



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2018 – 11:41 pm GMT

PDB ID : 3E8Q
Title : X-ray structure of rat arginase I-T135A: the unliganded complex
Authors : Shishova, E.Y.; Di Costanzo, L.; Emig, F.A.; Ash, D.E.; Christianson, D.W.
Deposited on : 2008-08-20
Resolution : 2.90 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

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

with specific help available everywhere you see the ⓘ symbol.

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	:	trunk30967
Percentile statistics	:	20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac	:	5.8.0158
CCP4	:	7.0 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk30967

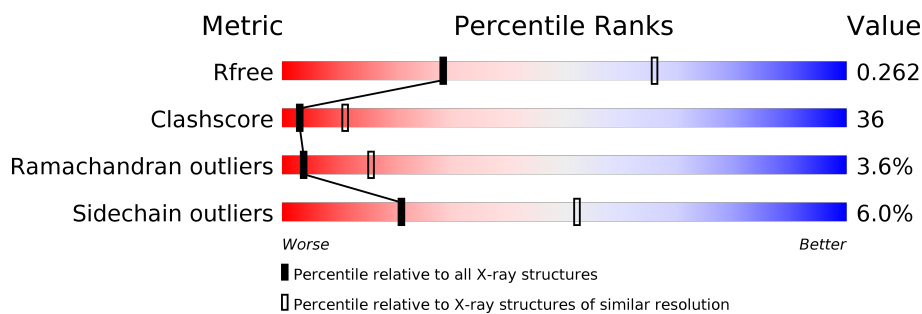
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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}	111664	1716 (2.90-2.90)
Clashscore	122126	1924 (2.90-2.90)
Ramachandran outliers	120053	1884 (2.90-2.90)
Sidechain outliers	120020	1886 (2.90-2.90)

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	323	
1	B	323	
1	C	323	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7078 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 Arginase-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	308	Total	C	N	O	S	0	0	0
			2342	1494	399	442	7			
1	B	308	Total	C	N	O	S	0	0	0
			2342	1494	399	442	7			
1	C	308	Total	C	N	O	S	0	0	0
			2342	1494	399	442	7			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	135	ALA	THR	ENGINEERED	UNP P07824
B	135	ALA	THR	ENGINEERED	UNP P07824
C	135	ALA	THR	ENGINEERED	UNP P07824

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	13	Total	O	0	0
			13	13		
3	B	14	Total	O	0	0
			14	14		

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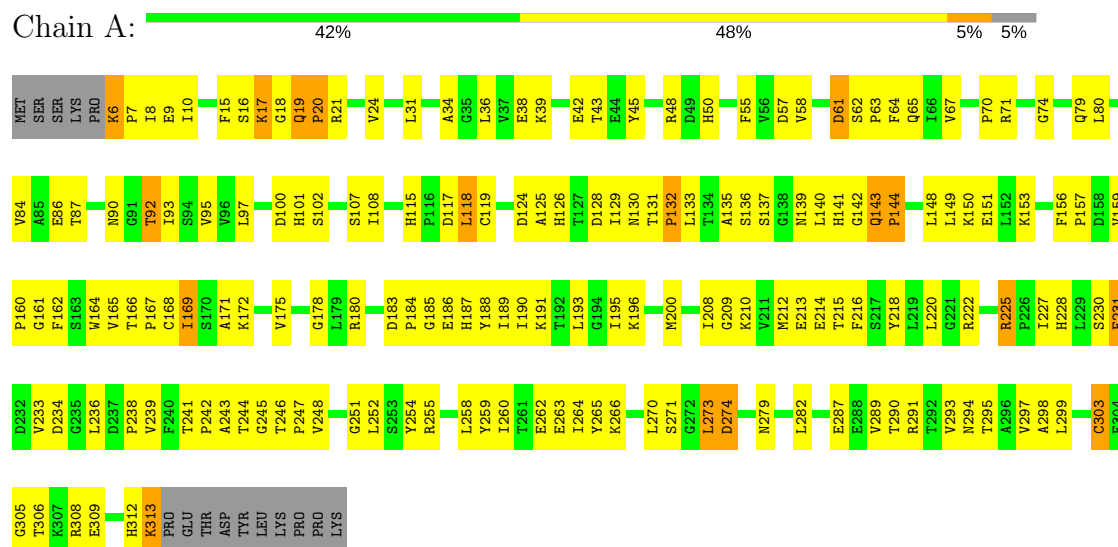
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	19	Total	O	0	0
			19	19		

