



Full wwPDB X-ray Structure Validation Report

Mar 1, 2014 – 02:05 AM GMT

PDB ID : 2V8H
Title : CRYSTAL STRUCTURE OF MUTANT E159A OF BETA-ALANINE SYNTHASE FROM SACCHAROMYCES KLUYVERI IN COMPLEX WITH ITS SUBSTRATE N-CARBAMYL-BETA-ALANINE
Authors : Lundgren, S.; Andersen, B.; Piskur, J.; Dobritsch, D.
Deposited on : 2007-08-08
Resolution : 2.00 Å(reported)

This is a full wwPDB validation 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/ValidationPDFNotes.html>

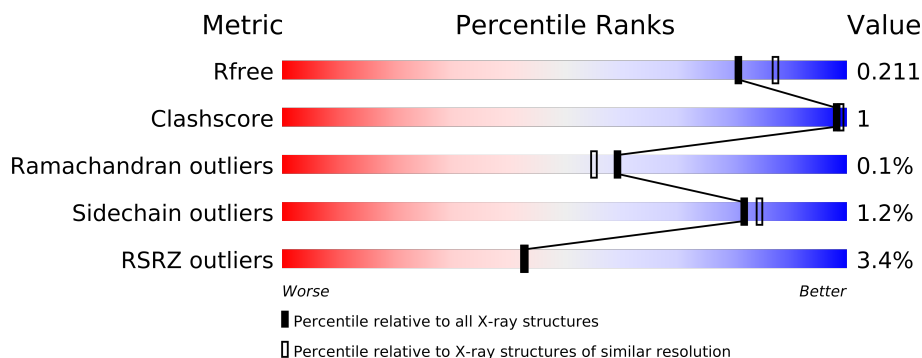
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.00 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}	66092	4888 (2.00-2.00)
Clashscore	79885	6188 (2.00-2.00)
Ramachandran outliers	78287	6102 (2.00-2.00)
Sidechain outliers	78261	6100 (2.00-2.00)
RSRZ outliers	66119	4890 (2.00-2.00)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	474	
1	B	474	
1	C	474	
1	D	474	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	URP	B	600	-	X
4	BCN	A	601	-	X
4	BCN	B	601	-	X
4	BCN	C	601	-	X
4	BCN	D	601	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 14629 atoms, of which 0 are hydrogen and 0 are deuterium.

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 BETA-ALANINE SYNTHASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	431	Total	C	N	O	S	0	9	0
			3390	2138	582	654	16			
1	B	431	Total	C	N	O	S	0	11	0
			3406	2151	586	652	17			
1	C	432	Total	C	N	O	S	0	4	0
			3370	2128	579	647	16			
1	D	431	Total	C	N	O	S	0	15	0
			3419	2163	588	652	16			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	159	ALA	GLU	ENGINEERED MUTATION	UNP Q96W94
A	456	GLN	-	EXPRESSION TAG	UNP Q96W94
A	457	PHE	-	EXPRESSION TAG	UNP Q96W94
A	458	PRO	-	EXPRESSION TAG	UNP Q96W94
A	459	GLY	-	EXPRESSION TAG	UNP Q96W94
A	460	ASP	-	EXPRESSION TAG	UNP Q96W94
A	461	ASP	-	EXPRESSION TAG	UNP Q96W94
A	462	ASP	-	EXPRESSION TAG	UNP Q96W94
A	463	ASP	-	EXPRESSION TAG	UNP Q96W94
A	464	LYS	-	EXPRESSION TAG	UNP Q96W94
A	465	HIS	-	EXPRESSION TAG	UNP Q96W94
A	466	HIS	-	EXPRESSION TAG	UNP Q96W94
A	467	HIS	-	EXPRESSION TAG	UNP Q96W94
A	468	HIS	-	EXPRESSION TAG	UNP Q96W94
A	469	HIS	-	EXPRESSION TAG	UNP Q96W94
A	470	HIS	-	EXPRESSION TAG	UNP Q96W94
A	471	HIS	-	EXPRESSION TAG	UNP Q96W94
A	472	HIS	-	EXPRESSION TAG	UNP Q96W94
A	473	SER	-	EXPRESSION TAG	UNP Q96W94
A	474	GLY	-	EXPRESSION TAG	UNP Q96W94
A	475	ASP	-	EXPRESSION TAG	UNP Q96W94

