



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 06:23 PM UTC

PDB ID : 3BE7 / pdb_00003be7
Title : Crystal structure of Zn-dependent arginine carboxypeptidase
Authors : Patskovsky, Y.; Ramagopal, U.A.; Toro, R.; Meyer, A.J.; Freeman, J.; Iizuka, M.; Bain, K.; Rodgers, L.; Raushel, F.; Sauder, J.M.; Burley, S.K.; Almo, S.C.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2007-11-16
Resolution : 2.30 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 types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

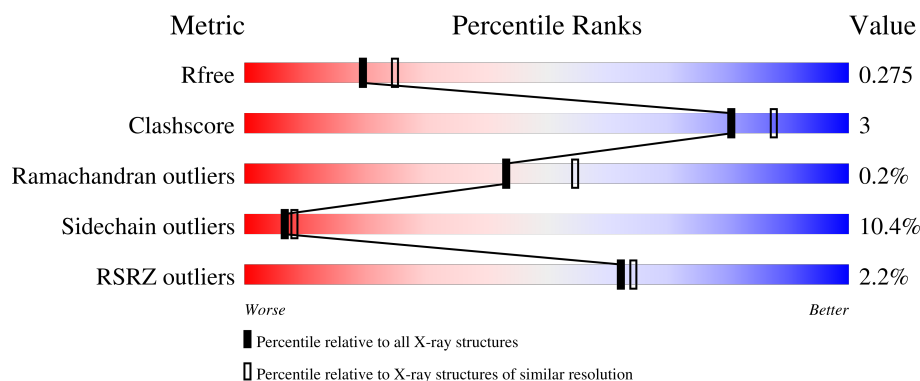
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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 ≥ 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	408	 2% 83% 14% ..
1	B	408	 2% 80% 16% ..
1	C	408	 % 82% 13% ..
1	D	408	 % 81% 13% ..
1	E	408	 2% 83% 13% .

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Mol	Chain	Length	Quality of chain
1	F	408	3% 82% 13%
1	G	408	3% 82% 12%
1	H	408	2% 83% 13%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 24963 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 Zn-dependent arginine carboxypeptidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	398	Total	C	N	O	S	0	9	0
			3081	1938	535	591	17			
1	B	395	Total	C	N	O	S	0	5	0
			3041	1914	531	580	16			
1	C	394	Total	C	N	O	S	0	2	0
			3010	1893	525	576	16			
1	D	395	Total	C	N	O	S	0	2	0
			3021	1900	527	578	16			
1	E	394	Total	C	N	O	S	0	2	0
			3010	1892	523	579	16			
1	F	395	Total	C	N	O	S	0	1	0
			3012	1894	523	578	17			
1	G	394	Total	C	N	O	S	0	2	0
			3012	1894	525	577	16			
1	H	395	Total	C	N	O	S	0	1	0
			3010	1892	523	579	16			

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	expression tag	PDB 3BE7
A	0	SER	-	expression tag	PDB 3BE7
A	1	LEU	-	expression tag	PDB 3BE7
A	399	GLU	-	expression tag	PDB 3BE7
A	400	GLY	-	expression tag	PDB 3BE7
A	401	HIS	-	expression tag	PDB 3BE7
A	402	HIS	-	expression tag	PDB 3BE7
A	403	HIS	-	expression tag	PDB 3BE7
A	404	HIS	-	expression tag	PDB 3BE7
A	405	HIS	-	expression tag	PDB 3BE7
A	406	HIS	-	expression tag	PDB 3BE7
B	-1	MET	-	expression tag	PDB 3BE7
B	0	SER	-	expression tag	PDB 3BE7