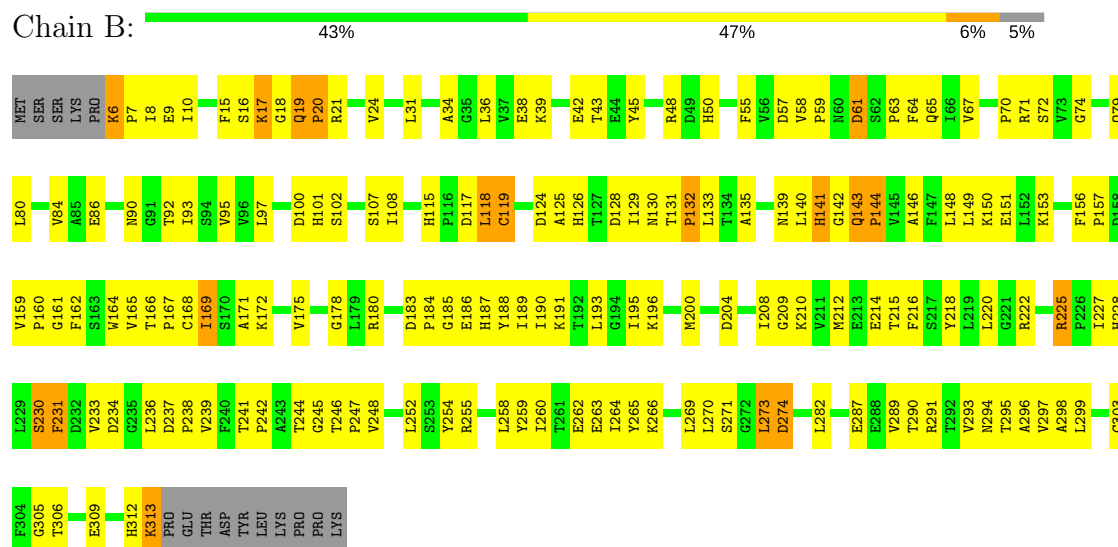
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

