Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 05:54 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.; Dobritzsch, D.
Deposited on	:	2007-08-08
Resolution	:	2.00 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
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:

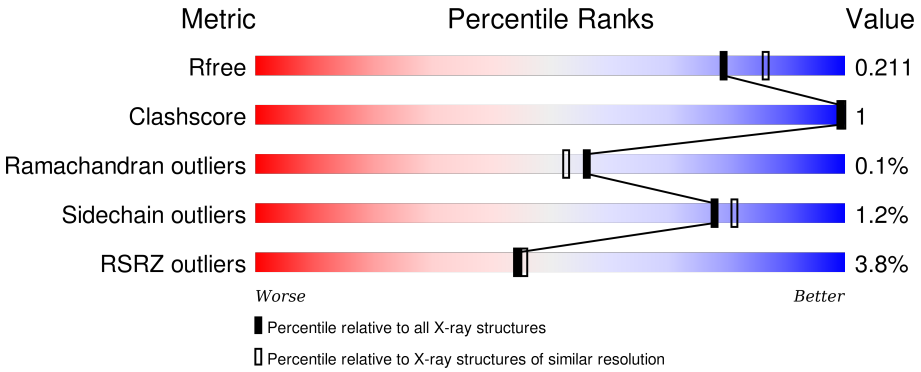
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)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

1 Overall quality at a glance

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

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}	91344	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (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. 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	474	2% 89% • 9%
1	B	474	5% 89% • 9%
1	C	474	5% 88% • 9%
1	D	474	2% 88% • 9%

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	B	600	-	-	-	X
4	BCN	A	601	-	-	-	X
4	BCN	B	601	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 14629 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 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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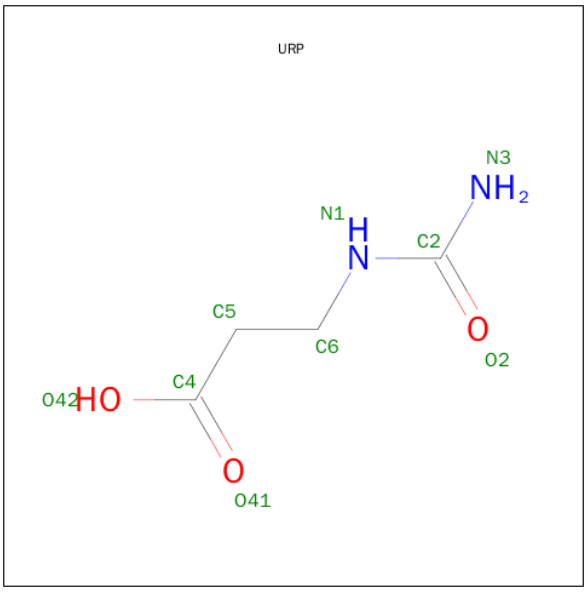
Chain	Residue	Modelled	Actual	Comment	Reference
D	159	ALA	GLU	ENGINEERED MUTATION	UNP Q96W94
D	456	GLN	-	EXPRESSION TAG	UNP Q96W94
D	457	PHE	-	EXPRESSION TAG	UNP Q96W94
D	458	PRO	-	EXPRESSION TAG	UNP Q96W94
D	459	GLY	-	EXPRESSION TAG	UNP Q96W94
D	460	ASP	-	EXPRESSION TAG	UNP Q96W94
D	461	ASP	-	EXPRESSION 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).

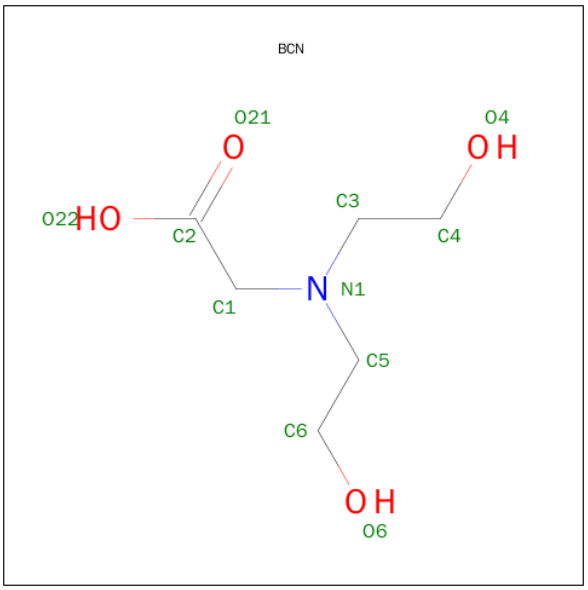
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	2	Total Zn 2 2	0	0
2	A	2	Total Zn 2 2	0	0
2	D	2	Total Zn 2 2	0	0
2	C	2	Total Zn 2 2	0	0