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Chain	Residue	Modelled	Actual	Comment	Reference
B	159	ALA	GLU	ENGINEERED MUTATION	UNP Q96W94
B	456	GLN	-	EXPRESSION TAG	UNP Q96W94
B	457	PHE	-	EXPRESSION TAG	UNP Q96W94
B	458	PRO	-	EXPRESSION TAG	UNP Q96W94
B	459	GLY	-	EXPRESSION TAG	UNP Q96W94
B	460	ASP	-	EXPRESSION TAG	UNP Q96W94
B	461	ASP	-	EXPRESSION TAG	UNP Q96W94
B	462	ASP	-	EXPRESSION TAG	UNP Q96W94
B	463	ASP	-	EXPRESSION TAG	UNP Q96W94
B	464	LYS	-	EXPRESSION TAG	UNP Q96W94
B	465	HIS	-	EXPRESSION TAG	UNP Q96W94
B	466	HIS	-	EXPRESSION TAG	UNP Q96W94
B	467	HIS	-	EXPRESSION TAG	UNP Q96W94
B	468	HIS	-	EXPRESSION TAG	UNP Q96W94
B	469	HIS	-	EXPRESSION TAG	UNP Q96W94
B	470	HIS	-	EXPRESSION TAG	UNP Q96W94
B	471	HIS	-	EXPRESSION TAG	UNP Q96W94
B	472	HIS	-	EXPRESSION TAG	UNP Q96W94
B	473	SER	-	EXPRESSION TAG	UNP Q96W94
B	474	GLY	-	EXPRESSION TAG	UNP Q96W94
B	475	ASP	-	EXPRESSION TAG	UNP Q96W94
C	159	ALA	GLU	ENGINEERED MUTATION	UNP Q96W94
C	456	GLN	-	EXPRESSION TAG	UNP Q96W94
C	457	PHE	-	EXPRESSION TAG	UNP Q96W94
C	458	PRO	-	EXPRESSION TAG	UNP Q96W94
C	459	GLY	-	EXPRESSION TAG	UNP Q96W94
C	460	ASP	-	EXPRESSION TAG	UNP Q96W94
C	461	ASP	-	EXPRESSION TAG	UNP Q96W94
C	462	ASP	-	EXPRESSION TAG	UNP Q96W94
C	463	ASP	-	EXPRESSION TAG	UNP Q96W94
C	464	LYS	-	EXPRESSION TAG	UNP Q96W94
C	465	HIS	-	EXPRESSION TAG	UNP Q96W94
C	466	HIS	-	EXPRESSION TAG	UNP Q96W94
C	467	HIS	-	EXPRESSION TAG	UNP Q96W94
C	468	HIS	-	EXPRESSION TAG	UNP Q96W94
C	469	HIS	-	EXPRESSION TAG	UNP Q96W94
C	470	HIS	-	EXPRESSION TAG	UNP Q96W94
C	471	HIS	-	EXPRESSION TAG	UNP Q96W94
C	472	HIS	-	EXPRESSION TAG	UNP Q96W94
C	473	SER	-	EXPRESSION TAG	UNP Q96W94
C	474	GLY	-	EXPRESSION TAG	UNP Q96W94
C	475	ASP	-	EXPRESSION TAG	UNP Q96W94