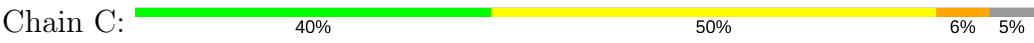
• Molecule 1: Arginase-1



• Molecule 1: Arginase-1



• Molecule 1: Arginase-1



T290	R291	T292	V293	N294	T295	A296	V297	A298	L299	C303	F304	G305	T306	E309	H312	K313	PRO	GLU	THR	ASP	TYR	LEU	LYS	PRO	PRO	PRO	LYS	G251	L252	S253	Y254	R255	E256	G257	L258	Y259	T260	T261	E262	E263	I264	Y265	K266	L269	L270	S271	G272	L273	D274	E277	V278	N279	L282	E287	E288	V289
R222	E151	L152	K153	F156	P157	D158	V159	P160	G161	F162	S163	M164	V165	T166	P167	C168	I169	S170	A171	K172	V175	G178	L179	R180	D183	P184	G185	E186	H187	Y188	I189	I190	K191	T192	L193	G194	I195	K196	Y197	M200	I208	G209	K210	V211	M212	E213	E214	T215	F216	S217	Y218	L219	L220	G221		
G74	E151	L152	K153	F156	P157	D158	V159	P160	G161	F162	S163	M164	V165	T166	P167	C168	I169	S170	A171	K172	V175	G178	L179	R180	D183	P184	G185	E186	H187	Y188	I189	I190	K191	T192	L193	G194	I195	K196	Y197	M200	I208	G209	K210	V211	M212	E213	E214	T215	F216	S217	Y218	L219	L220	G221		
G74	E151	L152	K153	F156	P157	D158	V159	P160	G161	F162	S163	M164	V165	T166	P167	C168	I169	S170	A171	K172	V175	G178	L179	R180	D183	P184	G185	E186	H187	Y188	I189	I190	K191	T192	L193	G194	I195	K196	Y197	M200	I208	G209	K210	V211	M212	E213	E214	T215	F216	S217	Y218	L219	L220	G221		
G74	E151	L152	K153	F156	P157	D158	V159	P160	G161	F162	S163	M164	V165	T166	P167	C168	I169	S170	A171	K172	V175	G178	L179	R180	D183	P184	G185	E186	H187	Y188	I189	I190	K191	T192	L193	G194	I195	K196	Y197	M200	I208	G209	K210	V211	M212	E213	E214	T215	F216	S217	Y218	L219	L220	G221		
G74	E151	L152	K153	F156	P157	D158	V159	P160	G161	F162	S163	M164	V165	T166	P167	C168	I169	S170	A171	K172	V175	G178	L179	R180	D183	P184	G185	E186	H187	Y188	I189	I190	K191	T192	L193	G194	I195	K196	Y197	M200	I208	G209	K210	V211	M212	E213	E214	T215	F216	S217	Y218	L219	L220	G221		
G74	E151	L152	K153	F156	P157	D158	V159	P160	G161	F162	S163	M164	V165	T166	P167	C168	I169	S170	A171	K172	V175	G178	L179	R180	D183	P184	G185	E186	H187	Y188	I189	I190	K191	T192	L193	G194	I195	K196	Y197	M200	I208	G209	K210	V211	M212	E213	E214	T215	F216	S217	Y218	L219	L220	G221		
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G74	E151	L152	K153	F156	P157	D158	V159	P160	G161	F162	S163	M164	V165	T166	P167	C168	I169	S170	A171	K172	V175	G178	L179	R180	D183	P184	G185	E186	H187	Y188	I189	I190	K191	T192	L193	G194	I195	K196	Y197	M200	I208	G209	K210	V211	M212	E213	E214	T215	F216	S217	Y218	L219	L220	G221		
G74	E151	L152	K153	F156	P157	D158	V159	P160	G161	F162	S163	M164	V165	T166	P167	C168	I169	S170	A171	K172	V175	G178	L179	R180	D183	P184	G185	E186	H187	Y188	I189	I190	K191	T192	L193	G194	I195	K196	Y197	M200	I208	G209	K210	V211	M212	E213	E214	T215	F216	S217	Y218	L219	L220	G221		
G74	E151	L152	K153	F156	P157	D158	V159	P160	G161	F162	S163	M164	V165	T166	P167	C168	I169	S170	A171	K172	V175	G178	L179	R180	D183	P184	G185	E186	H187	Y188	I189	I190	K191	T192	L193	G194	I195	K196	Y197	M200	I208	G209	K210	V211	M212	E213	E214	T215	F216	S217	Y218	L219	L220	G221		
G74	E151	L152	K153	F156	P157	D158	V159	P160	G161	F162	S163	M164	V165	T166	P167	C168	I169	S170	A171	K172	V175	G178	L179	R180	D183	P184	G185	E186	H187	Y188	I189	I190	K191	T192	L193	G194	I195	K196	Y197	M200	I208	G209	K210	V211	M212	E213	E214	T215	F216	S217	Y218	L219	L220	G221		
G74	E151	L152	K153	F156	P157	D158	V159	P160	G161	F162	S163	M164	V165	T166	P167	C168	I169	S170	A171	K172	V175	G178	L179	R180	D183	P184	G185	E186	H187	Y188	I189	I190	K191	T192	L193	G194	I195	K196	Y197	M200	I208	G209	K210	V211	M212	E213	E214	T215	F216	S217	Y218	L219	L220	G221		