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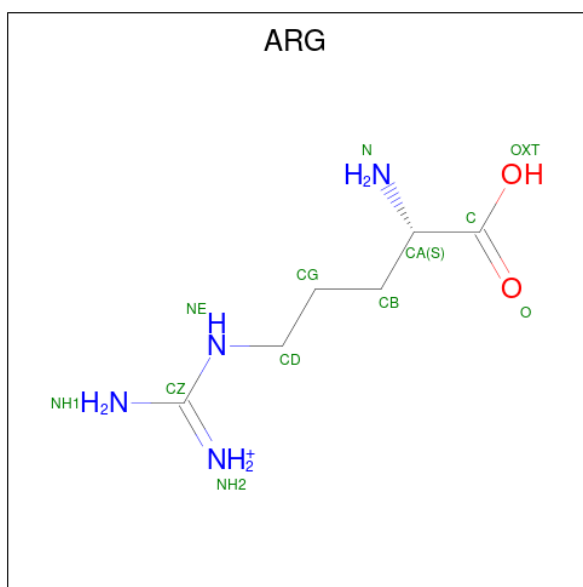
Chain	Residue	Modelled	Actual	Comment	Reference
B	1	LEU	-	expression tag	PDB 3BE7
B	399	GLU	-	expression tag	PDB 3BE7
B	400	GLY	-	expression tag	PDB 3BE7
B	401	HIS	-	expression tag	PDB 3BE7
B	402	HIS	-	expression tag	PDB 3BE7
B	403	HIS	-	expression tag	PDB 3BE7
B	404	HIS	-	expression tag	PDB 3BE7
B	405	HIS	-	expression tag	PDB 3BE7
B	406	HIS	-	expression tag	PDB 3BE7
C	-1	MET	-	expression tag	PDB 3BE7
C	0	SER	-	expression tag	PDB 3BE7
C	1	LEU	-	expression tag	PDB 3BE7
C	399	GLU	-	expression tag	PDB 3BE7
C	400	GLY	-	expression tag	PDB 3BE7
C	401	HIS	-	expression tag	PDB 3BE7
C	402	HIS	-	expression tag	PDB 3BE7
C	403	HIS	-	expression tag	PDB 3BE7
C	404	HIS	-	expression tag	PDB 3BE7
C	405	HIS	-	expression tag	PDB 3BE7
C	406	HIS	-	expression tag	PDB 3BE7
D	-1	MET	-	expression tag	PDB 3BE7
D	0	SER	-	expression tag	PDB 3BE7
D	1	LEU	-	expression tag	PDB 3BE7
D	399	GLU	-	expression tag	PDB 3BE7
D	400	GLY	-	expression tag	PDB 3BE7
D	401	HIS	-	expression tag	PDB 3BE7
D	402	HIS	-	expression tag	PDB 3BE7
D	403	HIS	-	expression tag	PDB 3BE7
D	404	HIS	-	expression tag	PDB 3BE7
D	405	HIS	-	expression tag	PDB 3BE7
D	406	HIS	-	expression tag	PDB 3BE7
E	-1	MET	-	expression tag	PDB 3BE7
E	0	SER	-	expression tag	PDB 3BE7
E	1	LEU	-	expression tag	PDB 3BE7
E	399	GLU	-	expression tag	PDB 3BE7
E	400	GLY	-	expression tag	PDB 3BE7
E	401	HIS	-	expression tag	PDB 3BE7
E	402	HIS	-	expression tag	PDB 3BE7
E	403	HIS	-	expression tag	PDB 3BE7
E	404	HIS	-	expression tag	PDB 3BE7
E	405	HIS	-	expression tag	PDB 3BE7
E	406	HIS	-	expression tag	PDB 3BE7

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-1	MET	-	expression tag	PDB 3BE7
F	0	SER	-	expression tag	PDB 3BE7
F	1	LEU	-	expression tag	PDB 3BE7
F	399	GLU	-	expression tag	PDB 3BE7
F	400	GLY	-	expression tag	PDB 3BE7
F	401	HIS	-	expression tag	PDB 3BE7
F	402	HIS	-	expression tag	PDB 3BE7
F	403	HIS	-	expression tag	PDB 3BE7
F	404	HIS	-	expression tag	PDB 3BE7
F	405	HIS	-	expression tag	PDB 3BE7
F	406	HIS	-	expression tag	PDB 3BE7
G	-1	MET	-	expression tag	PDB 3BE7
G	0	SER	-	expression tag	PDB 3BE7
G	1	LEU	-	expression tag	PDB 3BE7
G	399	GLU	-	expression tag	PDB 3BE7
G	400	GLY	-	expression tag	PDB 3BE7
G	401	HIS	-	expression tag	PDB 3BE7
G	402	HIS	-	expression tag	PDB 3BE7
G	403	HIS	-	expression tag	PDB 3BE7
G	404	HIS	-	expression tag	PDB 3BE7
G	405	HIS	-	expression tag	PDB 3BE7
G	406	HIS	-	expression tag	PDB 3BE7
H	-1	MET	-	expression tag	PDB 3BE7
H	0	SER	-	expression tag	PDB 3BE7
H	1	LEU	-	expression tag	PDB 3BE7
H	399	GLU	-	expression tag	PDB 3BE7
H	400	GLY	-	expression tag	PDB 3BE7
H	401	HIS	-	expression tag	PDB 3BE7
H	402	HIS	-	expression tag	PDB 3BE7
H	403	HIS	-	expression tag	PDB 3BE7
H	404	HIS	-	expression tag	PDB 3BE7
H	405	HIS	-	expression tag	PDB 3BE7
H	406	HIS	-	expression tag	PDB 3BE7