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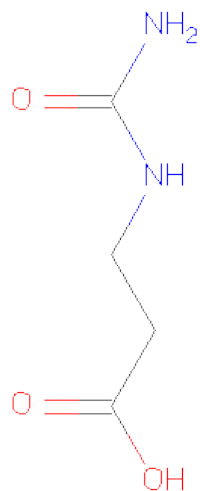
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Chain	Residue	Modelled	Actual	Comment	Reference
D	159	ALA	GLU	ENGINEERED MUTATION	UNP Q96W94
D	456	GLN	-	EXPRESSION TAG	UNP Q96W94
D	457	PHE	-	EXPRESSION TAG	UNP Q96W94
D	458	PRO	-	EXPRESSION TAG	UNP Q96W94
D	459	GLY	-	EXPRESSION TAG	UNP Q96W94
D	460	ASP	-	EXPRESSION TAG	UNP Q96W94
D	461	ASP	-	EXPRESSION TAG	UNP Q96W94
D	462	ASP	-	EXPRESSION TAG	UNP Q96W94
D	463	ASP	-	EXPRESSION TAG	UNP Q96W94
D	464	LYS	-	EXPRESSION TAG	UNP Q96W94
D	465	HIS	-	EXPRESSION TAG	UNP Q96W94
D	466	HIS	-	EXPRESSION TAG	UNP Q96W94
D	467	HIS	-	EXPRESSION TAG	UNP Q96W94
D	468	HIS	-	EXPRESSION TAG	UNP Q96W94
D	469	HIS	-	EXPRESSION TAG	UNP Q96W94
D	470	HIS	-	EXPRESSION TAG	UNP Q96W94
D	471	HIS	-	EXPRESSION TAG	UNP Q96W94
D	472	HIS	-	EXPRESSION TAG	UNP Q96W94
D	473	SER	-	EXPRESSION TAG	UNP Q96W94
D	474	GLY	-	EXPRESSION TAG	UNP Q96W94
D	475	ASP	-	EXPRESSION TAG	UNP Q96W94

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

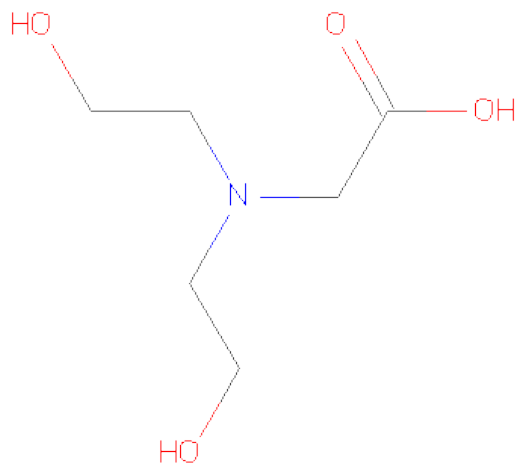
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	2	Total 2 Zn 2	0	0
2	A	2	Total 2 Zn 2	0	0
2	D	2	Total 2 Zn 2	0	0
2	C	2	Total 2 Zn 2	0	0

- Molecule 3 is N-(AMINOCARBONYL)-BETA-ALANINE (three-letter code: URP) (formula: C₄H₈N₂O₃).



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

- Molecule 4 is BICINE (three-letter code: BCN) (formula: C₆H₁₃NO₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			11	6	1	4		
4	B	1	Total	C	N	O	0	0
			11	6	1	4		
4	C	1	Total	C	N	O	0	0
			11	6	1	4		
4	D	1	Total	C	N	O	0	0
			11	6	1	4		

- Molecule 5 is water.

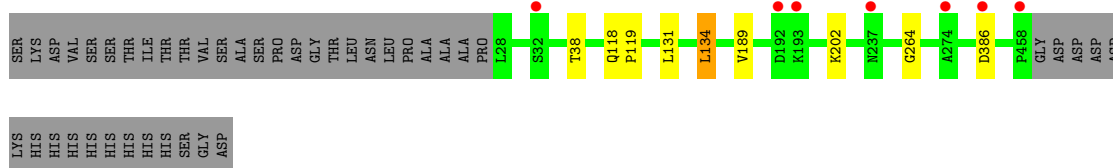
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	303	Total	O	0	0
			303	303		
5	B	204	Total	O	0	0
			204	204		
5	C	180	Total	O	0	0
			180	180		
5	D	269	Total	O	0	0
			269	269		

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.

