	544	GLY	-	EXPRESSION TAG	UNP Q9P903
B	545	ASP	-	EXPRESSION TAG	UNP Q9P903
B	546	ASP	-	EXPRESSION TAG	UNP Q9P903
B	547	ASP	-	EXPRESSION TAG	UNP Q9P903
B	548	ASP	-	EXPRESSION TAG	UNP Q9P903
B	549	LYS	-	EXPRESSION TAG	UNP Q9P903
B	550	HIS	-	EXPRESSION TAG	UNP Q9P903
B	551	HIS	-	EXPRESSION TAG	UNP Q9P903
B	552	HIS	-	EXPRESSION TAG	UNP Q9P903
B	553	HIS	-	EXPRESSION TAG	UNP Q9P903
B	554	HIS	-	EXPRESSION TAG	UNP Q9P903
B	555	HIS	-	EXPRESSION TAG	UNP Q9P903
B	556	HIS	-	EXPRESSION TAG	UNP Q9P903
B	557	HIS	-	EXPRESSION TAG	UNP Q9P903
B	558	SER	-	EXPRESSION TAG	UNP Q9P903
B	559	GLY	-	EXPRESSION TAG	UNP Q9P903
B	560	ASP	-	EXPRESSION TAG	UNP Q9P903
C	167	KCX	LYS	MODIFIED RESIDUE	UNP Q9P903
C	543	PRO	-	EXPRESSION TAG	UNP Q9P903
C	544	GLY	-	EXPRESSION TAG	UNP Q9P903
C	545	ASP	-	EXPRESSION TAG	UNP Q9P903
C	546	ASP	-	EXPRESSION TAG	UNP Q9P903
C	547	ASP	-	EXPRESSION TAG	UNP Q9P903
C	548	ASP	-	EXPRESSION TAG	UNP Q9P903
C	549	LYS	-	EXPRESSION TAG	UNP Q9P903
C	550	HIS	-	EXPRESSION TAG	UNP Q9P903
C	551	HIS	-	EXPRESSION TAG	UNP Q9P903
C	552	HIS	-	EXPRESSION TAG	UNP Q9P903
C	553	HIS	-	EXPRESSION TAG	UNP Q9P903
C	554	HIS	-	EXPRESSION TAG	UNP Q9P903
C	555	HIS	-	EXPRESSION TAG	UNP Q9P903
C	556	HIS	-	EXPRESSION TAG	UNP Q9P903
C	557	HIS	-	EXPRESSION TAG	UNP Q9P903
C	558	SER	-	EXPRESSION TAG	UNP Q9P903
C	559	GLY	-	EXPRESSION TAG	UNP Q9P903
C	560	ASP	-	EXPRESSION TAG	UNP Q9P903
D	167	KCX	LYS	MODIFIED RESIDUE	UNP Q9P903
D	543	PRO	-	EXPRESSION TAG	UNP Q9P903
D	544	GLY	-	EXPRESSION TAG	UNP Q9P903
D	545	ASP	-	EXPRESSION TAG	UNP Q9P903
D	546	ASP	-	EXPRESSION TAG	UNP Q9P903
D	547	ASP	-	EXPRESSION TAG	UNP Q9P903

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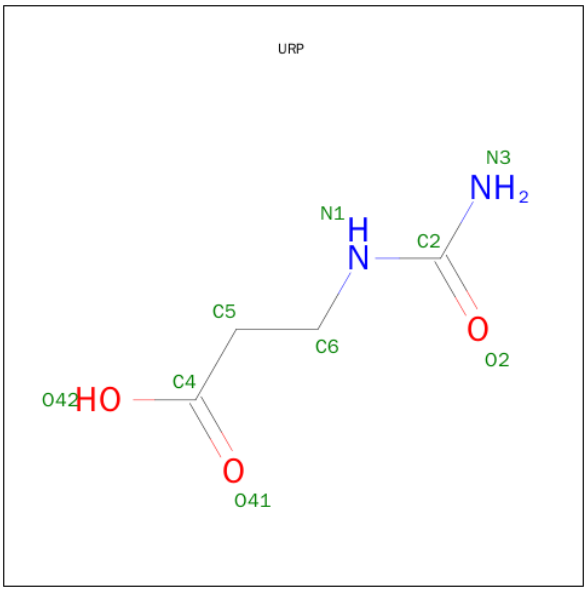
Chain	Residue	Modelled	Actual	Comment	Reference
D	548	ASP	-	EXPRESSION TAG	UNP Q9P903
D	549	LYS	-	EXPRESSION TAG	UNP Q9P903
D	550	HIS	-	EXPRESSION TAG	UNP Q9P903
D	551	HIS	-	EXPRESSION TAG	UNP Q9P903
D	552	HIS	-	EXPRESSION TAG	UNP Q9P903
D	553	HIS	-	EXPRESSION TAG	UNP Q9P903
D	554	HIS	-	EXPRESSION TAG	UNP Q9P903
D	555	HIS	-	EXPRESSION TAG	UNP Q9P903
D	556	HIS	-	EXPRESSION TAG	UNP Q9P903
D	557	HIS	-	EXPRESSION TAG	UNP Q9P903
D	558	SER	-	EXPRESSION TAG	UNP Q9P903
D	559	GLY	-	EXPRESSION TAG	UNP Q9P903
D	560	ASP	-	EXPRESSION TAG	UNP Q9P903