- Molecule 2 is ARGinine (CCD ID: ARG) (formula: $C_6H_{15}N_4O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			12	6	4	2		
2	B	1	Total	C	N	O	0	0
			12	6	4	2		
2	C	1	Total	C	N	O	0	0
			12	6	4	2		
2	D	1	Total	C	N	O	0	0
			12	6	4	2		
2	E	1	Total	C	N	O	0	0
			12	6	4	2		
2	F	1	Total	C	N	O	0	0
			12	6	4	2		
2	G	1	Total	C	N	O	0	0
			12	6	4	2		
2	H	1	Total	C	N	O	0	0
			12	6	4	2		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		
3	E	1	Total	C	O	0	0
			6	3	3		
3	E	1	Total	C	O	0	0
			6	3	3		
3	F	1	Total	C	O	0	0
			6	3	3		
3	F	1	Total	C	O	0	0
			6	3	3		
3	F	1	Total	C	O	0	0
			6	3	3		
3	G	1	Total	C	O	0	0
			6	3	3		
3	H	1	Total	C	O	0	0
			6	3	3		
3	H	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	H	1	Total	C	O	0	0
			6	3	3		
3	H	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	F	1	Total	Mg	0	0
			1	1		
4	H	1	Total	Mg	0	0
			1	1		

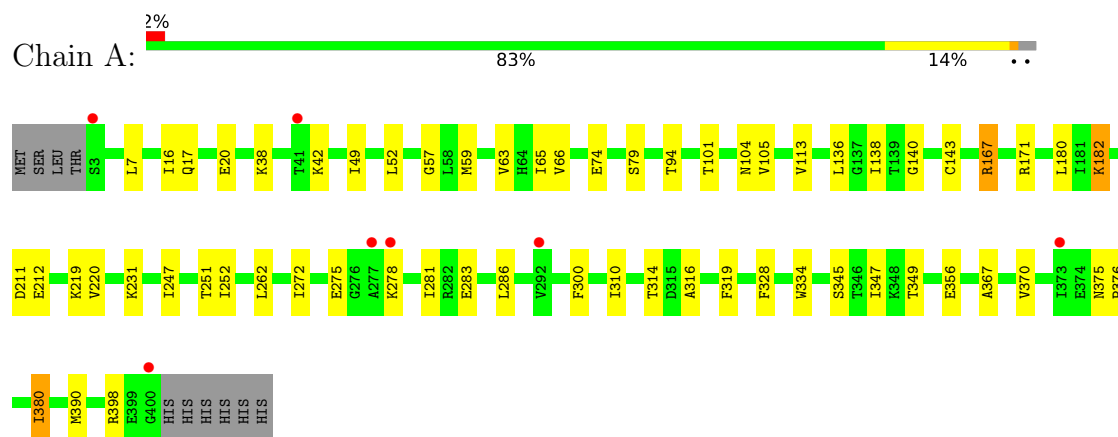
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	65	Total	O	0	0
			65	65		
5	B	57	Total	O	0	0
			57	57		
5	C	60	Total	O	0	0
			60	60		
5	D	65	Total	O	0	0
			65	65		
5	E	78	Total	O	0	0
			78	78		
5	F	75	Total	O	0	0
			75	75		
5	G	82	Total	O	0	0
			82	82		
5	H	90	Total	O	0	0
			90	90		