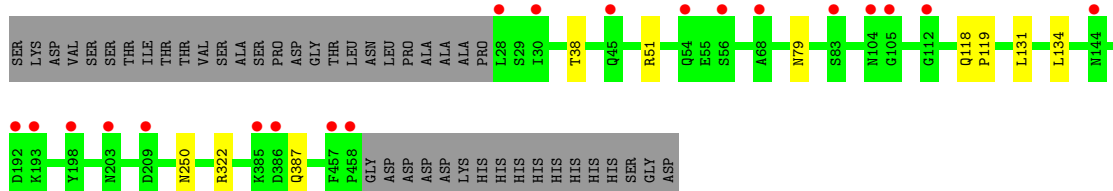
• Molecule 1: BETA-ALANINE SYNTHASE

Chain A:



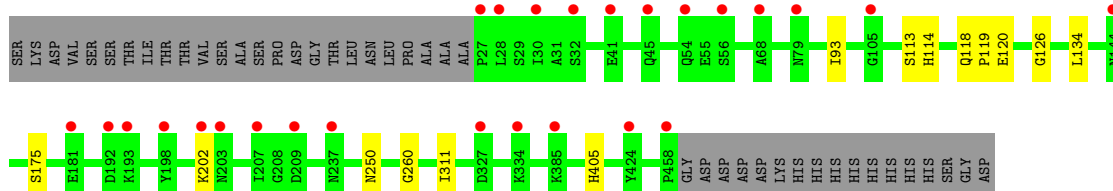
• Molecule 1: BETA-ALANINE SYNTHASE

Chain B:



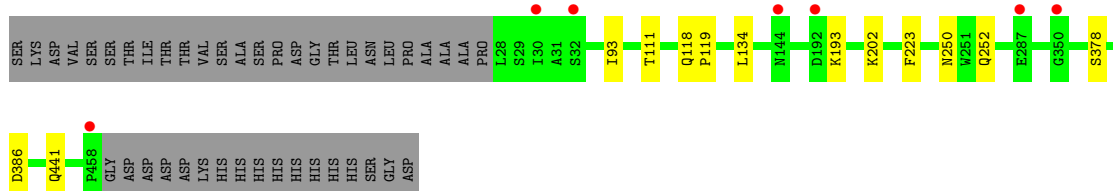
• Molecule 1: BETA-ALANINE SYNTHASE

Chain C:



• Molecule 1: BETA-ALANINE SYNTHASE

Chain D:



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	49.78Å 218.30Å 81.58Å 90.00° 92.19° 90.00°	Depositor
Resolution (Å)	19.76 – 2.00 19.76 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.6 (19.76-2.00) 99.6 (19.76-2.00)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.28 (at 2.01Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.178 , 0.208 0.181 , 0.211	Depositor DCC
R_{free} test set	5792 reflections (5.25%)	DCC
Wilson B-factor (Å ²)	21.5	Xtriage
Anisotropy	0.889	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 42.9	EDS
Estimated twinning fraction	0.053 for h,-k,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	1 of 116113 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	14629	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.55% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BCN, URP, ZN

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	0/3486	0.55	0/4723
1	B	0.41	0/3517	0.52	0/4762
1	C	0.40	0/3461	0.52	0/4690
1	D	0.44	0/3542	0.54	0/4797
All	All	0.43	0/14006	0.53	0/18972

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	C	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	120	GLU	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the

Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3390	0	3283	4	0
1	B	3406	0	3322	3	0
1	C	3370	0	3266	6	0
1	D	3419	0	3352	5	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	9	0	7	0	0
3	B	9	0	7	0	0
3	C	9	0	7	0	0
3	D	9	0	7	0	0
4	A	11	0	12	0	0
4	B	11	0	12	0	0
4	C	11	0	12	0	0
4	D	11	0	12	0	0
5	A	303	0	0	0	0
5	B	204	0	0	0	0
5	C	180	0	0	0	1
5	D	269	0	0	1	1
All	All	14629	0	13299	17	1

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 1.