G74	E151	L152	K153	F156	P157	D158	V159	P160	G161	F162	S163	M164	V165	T166	P167	C168	I169	S170	A171	K172	V175	G178	L179	R180	D183	P184	G185	E186	H187	Y188	I189	I190	K191	T192	L193	G194	I195	K196	Y197	M200	I208	G209	K210	V211	M212	E213	E214	T215	F216	S217	Y218	L219	L220	G221		
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G74	E151	L152	K153	F156	P157	D158	V159	P160	G161	F162	S163	M164	V165	T166	P167	C168	I169	S170	A171	K172	V175	G178	L179	R180	D183	P184	G185	E186	H187	Y188	I189	I190	K191	T192	L193	G194	I195	K196	Y197	M200	I208	G209	K210	V211	M212	E213	E214	T215	F216	S217	Y218	L219	L220	G221		
G74	E151	L152	K153	F156	P157	D158	V159	P160	G161	F162	S163	M164	V165	T166	P167	C168	I169	S170	A171	K172	V175	G178	L179	R180	D183	P184	G185	E186	H187	Y188	I189	I190	K191	T192	L193	G194	I195	K196	Y197	M200	I208	G209	K210	V211	M212	E213	E214	T215	F216	S217	Y218	L219	L220	G221		
G74	E151	L152	K153	F156	P157	D158	V159	P160	G161	F162	S163	M164	V165	T166	P167	C168	I169	S170	A171	K172	V175	G178	L179	R180	D183	P184	G185	E186	H187	Y188	I189	I190	K191	T192	L193	G194	I195	K196	Y197	M200	I208	G209	K210	V211	M212	E213	E214	T215	F216	S217	Y218	L219	L220	G221		
G74	E151	L152	K153	F156	P157	D158	V159	P160	G161	F162	S163	M164	V165	T166	P167	C168	I169	S170	A171	K172	V175	G178	L179	R180	D183	P184	G185	E186	H187	Y188	I189	I190	K191	T192	L193	G194	I195	K196	Y197	M200	I208	G209	K210	V211	M212	E213	E214	T215	F216	S217	Y218	L219	L220	G221		
G74	E151	L152	K153	F156	P157	D158	V159	P160	G161	F162	S163	M164	V165	T166	P167	C168	I169	S170	A171	K172	V175	G178	L179	R180	D183	P184	G185	E186	H187	Y188	I189	I190	K191	T192	L193	G194	I195	K196	Y197	M200	I208	G209	K210	V211	M212	E213	E214	T215	F216	S217	Y218	L219	L220	G221		
G74	E151	L152	K153	F156	P157	D158	V159	P160	G161	F162	S163	M164	V165	T166	P167	C168	I169	S170	A171	K172	V175	G178	L179	R180	D183	P184	G185	E186	H187	Y188	I189	I190	K191	T192	L193	G194	I195	K196	Y197	M200	I208	G209	K210	V211	M212	E213	E214	T215	F216	S217	Y218	L219	L220	G221		
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G74	E151	L152	K153	F156	P157	D158	V159	P160	G161	F162	S163	M164	V165	T166	P167	C168	I169	S170	A171	K172	V175	G178	L179	R180	D183	P184	G185	E186	H187	Y188	I189	I190	K191	T192	L193	G194	I195	K196	Y197	M200	I208	G209	K210	V211	M212	E213	E214	T215	F216	S217	Y218	L219	L220	G221		
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G74	E151	L152	K153	F156	P157	D158	V159	P160	G161	F162	S163	M164	V165	T166	P167	C168	I169	S170	A171	K172	V175	G178	L179	R180	D183	P184	G185	E186	H187	Y188	I189	I190	K191	T192	L193	G194	I195	K196	Y197	M200	I208	G209	K210	V211	M212	E213	E214	T215	F216	S217	Y218	L219	L220	G221		
G74	E151	L152	K153	F156	P157	D158	V159	P160	G161	F162	S163	M164	V165	T166	P167	C168	I169	S170	A171	K172	V175	G178	L179	R180	D183	P184	G185	E186	H187	Y188	I189	I190	K191	T192	L193	G194	I195	K196	Y197	M200	I208	G209	K210	V211	M212	E213	E214	T215	F216	S217	Y218	L219	L220	G221		
G74	E151	L152	K153	F156	P157	D158	V159	P160	G161	F162	S163	M164	V165	T166	P167	C168	I169	S170	A171	K172	V175	G178	L179	R180	D183	P184	G185	E186	H187	Y188	I189	I190	K191	T192	L193	G194	I195	K196	Y197	M200	I208	G209	K210	V211	M212	E213	E214	T215	F216	S217	Y218	L219	L220	G221		
G74	E151	L152	K153	F156	P157	D158	V159	P160	G161	F162	S163	M164	V165	T166	P167	C168	I169	S170	A171	K172	V175	G178	L179	R180	D183	P184	G185	E186	H187	Y188	I189	I190	K191	T192	L193	G194	I195	K196	Y197	M200	I208															