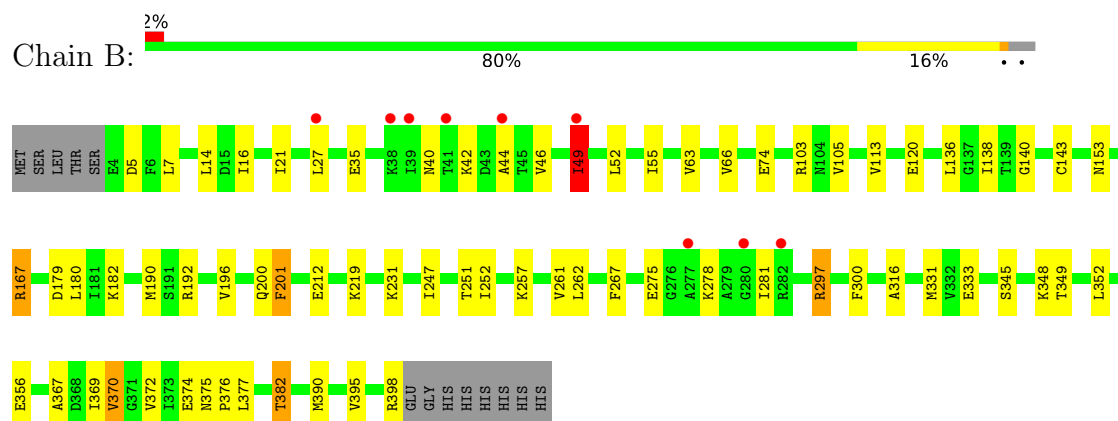
3 Residue-property plots [i](#)

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.

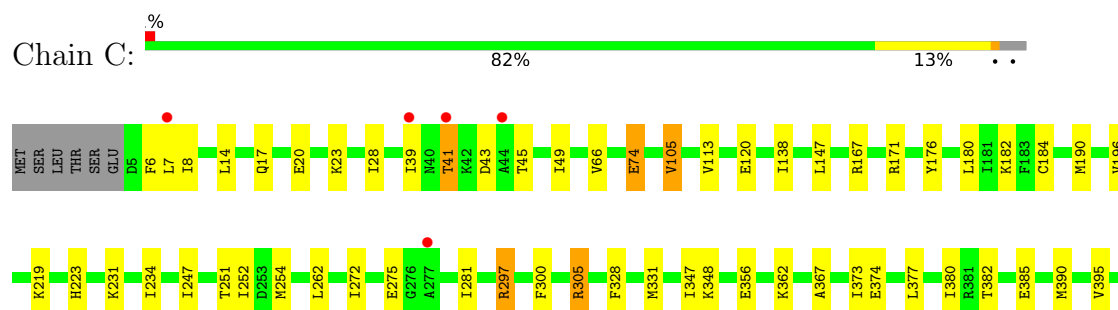
- Molecule 1: Zn-dependent arginine carboxypeptidase



- Molecule 1: Zn-dependent arginine carboxypeptidase



- Molecule 1: Zn-dependent arginine carboxypeptidase



R398
GLU
GLY
HIS
HIS
HIS
HIS
HIS
HIS

- Molecule 1: Zn-dependent arginine carboxypeptidase

Chain D:  81% 13% ..

MET SER LEU THR SER E4 D5 D6 L7 I8 K9 I16 E20 E21 E22 K23 K38 K39 N40 T41 D42 D43 A44 T45 V46 I49 P50 D51 L54 V63 H64 I65 V66 E92 V105 V113 E120 L136 C143 L148 N153 R167 R171

R174 L180 I181 K182 M190 V196 Q200 F201 E212 K219 H223 K231 I247 T251 I252 D253 M254 L262 K277 K278 I281 R297 M301 A316 F328 M331 W334 K348 A367 D368 I369 I373 E374 I380 R381 T382

M390 V395 R398 GLU GLY HIS HIS HIS HIS HIS HIS

- Molecule 1: Zn-dependent arginine carboxypeptidase

Chain E:  83% 13% .

MET SER LEU THR SER GLU D5 D6 L7 K11 E20 E21 E22 R29 K32 E35 I39 N40 T41 A44 T45 I49 P50 D51 V63 V66 E74 S75 I76 V105 V113 L136 G137 I138 T139 G140 C143 L148 M153 R167 D179

C184 M190 V196 H223 L228 S240 V241 E242 D249 L262 K277 K278 A279 G280 I281 K295 R306 A316 F328 M331 V332 E333 I347 L352 E356 A367 D368 I369 E374 I380 R381 T382 M390 V395 R398 GLY

HIS HIS HIS HIS HIS HIS HIS

- Molecule 1: Zn-dependent arginine carboxypeptidase

Chain F:  82% 13% ..