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



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

- Molecule 4 is BICINE (three-letter code: BCN) (formula: $C_6H_{13}NO_4$).



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.

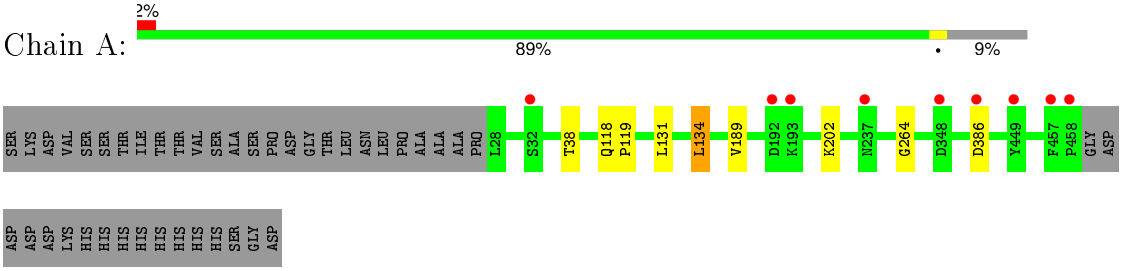
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	303	Total	O	0	0
			303	303		
5	B	204	Total	O	0	0
			204	204		
5	C	180	Total	O	0	0
			180	180		
5	D	269	Total	O	0	0
			269	269		

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.

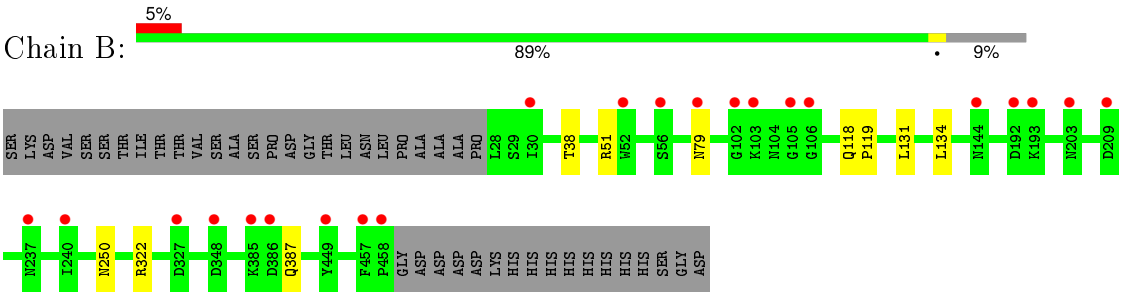
- Molecule 1: BETA-ALANINE SYNTHASE

Chain A:



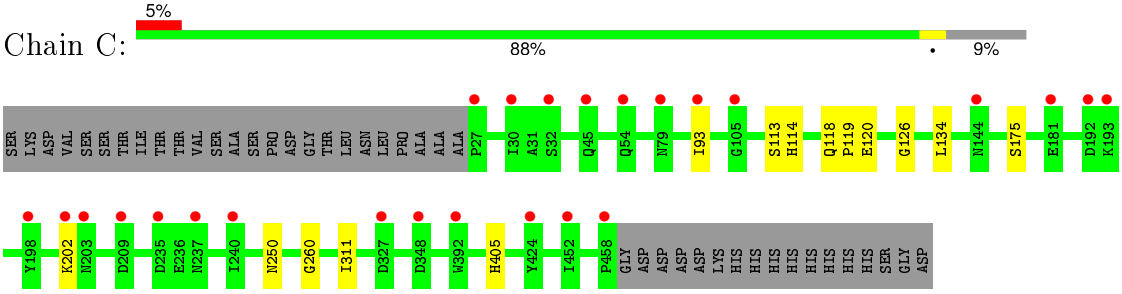
- Molecule 1: BETA-ALANINE SYNTHASE

Chain B:



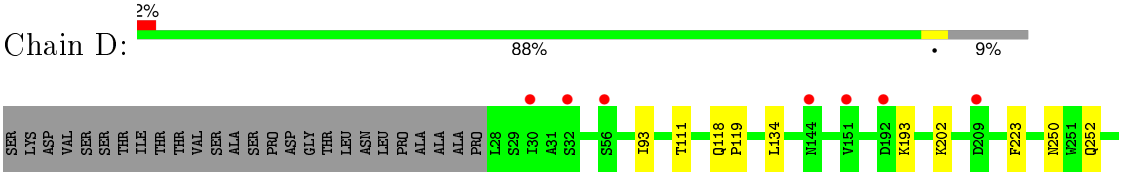
- Molecule 1: BETA-ALANINE SYNTHASE

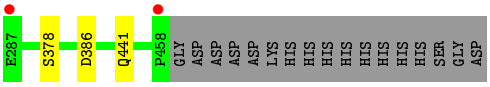
Chain C:



- Molecule 1: BETA-ALANINE SYNTHASE

Chain D:




E287
S378
D386
Q441
P458
GLY
ASP
ASP
ASP
ASP
LYS
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	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
$< I/\sigma(I) >$ [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)	0.38 , 49.7	EDS
Estimated twinning fraction	0.053 for h,-k,-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	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.*

[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

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 Too-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 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	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

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 (17) 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: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	Interatomic distance (Å)	Clash overlap (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	Interatomic distance (Å)	Clash overlap (Å)
5:C:2137:HOH:O	5:D:2221:HOH:O[2_656]	2.11	0.09

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	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%)	52	48
1	D	444/474 (94%)	436 (98%)	8 (2%)	0	100	100
All	All	1757/1896 (93%)	1726 (98%)	30 (2%)	1 (0%)	56	53

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	113	SER

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	365/392 (93%)	361 (99%)	4 (1%)	80	83
1	B	368/392 (94%)	362 (98%)	6 (2%)	70	73
1	C	361/392 (92%)	358 (99%)	3 (1%)	86	89
1	D	371/392 (95%)	365 (98%)	6 (2%)	70	73
All	All	1465/1568 (93%)	1446 (99%)	19 (1%)	78	79

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

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Mol	Chain	Res	Type
1	C	250	ASN
1	C	401	GLN
1	D	250	ASN
1	D	401	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 carbohydrates in this entry.

5.6 Ligand geometry (i)

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	5,8,8	0.61	0	6,9,9	0.82	0
4	BCN	A	601	-	7,10,10	0.42	0	8,11,11	0.88	0
3	URP	B	600	2	5,8,8	0.48	0	6,9,9	0.72	0
4	BCN	B	601	-	7,10,10	0.31	0	8,11,11	1.15	1 (12%)
3	URP	C	600	2	5,8,8	0.52	0	6,9,9	0.87	0
4	BCN	C	601	-	7,10,10	0.38	0	8,11,11	0.71	0
3	URP	D	600	2	5,8,8	0.48	0	6,9,9	0.74	0
4	BCN	D	601	-	7,10,10	0.30	0	8,11,11	1.48	1 (12%)

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	-	0/4/6/6	0/0/0/0
4	BCN	A	601	-	-	0/8/10/10	0/0/0/0
3	URP	B	600	2	-	0/4/6/6	0/0/0/0
4	BCN	B	601	-	-	0/8/10/10	0/0/0/0
3	URP	C	600	2	-	0/4/6/6	0/0/0/0
4	BCN	C	601	-	-	0/8/10/10	0/0/0/0
3	URP	D	600	2	-	0/4/6/6	0/0/0/0
4	BCN	D	601	-	-	0/8/10/10	0/0/0/0

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	D	601	BCN	C2-C1-N1	-3.37	108.54	113.53
4	B	601	BCN	C2-C1-N1	-2.07	110.46	113.53

