



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 30, 2024 – 09:10 PM EST

PDB ID : 1JAW
Title : AMINOPEPTIDASE P FROM E. COLI LOW PH FORM
Authors : Wilce, M.C.J.; Bond, C.S.; Lilley, P.E.; Dixon, N.E.; Freeman, H.C.; Guss, J.M.
Deposited on : 1997-12-22
Resolution : 2.70 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

<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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

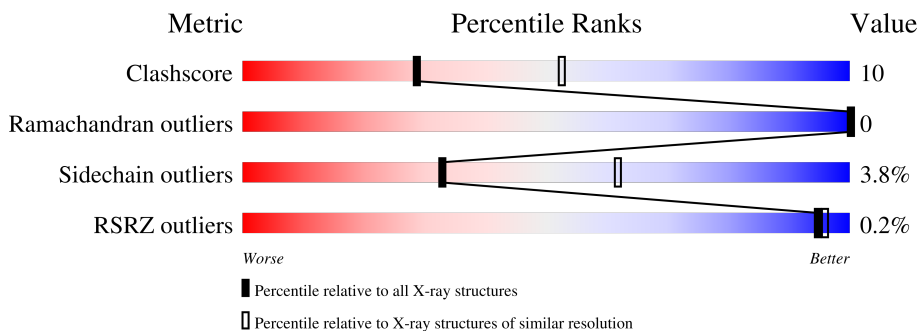
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	440	78% 20% ..

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	ACT	A	443	-	X	-	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3768 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 AMINOPEPTIDASE P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	440	3500	2202	618	665	15	0	0	0

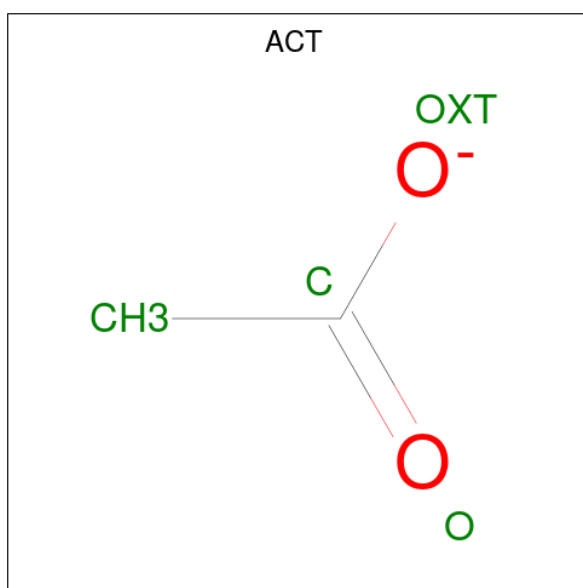
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	89	TYR	PHE	conflict	UNP P15034

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

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

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



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

- Molecule 4 is water.

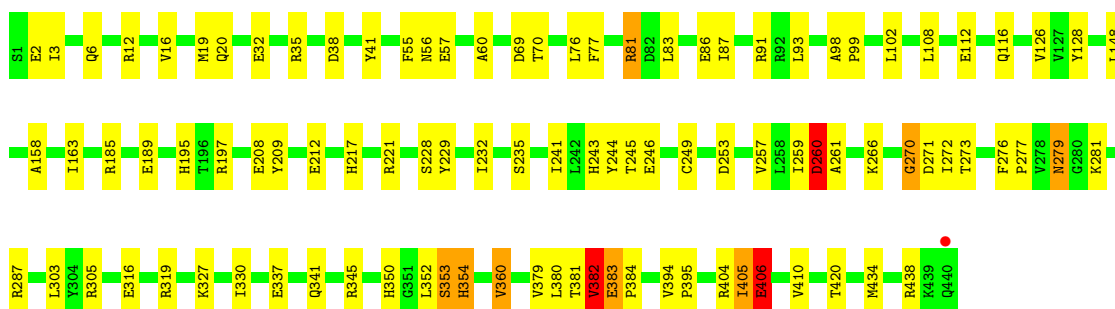
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	262	Total	O	0	0
			262	262		

3 Residue-property plots

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: AMINOPEPTIDASE P

Chain A:  78% 20% ..



4 Data and refinement statistics

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, α , β , γ	139.71Å 139.71Å 230.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.70 27.74 – 2.70	Depositor EDS
% Data completeness (in resolution range)	83.1 (50.00-2.70) 83.1 (27.74-2.70)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.50 (at 2.72Å)	Xtrriage
Refinement program	X-PLOR 3.8	Depositor
R, R_{free}	0.182 , 0.227 0.185 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	38.0	Xtrriage
Anisotropy	0.512	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 50.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3768	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.21% 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: ACT, 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	0.92	21/3572 (0.6%)	0.83	12/4837 (0.2%)

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	6

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	406	GLU	CB-CG	-17.51	1.18	1.52
1	A	383	GLU	C-O	17.10	1.55	1.23
1	A	406	GLU	CD-OE1	15.95	1.43	1.25
1	A	406	GLU	CD-OE2	12.82	1.39	1.25
1	A	405	ILE	C-N	12.47	1.62	1.34
1	A	270	GLY	C-N	11.96	1.61	1.34
1	A	406	GLU	C-N	-11.64	1.07	1.34
1	A	260	ASP	CA-C	11.58	1.83	1.52
1	A	271	ASP	CA-C	-8.90	1.29	1.52
1	A	271	ASP	N-CA	8.72	1.63	1.46
1	A	354	HIS	C-O	8.40	1.39	1.23
1	A	271	ASP	CA-CB	-8.38	1.35	1.53
1	A	406	GLU	CA-C	7.44	1.72	1.52
1	A	260	ASP	CA-CB	-7.16	1.38	1.53
1	A	271	ASP	CG-OD2	7.07	1.41	1.25
1	A	353	SER	C-N	6.49	1.49	1.34
1	A	406	GLU	CG-CD	-6.39	1.42	1.51
1	A	354	HIS	C-N	5.72	1.47	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	259	ILE	C-N	5.54	1.46	1.34
1	A	354	HIS	CA-C	5.34	1.66	1.52
1	A	260	ASP	C-N	-5.15	1.22	1.34