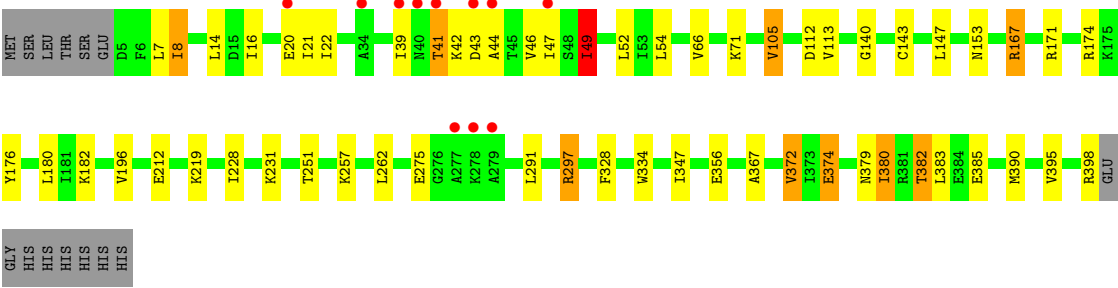
MET SER LEU THR SER E4 D5 D6 L7 I8 K11 D15 I16 Q17 T18 G19 E20 R29 K32 K38 K39 N40 T41 D42 D43 A44 T45 V46 I47 S48 I49 P50 D51 L52 V63 H64 I65 V66 S70 I76 V105 V113 L130 L136 G137 I138 R167

R174 L180 I181 K182 S191 V196 F201 E212 H223 K231 I247 T251 I252 K257 L262 F267 V268 A271 V292 R297 R305 A316 F328 M331 T349 I355 A367 V372 I373 E374 N379 I380 R381 T382

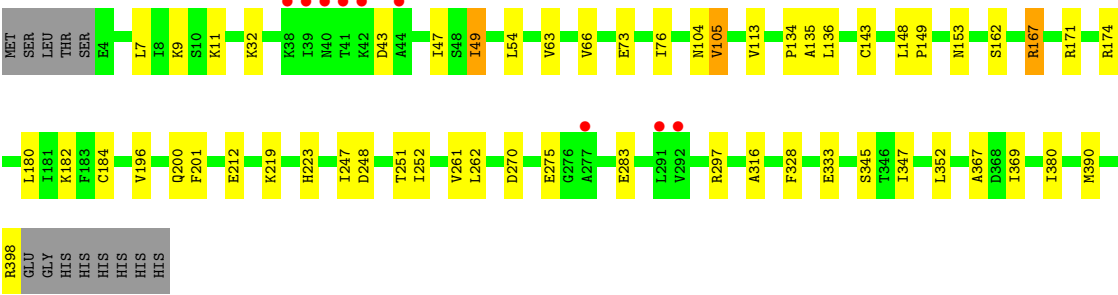
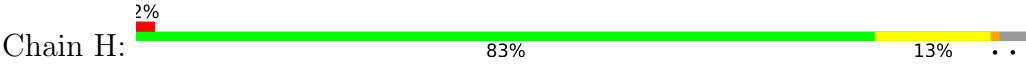
E385 M390 R398 GLU GLY HIS HIS HIS HIS HIS HIS

- Molecule 1: Zn-dependent arginine carboxypeptidase

Chain G:  82% 12% ..



• Molecule 1: Zn-dependent arginine carboxypeptidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	113.42Å 146.58Å 255.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.30 20.00 – 2.30	Depositor EDS
% Data completeness (in resolution range)	96.0 (20.00-2.30) 95.8 (20.00-2.30)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.13 (at 2.16Å)	Xtriage
Refinement program	REFMAC 5.3.0034	Depositor
R, R_{free}	0.226 , 0.280 0.223 , 0.275	Depositor DCC
R_{free} test set	6570 reflections (2.85%)	wwPDB-VP
Wilson B-factor (Å ²)	30.0	Xtriage
Anisotropy	0.153	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 42.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	24963	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.03% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, GOL

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	0/3153	0.83	0/4248
1	B	0.48	0/3103	0.86	0/4181
1	C	0.47	0/3063	0.88	0/4131
1	D	0.49	0/3074	0.85	2/4144 (0.0%)
1	E	0.47	0/3060	0.87	2/4127 (0.0%)
1	F	0.47	0/3062	0.84	0/4129
1	G	0.47	0/3065	0.87	2/4133 (0.0%)
1	H	0.47	0/3060	0.86	4/4127 (0.1%)
All	All	0.47	0/24640	0.86	10/33220 (0.0%)