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 3 is N-(AMINOCARBONYL)-BETA-ALANINE (three-letter code: URP) (formula: $C_4H_8N_2O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	9	4	2	3	0	0
			Total	C	N	O		
3	B	1	9	4	2	3	0	0

- Molecule 4 is water.

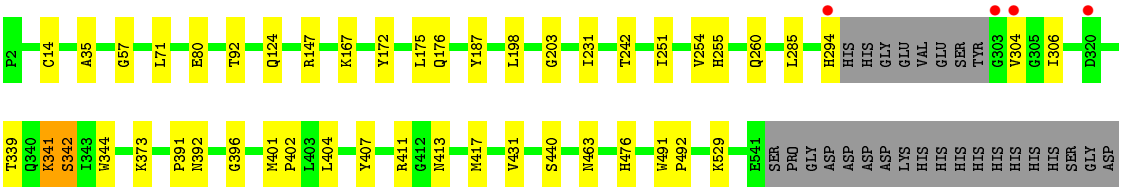
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	218	218	218	0	0
			Total	O		
4	B	191	191	191	0	0
			Total	O		
4	C	200	200	200	0	0
			Total	O		
4	D	186	186	186	0	0

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: dihydropyrimidinase

Chain A:

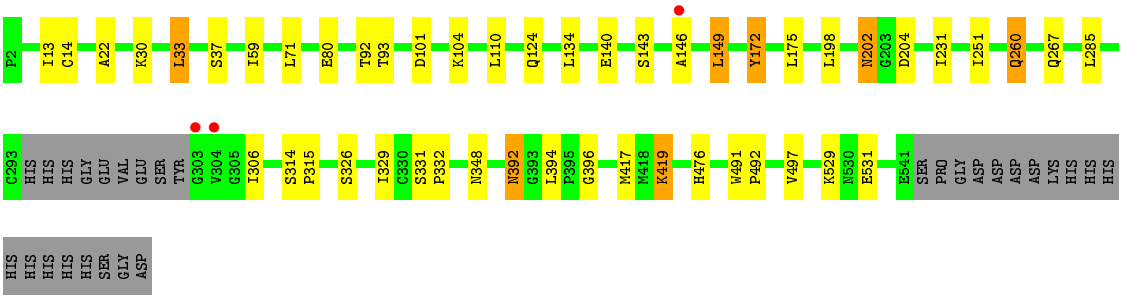


- Molecule 1: dihydropyrimidinase

Chain B:

- Molecule 1: dihydropyrimidinase

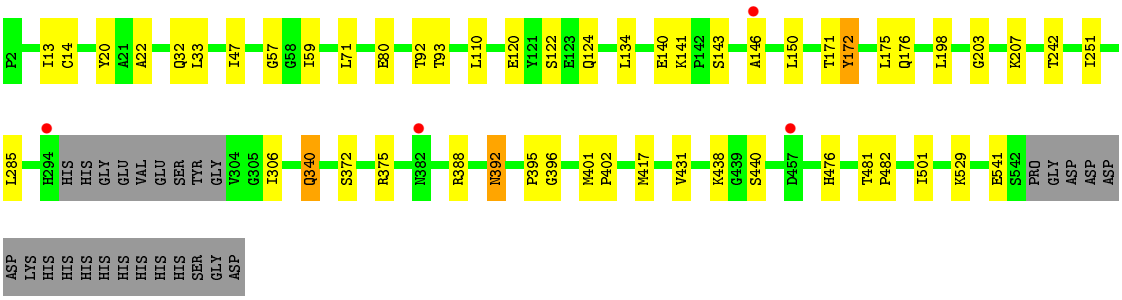
Chain C:



- Molecule 1: dihydropyrimidinase

Chain D:

%
86%
9%
5%


P2 I13 C14 Y20 A21 A22 Q32 L33 I47 G57 G58 I59 L71 E80 T92 T93 L110 E120 Y121 S122 E123 Q124 L134 E140 K141 P142 S143 A146 L150 T171 Y172 L175 Q176 L198 G203 K207 T242 I251
L285 H294 HIS HIS GLY GLU VAL GLU SER TYR GLY V304 G305 I306 Q340 S372 R375 N382 R388 N392 P395 G396 M401 P402 M417 V431 K438 G439 S440 D457 H476 T481 P482 I501 K529 E541 S542 PRO GLY ASP ASP ASP
ASP LYS HIS HIS HIS HIS HIS HIS HIS HIS SER GLY ASP

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	91.14Å 73.03Å 164.10Å 90.00° 91.98° 90.00°	Depositor
Resolution (Å)	44.37 – 2.45 44.28 – 2.45	Depositor EDS
% Data completeness (in resolution range)	97.3 (44.37-2.45) 90.9 (44.28-2.45)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$< I/\sigma(I) >$ [1]	2.89 (at 2.45Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.182 , 0.237 0.189 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å^2)	17.7	Xtriage
Anisotropy	0.592	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	(Not available) , (Not available)	EDS
Estimated twinning fraction	0.177 for h,-k,-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Outliers	0 of 79571 reflections	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	17433	wwPDB-VP
Average B, all atoms (Å^2)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.99% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: ZN, URP, KCX

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	0.46	0/4239	0.57	0/5752
1	B	0.46	0/4239	0.58	0/5752
1	C	0.45	0/4228	0.58	1/5737 (0.0%)
1	D	0.43	0/4241	0.56	0/5755
All	All	0.45	0/16947	0.57	1/22996 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	149	LEU	CA-CB-CG	5.50	127.95	115.30

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	4155	0	4084	23	0
1	B	4155	0	4084	27	0
1	C	4145	0	4077	28	0
1	D	4157	0	4086	27	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	9	0	7	0	0
3	B	9	0	7	1	0
4	A	218	0	0	1	0
4	B	191	0	0	1	0
4	C	200	0	0	2	0
4	D	186	0	0	2	0
All	All	17433	0	16345	100	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 3.

The worst 5 of 100 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:198:LEU:HD12	1:A:251:ILE:HD11	1.29	1.08
1:C:198:LEU:HD12	1:C:251:ILE:HD11	1.32	1.07
1:D:198:LEU:HD12	1:D:251:ILE:HD11	1.35	1.04
1:B:198:LEU:HD12	1:B:251:ILE:HD11	1.46	0.96
1:C:260:GLN:HE21	1:C:260:GLN:H	1.33	0.76

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	528/559 (94%)	508 (96%)	18 (3%)	2 (0%)	39	49
1	B	528/559 (94%)	512 (97%)	14 (3%)	2 (0%)	39	49
1	C	527/559 (94%)	513 (97%)	12 (2%)	2 (0%)	39	49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	528/559 (94%)	516 (98%)	10 (2%)	2 (0%)	39	49
All	All	2111/2236 (94%)	2049 (97%)	54 (3%)	8 (0%)	39	49

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	172	TYR
1	B	172	TYR
1	C	172	TYR
1	D	172	TYR
1	A	396	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	456/479 (95%)	445 (98%)	11 (2%)	57	73
1	B	456/479 (95%)	445 (98%)	11 (2%)	57	73
1	C	455/479 (95%)	444 (98%)	11 (2%)	57	73
1	D	457/479 (95%)	443 (97%)	14 (3%)	47	64
All	All	1824/1916 (95%)	1777 (97%)	47 (3%)	54	70

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	511	GLU
1	C	260	GLN
1	D	476	HIS
1	C	37	SER
1	C	392	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	318	ASN
1	B	392	ASN
1	C	260	GLN
1	B	260	GLN
1	C	202	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues are modelled in this entry.