4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	87.40Å 87.40Å 100.82Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	25.13 – 2.90 25.13 – 2.80	Depositor EDS
% Data completeness (in resolution range)	98.4 (25.13-2.90) 96.3 (25.13-2.80)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.79 (at 2.80Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.263 , 0.296 0.265 , 0.262	Depositor DCC
R_{free} test set	1056 reflections (5.19%)	wwPDB-VP
Wilson B-factor (Å ²)	37.8	Xtriage
Anisotropy	0.964	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 27.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.096 for -h,-k,l 0.348 for h,-h-k,-l 0.095 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	7078	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.41% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: MN

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	0.45	1/2393 (0.0%)	0.65	0/3248
1	B	0.44	1/2393 (0.0%)	0.66	0/3248
1	C	0.41	0/2393	0.66	0/3248
All	All	0.43	2/7179 (0.0%)	0.66	0/9744

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	119	CYS	CB-SG	-5.48	1.72	1.81
1	A	303	CYS	CB-SG	-5.05	1.73	1.81

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	2342	0	2374	165	0
1	B	2342	0	2374	178	0
1	C	2342	0	2374	180	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	13	0	0	0	0
3	B	14	0	0	0	0
3	C	19	0	0	1	0
All	All	7078	0	7122	507	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 36.

The worst 5 of 507 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:290:THR:HG22	1:C:294:ASN:HD21	1.31	0.95
1:B:290:THR:HG22	1:B:294:ASN:HD21	1.34	0.92
1:C:234:ASP:HB3	1:C:244:THR:HG21	1.52	0.90
1:B:234:ASP:HB3	1:B:244:THR:HG21	1.55	0.89
1:A:290:THR:HG22	1:A:294:ASN:HD21	1.39	0.86

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	306/323 (95%)	260 (85%)	35 (11%)	11 (4%)	4	16
1	B	306/323 (95%)	262 (86%)	33 (11%)	11 (4%)	4	16
1	C	306/323 (95%)	259 (85%)	36 (12%)	11 (4%)	4	16
All	All	918/969 (95%)	781 (85%)	104 (11%)	33 (4%)	4	16

5 of 33 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	17	LYS
1	B	17	LYS
1	C	17	LYS
1	C	67	VAL
1	A	61	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	257/272 (94%)	242 (94%)	15 (6%)	22	54
1	B	257/272 (94%)	241 (94%)	16 (6%)	20	51
1	C	257/272 (94%)	242 (94%)	15 (6%)	22	54
All	All	771/816 (94%)	725 (94%)	46 (6%)	21	52

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	101	HIS
1	B	230	SER
1	C	273	LEU
1	B	118	LEU
1	B	169	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	65	GLN
1	B	79	GLN
1	C	79	GLN
1	B	19	GLN
1	C	65	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 6 ligands modelled in this entry, 6 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 ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.