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	A	0	4
1	B	0	5
1	C	0	2
1	D	0	4
1	E	0	3
1	F	0	3
1	G	0	6
1	H	0	2
All	All	0	29

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	148	LEU	CA-C-N	5.83	126.38	120.38
1	H	148	LEU	C-N-CA	5.83	126.38	120.38
1	H	149	PRO	CA-C-N	5.68	126.06	119.47
1	H	149	PRO	C-N-CA	5.68	126.06	119.47
1	E	148	LEU	CA-C-N	5.60	123.75	119.66

There are no chirality outliers.

5 of 29 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	104	ASN	Peptide
1	A	143	CYS	Peptide
1	A	334	TRP	Peptide
1	A	49	ILE	Peptide
1	B	40	ASN	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	3081	0	3102	18	0
1	B	3041	0	3069	18	0
1	C	3010	0	3025	18	0
1	D	3021	0	3037	19	0
1	E	3010	0	3015	14	0
1	F	3012	0	3020	20	0
1	G	3012	0	3024	14	0
1	H	3010	0	3016	15	0
2	A	12	0	12	0	0
2	B	12	0	12	0	0
2	C	12	0	12	0	0
2	D	12	0	12	0	0
2	E	12	0	12	0	0
2	F	12	0	12	0	0
2	G	12	0	12	0	0
2	H	12	0	12	0	0
3	A	12	0	16	0	0
3	B	6	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	6	0	8	0	0
3	D	12	0	16	0	0
3	E	12	0	16	0	0
3	F	18	0	24	0	0
3	G	6	0	8	0	0
3	H	24	0	32	2	0
4	F	1	0	0	0	0
4	H	1	0	0	0	0
5	A	65	0	0	0	0
5	B	57	0	0	0	0
5	C	60	0	0	0	0
5	D	65	0	0	0	0
5	E	78	0	0	0	0
5	F	75	0	0	0	0
5	G	82	0	0	0	0
5	H	90	0	0	0	0
All	All	24963	0	24532	127	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 127 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:B:374:GLU:H	1:B:382:THR:HG21	1.51	0.75
1:D:231:LYS:HG2	1:D:251:THR:HG21	1.78	0.66
1:C:231:LYS:HG2	1:C:251:THR:HG21	1.81	0.61
1:F:167:ARG:HH21	1:F:212:GLU:HG2	1.65	0.60
1:D:5:ASP:OD2	1:D:5:ASP:N	2.30	0.59

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	405/408 (99%)	387 (96%)	18 (4%)	0	100	100
1	B	398/408 (98%)	380 (96%)	16 (4%)	2 (0%)	24	31
1	C	394/408 (97%)	373 (95%)	21 (5%)	0	100	100
1	D	395/408 (97%)	376 (95%)	19 (5%)	0	100	100
1	E	394/408 (97%)	378 (96%)	16 (4%)	0	100	100
1	F	394/408 (97%)	375 (95%)	17 (4%)	2 (0%)	24	31
1	G	394/408 (97%)	374 (95%)	18 (5%)	2 (0%)	24	31
1	H	394/408 (97%)	380 (96%)	14 (4%)	0	100	100
All	All	3168/3264 (97%)	3023 (95%)	139 (4%)	6 (0%)	43	55

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	201	PHE
1	F	201	PHE
1	G	41	THR
1	G	43	ASP
1	F	50	PRO

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	329/330 (100%)	298 (91%)	31 (9%)	8	11
1	B	323/330 (98%)	283 (88%)	40 (12%)	4	5
1	C	319/330 (97%)	287 (90%)	32 (10%)	7	9
1	D	320/330 (97%)	282 (88%)	38 (12%)	5	6
1	E	319/330 (97%)	289 (91%)	30 (9%)	8	11
1	F	319/330 (97%)	287 (90%)	32 (10%)	7	9

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	G	319/330 (97%)	281 (88%)	38 (12%)	5 6
1	H	319/330 (97%)	288 (90%)	31 (10%)	8 10
All	All	2567/2640 (97%)	2295 (89%)	272 (11%)	7 8