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^{th} 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%)	0.26	9 (2%)	67	67	23, 27, 31, 37	0
1	B	431/474 (90%)	0.45	22 (5%)	32	33	23, 27, 30, 35	0
1	C	432/474 (91%)	0.52	25 (5%)	26	28	23, 27, 30, 37	0
1	D	431/474 (90%)	0.26	9 (2%)	67	67	24, 27, 30, 40	0
All	All	1725/1896 (90%)	0.37	65 (3%)	44	45	23, 27, 30, 40	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	192	ASP	6.8
1	D	458	PRO	5.4
1	A	458	PRO	5.3
1	C	105	GLY	5.2
1	C	193	LYS	5.1
1	C	192	ASP	4.9
1	C	458	PRO	4.7
1	B	458	PRO	4.1
1	C	209	ASP	4.0
1	B	193	LYS	3.8
1	B	105	GLY	3.8
1	C	203	ASN	3.6
1	A	193	LYS	3.5
1	B	102	GLY	3.5
1	B	30	ILE	3.2
1	C	144	ASN	3.2
1	B	56	SER	3.1
1	C	327	ASP	2.9
1	C	27	PRO	2.9
1	D	32	SER	2.8
1	C	235	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	202	LYS	2.7
1	B	348	ASP	2.7
1	B	449	TYR	2.7
1	B	457	PHE	2.7
1	C	54	GLN	2.6
1	B	386	ASP	2.6
1	A	192	ASP	2.6
1	A	237	ASN	2.6
1	B	79	ASN	2.6
1	C	237	ASN	2.5
1	C	93	ILE	2.5
1	D	144	ASN	2.5
1	C	181	GLU	2.4
1	A	386	ASP	2.4
1	B	144	ASN	2.4
1	B	209	ASP	2.4
1	B	240	ILE	2.4
1	B	103	LYS	2.4
1	A	32[A]	SER	2.3
1	B	106	GLY	2.3
1	D	151[A]	VAL	2.3
1	C	240	ILE	2.3
1	D	30	ILE	2.3
1	C	198	TYR	2.2
1	B	192	ASP	2.2
1	C	45	GLN	2.2
1	A	348	ASP	2.2
1	C	79	ASN	2.2
1	B	385	LYS	2.2
1	A	457	PHE	2.1
1	C	30	ILE	2.1
1	B	237	ASN	2.1
1	A	449	TYR	2.1
1	C	424	TYR	2.1
1	B	203	ASN	2.1
1	C	348	ASP	2.1
1	B	52	TRP	2.1
1	C	32	SER	2.1
1	B	327	ASP	2.0
1	C	392	TRP	2.0
1	C	452	ILE	2.0
1	D	56	SER	2.0

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Mol	Chain	Res	Type	RSRZ
1	D	209	ASP	2.0
1	D	287	GLU	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 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^{th} 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
4	BCN	A	601	11/11	0.69	0.22	4.32	58,61,61,61	0
3	URP	B	600	9/9	0.88	0.18	2.48	33,35,36,37	0
4	BCN	B	601	11/11	0.68	0.20	2.00	51,52,53,53	0
4	BCN	D	601	11/11	0.78	0.20	1.97	51,51,52,52	0
2	ZN	B	500	1/1	0.99	0.17	1.97	49,49,49,49	0
2	ZN	C	501	1/1	0.98	0.15	1.48	35,35,35,35	1
3	URP	D	600	9/9	0.95	0.16	1.32	32,33,35,36	0
4	BCN	C	601	11/11	0.66	0.18	1.23	46,47,47,48	0
3	URP	A	600	9/9	0.93	0.14	0.63	33,33,36,37	0
3	URP	C	600	9/9	0.93	0.13	0.12	33,34,35,36	0
2	ZN	A	501	1/1	0.98	0.11	-0.71	32,32,32,32	1
2	ZN	A	500	1/1	0.98	0.09	-1.48	46,46,46,46	0
2	ZN	D	501	1/1	0.93	0.10	-1.61	30,30,30,30	1
2	ZN	D	500	1/1	0.99	0.08	-1.71	47,47,47,47	0
2	ZN	B	501	1/1	0.88	0.10	-1.92	39,39,39,39	1
2	ZN	C	500	1/1	0.97	0.07	-2.13	46,46,46,46	0

6.5 Other polymers (i)

There are no such residues in this entry.