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	$\#\|Z\| > 2$
1	KCX	A	167	1,2	7,11,12	0.58	0	7,12,14	1.50	2 (28%)
1	KCX	B	167	1,2	7,11,12	0.58	0	7,12,14	1.38	1 (14%)
1	KCX	C	167	1,2	7,11,12	0.49	0	7,12,14	1.22	2 (28%)
1	KCX	D	167	1,2	7,11,12	0.67	0	7,12,14	1.32	2 (28%)

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
1	KCX	A	167	1,2	-	0/6/10/12	0/0/0/0
1	KCX	B	167	1,2	-	0/6/10/12	0/0/0/0
1	KCX	C	167	1,2	-	0/6/10/12	0/0/0/0
1	KCX	D	167	1,2	-	0/6/10/12	0/0/0/0

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	167	KCX	CE-NZ-CX	-3.13	119.95	123.49
1	D	167	KCX	CE-NZ-CX	-2.54	120.61	123.49
1	B	167	KCX	CE-NZ-CX	-2.44	120.73	123.49
1	C	167	KCX	CE-NZ-CX	-2.23	120.97	123.49
1	D	167	KCX	O-C-CA	-2.17	119.83	125.49

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	167	KCX	2	0

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 10 ligands modelled in this entry, 8 are monoatomic - leaving 2 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	$\#\|Z\| > 2$
3	URP	A	604	2	5,8,8	0.90	0	6,9,9	2.64	3 (50%)
3	URP	B	604	2	5,8,8	0.78	0	6,9,9	2.93	4 (66%)

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
3	URP	A	604	2	-	0/4/6/6	0/0/0/0
3	URP	B	604	2	-	0/4/6/6	0/0/0/0

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	604	URP	C5-C6-N1	-3.89	102.49	111.97
3	A	604	URP	C5-C6-N1	-3.83	102.62	111.97
3	B	604	URP	O2-C2-N3	-2.18	119.56	123.30
3	A	604	URP	N3-C2-N1	2.66	119.42	116.17
3	B	604	URP	N3-C2-N1	2.97	119.80	116.17

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	604	URP	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 (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, 95th 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^2)	Q<0.9
1	A	531/559 (94%)	-0.63	4 (0%)	87	89	21, 23, 25, 32	1 (0%)
1	B	531/559 (94%)	-0.58	4 (0%)	87	89	20, 23, 25, 33	1 (0%)
1	C	530/559 (94%)	-0.55	3 (0%)	90	91	21, 23, 25, 33	0
1	D	531/559 (94%)	-0.53	4 (0%)	87	89	21, 23, 25, 31	0
All	All	2123/2236 (94%)	-0.57	15 (0%)	89	90	20, 23, 25, 33	2 (0%)

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	304	VAL	4.2
1	D	146	ALA	4.1
1	D	294	HIS	3.8
1	B	294	HIS	3.7
1	C	304	VAL	3.5

6.2 Non-standard residues in protein, DNA, RNA chains (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, 95th 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^2)	Q<0.9
1	KCX	B	167	12/13	0.97	0.11	-	22,23,30,31	3
1	KCX	A	167	12/13	0.94	0.13	-	22,24,30,31	3
1	KCX	D	167	12/13	0.92	0.16	-	22,24,30,30	3
1	KCX	C	167	12/13	0.94	0.12	-	22,23,30,31	3

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, 95th 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^2)	Q<0.9
3	URP	B	604	9/9	0.86	0.28	8.42	42,44,47,47	0
3	URP	A	604	9/9	0.89	0.25	6.35	44,46,49,49	0
2	ZN	B	602	1/1	0.97	0.12	0.43	50,50,50,50	0
2	ZN	D	602	1/1	0.96	0.12	0.25	46,46,46,46	0
2	ZN	C	602	1/1	0.99	0.11	-0.13	45,45,45,45	0
2	ZN	A	602	1/1	0.97	0.10	-0.22	48,48,48,48	0
2	ZN	C	601	1/1	0.99	0.05	-	39,39,39,39	0
2	ZN	B	601	1/1	1.00	0.10	-	32,32,32,32	0
2	ZN	D	601	1/1	0.99	0.06	-	36,36,36,36	0
2	ZN	A	601	1/1	0.99	0.10	-	34,34,34,34	0

6.5 Other polymers (i)

There are no such residues in this entry.