All (17) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:118:GLN:HB3	1:C:119:PRO:HD2	1.55	0.88
1:D:252:GLN:HG3	5:D:2147:HOH:O	2.01	0.59
1:C:118:GLN:HB3	1:C:119:PRO:CD	2.33	0.56
1:A:264:GLY:HA2	1:B:322:ARG:HD2	1.91	0.52
1:C:175:SER:HB2	1:C:405:HIS:CD2	2.47	0.49
1:A:38:THR:HG22	1:A:131:LEU:HD13	1.95	0.49
1:D:118:GLN:HB3	1:D:119:PRO:HD2	1.95	0.48
1:D:93:ILE:O	1:D:93:ILE:HG13	2.14	0.48
1:C:93:ILE:HG13	1:C:93:ILE:O	2.14	0.48
1:A:134:LEU:O	1:A:134:LEU:HD22	2.14	0.47
1:A:118:GLN:HB3	1:A:119:PRO:HD2	1.98	0.45
1:B:118:GLN:HB3	1:B:119:PRO:HD2	2.00	0.43
1:D:378:SER:OG	1:D:441:GLN:HB3	2.20	0.42
1:D:111:THR:HA	1:D:223:PHE:O	2.20	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:38:THR:HG22	1:B:131:LEU:HD13	2.03	0.41
1:C:114:HIS:CE1	1:C:126:GLY:HA3	2.56	0.41
1:C:260:GLY:HA2	1:C:311:ILE:O	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:C:2137:HOH:O	5:D:2221:HOH:O[2_656]	2.11	0.09

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	438/474 (92%)	429 (98%)	9 (2%)	0	100	100
1	B	441/474 (93%)	434 (98%)	7 (2%)	0	100	100
1	C	434/474 (92%)	427 (98%)	6 (1%)	1 (0%)	56	51
1	D	444/474 (94%)	436 (98%)	8 (2%)	0	100	100
All	All	1757/1896 (93%)	1726 (98%)	30 (2%)	1 (0%)	59	55

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	113	SER

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	365/392 (93%)	361 (99%)	4 (1%)	84	86
1	B	368/392 (94%)	362 (98%)	6 (2%)	75	77
1	C	361/392 (92%)	358 (99%)	3 (1%)	89	92
1	D	371/392 (95%)	365 (98%)	6 (2%)	75	77
All	All	1465/1568 (93%)	1446 (99%)	19 (1%)	82	82

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	134	LEU
1	A	189	VAL
1	A	202	LYS
1	A	386	ASP
1	B	51[A]	ARG
1	B	51[B]	ARG
1	B	79	ASN
1	B	134	LEU
1	B	250	ASN
1	B	387	GLN
1	C	134	LEU
1	C	202	LYS
1	C	250	ASN
1	D	134	LEU
1	D	193	LYS
1	D	202	LYS
1	D	250	ASN
1	D	386[A]	ASP
1	D	386[B]	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	79	ASN
1	A	250	ASN
1	A	290	GLN
1	A	441	GLN
1	B	250	ASN
1	B	387	GLN
1	C	250	ASN
1	C	401	GLN

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Mol	Chain	Res	Type
1	D	250	ASN
1	D	401	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 16 ligands modelled in this entry, 8 are monoatomic - leaving 8 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	600	2	8,8,8	0.89	0	9,9,9	1.10	0
4	BCN	A	601	-	10,10,10	0.63	0	11,11,11	0.85	0
3	URP	B	600	2	8,8,8	0.89	0	9,9,9	0.93	0
4	BCN	B	601	-	10,10,10	0.55	0	11,11,11	1.07	0
3	URP	C	600	2	8,8,8	0.81	0	9,9,9	1.13	0
4	BCN	C	601	-	10,10,10	0.63	0	11,11,11	0.74	0
3	URP	D	600	2	8,8,8	0.85	0	9,9,9	1.00	0
4	BCN	D	601	-	10,10,10	0.59	0	11,11,11	1.03	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
3	URP	A	600	2	-	0/6/6/6	0/0/0/0
4	BCN	A	601	-	-	0/10/10/10	0/0/0/0
3	URP	B	600	2	-	0/6/6/6	0/0/0/0
4	BCN	B	601	-	-	0/10/10/10	0/0/0/0
3	URP	C	600	2	-	0/6/6/6	0/0/0/0
4	BCN	C	601	-	-	0/10/10/10	0/0/0/0
3	URP	D	600	2	-	0/6/6/6	0/0/0/0
4	BCN	D	601	-	-	0/10/10/10	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.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 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	431/474 (90%)	0.31	7 (1%) 68 69	23, 27, 31, 37	0
1	B	431/474 (90%)	0.34	20 (4%) 31 30	23, 27, 30, 35	0
1	C	432/474 (91%)	0.41	26 (6%) 21 20	23, 27, 30, 37	0
1	D	431/474 (90%)	0.23	7 (1%) 68 69	24, 27, 30, 40	0
All	All	1725/1896 (90%)	0.32	60 (3%) 43 41	23, 27, 30, 40	0