5 of 272 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	347	ILE
1	G	385	GLU
1	H	248	ASP
1	C	348	LYS
1	C	305	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	296	GLN
1	G	360	GLN
1	D	125	ASN
1	D	109	ASN
1	H	17	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 26 ligands modelled in this entry, 2 are monoatomic - leaving 24 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	GOL	H	506	-	5,5,5	0.35	0	5,5,5	0.39	0
3	GOL	D	502	-	5,5,5	0.38	0	5,5,5	0.34	0
3	GOL	A	502	-	5,5,5	0.42	0	5,5,5	0.29	0
2	ARG	E	501	-	10,11,11	0.76	1 (10%)	9,13,13	0.95	1 (11%)
2	ARG	G	501	-	10,11,11	0.76	1 (10%)	9,13,13	0.86	1 (11%)
2	ARG	A	501	-	10,11,11	0.73	1 (10%)	9,13,13	0.85	1 (11%)
3	GOL	G	502	-	5,5,5	0.40	0	5,5,5	0.33	0
2	ARG	D	501	-	10,11,11	0.77	1 (10%)	9,13,13	1.00	1 (11%)
3	GOL	F	505	-	5,5,5	0.37	0	5,5,5	0.25	0
3	GOL	B	502	-	5,5,5	0.36	0	5,5,5	0.28	0
3	GOL	E	503	-	5,5,5	0.40	0	5,5,5	0.20	0
3	GOL	F	504	-	5,5,5	0.35	0	5,5,5	0.40	0
3	GOL	A	503	-	5,5,5	0.36	0	5,5,5	0.44	0
3	GOL	C	502	-	5,5,5	0.37	0	5,5,5	0.51	0
3	GOL	H	505	-	5,5,5	0.36	0	5,5,5	0.47	0
3	GOL	D	503	-	5,5,5	0.38	0	5,5,5	0.39	0
3	GOL	H	503	-	5,5,5	0.35	0	5,5,5	0.33	0
2	ARG	F	501	-	10,11,11	0.76	1 (10%)	9,13,13	0.90	1 (11%)
3	GOL	F	506	-	5,5,5	0.40	0	5,5,5	0.26	0
2	ARG	C	501	-	10,11,11	0.76	1 (10%)	9,13,13	0.95	1 (11%)
3	GOL	E	502	-	5,5,5	0.37	0	5,5,5	0.29	0
3	GOL	H	504	-	5,5,5	0.37	0	5,5,5	0.22	0
2	ARG	H	501	-	10,11,11	0.78	1 (10%)	9,13,13	0.92	1 (11%)
2	ARG	B	501	-	10,11,11	0.73	1 (10%)	9,13,13	0.79	1 (11%)

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 Torsions and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	H	506	-	-	4/4/4/4	-
3	GOL	D	502	-	-	4/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	A	502	-	-	4/4/4/4	-
2	ARG	E	501	-	-	3/11/11/11	-
2	ARG	G	501	-	-	2/11/11/11	-
2	ARG	A	501	-	-	2/11/11/11	-
3	GOL	G	502	-	-	3/4/4/4	-
2	ARG	D	501	-	-	3/11/11/11	-
3	GOL	F	505	-	-	2/4/4/4	-
3	GOL	B	502	-	-	0/4/4/4	-
3	GOL	E	503	-	-	2/4/4/4	-
3	GOL	F	504	-	-	2/4/4/4	-
3	GOL	A	503	-	-	3/4/4/4	-
3	GOL	C	502	-	-	2/4/4/4	-
3	GOL	H	505	-	-	2/4/4/4	-
3	GOL	D	503	-	-	2/4/4/4	-
3	GOL	H	503	-	-	3/4/4/4	-
2	ARG	F	501	-	-	1/11/11/11	-
3	GOL	F	506	-	-	0/4/4/4	-
2	ARG	C	501	-	-	2/11/11/11	-
3	GOL	E	502	-	-	2/4/4/4	-
3	GOL	H	504	-	-	3/4/4/4	-
2	ARG	H	501	-	-	1/11/11/11	-
2	ARG	B	501	-	-	1/11/11/11	-

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	501	ARG	OXT-C	-2.35	1.23	1.30
2	D	501	ARG	OXT-C	-2.34	1.23	1.30
2	F	501	ARG	OXT-C	-2.33	1.23	1.30
2	C	501	ARG	OXT-C	-2.33	1.23	1.30
2	E	501	ARG	OXT-C	-2.32	1.23	1.30

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	501	ARG	OXT-C-O	-2.89	117.53	124.08
2	E	501	ARG	OXT-C-O	-2.71	117.93	124.08
2	C	501	ARG	OXT-C-O	-2.65	118.08	124.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	501	ARG	OXT-C-O	-2.59	118.19	124.08
2	H	501	ARG	OXT-C-O	-2.55	118.30	124.08

There are no chirality outliers.