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	192	ASP	7.0
1	C	105	GLY	5.4
1	D	458	PRO	5.0
1	B	458	PRO	4.6
1	C	458	PRO	4.3
1	C	203	ASN	4.3
1	C	192	ASP	4.2
1	C	193	LYS	4.1
1	C	27	PRO	4.0
1	A	458	PRO	3.9
1	B	105	GLY	3.9
1	C	54	GLN	3.8
1	C	209	ASP	3.6
1	C	237	ASN	3.4
1	C	144	ASN	3.4
1	A	32[A]	SER	3.3
1	C	30	ILE	3.1
1	A	193	LYS	3.0
1	C	198	TYR	3.0
1	B	193	LYS	2.9
1	C	327	ASP	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	79	ASN	2.8
1	C	181	GLU	2.8
1	B	30	ILE	2.7
1	B	192	ASP	2.7
1	B	385	LYS	2.7
1	B	144	ASN	2.7
1	B	203	ASN	2.6
1	C	202	LYS	2.6
1	D	144	ASN	2.6
1	A	192	ASP	2.6
1	B	209	ASP	2.5
1	C	207	ILE	2.5
1	B	83	SER	2.5
1	D	350	GLY	2.5
1	A	274	ALA	2.5
1	B	112	GLY	2.4
1	C	28	LEU	2.4
1	D	287	GLU	2.4
1	A	237	ASN	2.4
1	C	45	GLN	2.4
1	B	56	SER	2.4
1	C	385	LYS	2.4
1	B	28	LEU	2.3
1	B	198	TYR	2.3
1	C	334	LYS	2.3
1	A	386	ASP	2.3
1	B	104	ASN	2.2
1	B	386	ASP	2.2
1	C	56	SER	2.2
1	D	30	ILE	2.2
1	C	32	SER	2.2
1	B	457	PHE	2.1
1	C	41	GLU	2.1
1	B	54	GLN	2.1
1	B	45	GLN	2.0
1	C	424	TYR	2.0
1	B	68	ALA	2.0
1	C	68	ALA	2.0
1	D	32	SER	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, 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	BCN	B	601	11/11	0.19	3.68	51,52,53,53	0
3	URP	B	600	9/9	0.18	3.62	33,35,36,37	0
4	BCN	A	601	11/11	0.22	3.53	58,61,61,61	0
4	BCN	C	601	11/11	0.18	2.18	46,47,47,48	0
4	BCN	D	601	11/11	0.18	2.06	51,51,52,52	0
3	URP	D	600	9/9	0.15	0.85	32,33,35,36	0
3	URP	A	600	9/9	0.17	0.71	33,33,36,37	0
3	URP	C	600	9/9	0.12	0.63	33,34,35,36	0
2	ZN	B	500	1/1	0.11	0.17	49,49,49,49	0
2	ZN	C	501	1/1	0.09	-0.89	35,35,35,35	1
2	ZN	B	501	1/1	0.08	-2.40	39,39,39,39	1
2	ZN	A	501	1/1	0.07	-2.59	32,32,32,32	1
2	ZN	C	500	1/1	0.03	-2.94	46,46,46,46	0
2	ZN	D	501	1/1	0.11	-3.78	30,30,30,30	1
2	ZN	A	500	1/1	0.06	-3.99	46,46,46,46	0
2	ZN	D	500	1/1	0.06	-4.79	47,47,47,47	0

6.5 Other polymers ⓘ

There are no such residues in this entry.