5 of 53 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	502	GOL	O2-C2-C3-O3
3	A	503	GOL	O1-C1-C2-O2
3	A	503	GOL	O1-C1-C2-C3
3	C	502	GOL	C1-C2-C3-O3
3	D	502	GOL	O1-C1-C2-C3

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	504	GOL	2	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	398/408 (97%)	-0.04	7 (1%) 67 69	19, 46, 81, 117	9 (2%)
1	B	395/408 (96%)	-0.02	9 (2%) 61 63	11, 45, 84, 117	5 (1%)
1	C	394/408 (96%)	-0.07	5 (1%) 75 76	20, 47, 82, 119	2 (0%)
1	D	395/408 (96%)	-0.09	6 (1%) 72 73	13, 44, 81, 119	2 (0%)
1	E	394/408 (96%)	-0.26	9 (2%) 61 63	18, 41, 77, 117	2 (0%)
1	F	395/408 (96%)	-0.02	14 (3%) 47 49	19, 45, 84, 117	1 (0%)
1	G	394/408 (96%)	-0.04	11 (2%) 55 57	22, 45, 81, 118	2 (0%)
1	H	395/408 (96%)	-0.21	9 (2%) 61 63	17, 42, 78, 117	1 (0%)
All	All	3160/3264 (96%)	-0.10	70 (2%) 62 64	11, 45, 81, 119	24 (0%)

The worst 5 of 70 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	400	GLY	4.6
1	F	268	VAL	4.5
1	D	39	ILE	3.8
1	E	44	ALA	3.7
1	G	47	ILE	3.7

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 oligosaccharides 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. 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	B-factors(Å ²)	Q<0.9
3	GOL	H	503	6/6	0.82	0.14	59,64,75,75	0
3	GOL	F	504	6/6	0.83	0.16	52,80,84,93	0
2	ARG	G	501	12/12	0.83	0.12	49,56,63,64	0
3	GOL	F	505	6/6	0.85	0.12	46,58,70,77	0
3	GOL	E	503	6/6	0.87	0.15	58,76,86,94	0
3	GOL	D	502	6/6	0.87	0.12	51,56,65,75	0
3	GOL	C	502	6/6	0.88	0.14	44,58,60,97	0
2	ARG	H	501	12/12	0.88	0.12	38,60,64,74	0
3	GOL	H	504	6/6	0.88	0.13	52,67,71,75	0
3	GOL	H	505	6/6	0.88	0.12	48,67,75,79	0
2	ARG	D	501	12/12	0.89	0.11	44,54,70,74	0
2	ARG	E	501	12/12	0.90	0.10	67,69,77,80	0
3	GOL	D	503	6/6	0.91	0.10	57,60,76,80	0
2	ARG	C	501	12/12	0.91	0.08	25,49,55,56	0
3	GOL	F	506	6/6	0.91	0.12	42,60,68,74	0
3	GOL	A	502	6/6	0.92	0.09	49,59,61,76	0
3	GOL	A	503	6/6	0.93	0.11	47,62,63,93	0
3	GOL	H	506	6/6	0.93	0.09	35,63,76,80	0
2	ARG	F	501	12/12	0.94	0.08	36,43,60,62	0
2	ARG	B	501	12/12	0.96	0.06	31,39,53,57	0
3	GOL	E	502	6/6	0.96	0.07	40,49,68,68	0
3	GOL	B	502	6/6	0.96	0.07	37,53,68,72	0
3	GOL	G	502	6/6	0.96	0.09	26,39,42,51	0
2	ARG	A	501	12/12	0.97	0.05	17,35,47,51	0
4	MG	F	503	1/1	0.97	0.06	34,34,34,34	0
4	MG	H	502	1/1	0.98	0.04	37,37,37,37	0

6.5 Other polymers ⓘ

There are no such residues in this entry.