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	270	GLY	O-C-N	-10.83	105.37	122.70
1	A	406	GLU	OE1-CD-OE2	-10.18	111.09	123.30
1	A	405	ILE	O-C-N	-9.29	107.84	122.70
1	A	354	HIS	O-C-N	8.51	136.31	122.70
1	A	345	ARG	C-N-CD	8.26	145.75	128.40
1	A	406	GLU	C-N-CA	7.04	139.30	121.70
1	A	271	ASP	CB-CG-OD2	6.77	124.39	118.30
1	A	354	HIS	CA-C-N	-5.95	104.11	117.20
1	A	270	GLY	CA-C-N	5.80	129.97	117.20
1	A	260	ASP	N-CA-CB	5.80	121.04	110.60
1	A	382	VAL	C-N-CA	-5.58	107.76	121.70
1	A	271	ASP	N-CA-C	-5.08	97.27	111.00

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	260	ASP	Mainchain
1	A	270	GLY	Mainchain
1	A	353	SER	Mainchain
1	A	382	VAL	Mainchain
1	A	405	ILE	Mainchain
1	A	406	GLU	Mainchain

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	3500	0	3428	67	0
2	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	4	0	3	1	0
4	A	262	0	0	6	0
All	All	3768	0	3431	67	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 10.

All (67) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:ASP:CA	1:A:260:ASP:C	1.83	1.44
1:A:2:GLU:HG3	1:A:3:ILE:N	1.84	0.93
1:A:2:GLU:HG3	1:A:3:ILE:H	1.38	0.88
1:A:6:GLN:NE2	4:A:583:HOH:O	2.22	0.72
1:A:327:LYS:HB3	1:A:327:LYS:NZ	2.03	0.71
1:A:434:MET:O	1:A:438:ARG:HD2	1.95	0.67
1:A:260:ASP:CA	1:A:261:ALA:N	2.58	0.64
1:A:337:GLU:O	1:A:341:GLN:HG2	1.97	0.64
1:A:2:GLU:OE1	1:A:266:LYS:HD2	1.99	0.62
1:A:229:TYR:CD1	1:A:360:VAL:HG11	2.34	0.62
1:A:379:VAL:HG22	1:A:410:VAL:HG13	1.82	0.62
1:A:208:GLU:HG3	1:A:249:CYS:O	2.01	0.61
1:A:260:ASP:C	1:A:260:ASP:CB	2.64	0.60
1:A:86:GLU:HG2	1:A:91:ARG:HA	1.83	0.59
1:A:20:GLN:OE1	1:A:126:VAL:HG21	2.03	0.58
1:A:217:HIS:CE1	1:A:221:ARG:HH21	2.22	0.58
1:A:279:ASN:HD22	1:A:281:LYS:H	1.50	0.58
1:A:279:ASN:ND2	1:A:281:LYS:H	2.02	0.57
1:A:16:VAL:HA	1:A:19:MET:HE3	1.86	0.56
1:A:354:HIS:CE1	1:A:381:THR:HG21	2.40	0.56
1:A:303:LEU:HD11	1:A:316:GLU:HG2	1.87	0.56
1:A:86:GLU:HG3	4:A:600:HOH:O	2.08	0.54
1:A:260:ASP:C	1:A:260:ASP:N	2.56	0.53
1:A:232:ILE:HG23	1:A:244:TYR:O	2.09	0.53
1:A:98:ALA:HB3	1:A:99:PRO:HD3	1.91	0.52
1:A:76:LEU:HD22	1:A:102:LEU:HD12	1.92	0.51
1:A:244:TYR:CE1	1:A:246:GLU:HG2	2.46	0.51
1:A:350:HIS:HE1	1:A:383:GLU:O	1.94	0.50
1:A:352:LEU:HD11	1:A:384:PRO:HG3	1.94	0.50
1:A:279:ASN:HD22	1:A:279:ASN:C	2.16	0.49
1:A:273:THR:CB	1:A:406:GLU:HB3	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:148:LEU:HB2	1:A:158:ALA:HB2	1.93	0.49
1:A:235:SER:HB3	1:A:257:VAL:HG23	1.95	0.49
1:A:273:THR:HG21	1:A:404:ARG:HB3	1.94	0.49
1:A:360:VAL:HG22	4:A:469:HOH:O	2.13	0.48
1:A:249:CYS:SG	4:A:574:HOH:O	2.60	0.48
1:A:32:GLU:HG3	4:A:624:HOH:O	2.13	0.48
1:A:108:LEU:HD13	1:A:116:GLN:HG3	1.96	0.47
1:A:93:LEU:HD21	1:A:98:ALA:HA	1.97	0.47
1:A:383:GLU:HB3	1:A:406:GLU:HB2	1.97	0.47
1:A:260:ASP:CA	1:A:260:ASP:O	2.51	0.46
1:A:327:LYS:HB3	1:A:327:LYS:HZ2	1.76	0.46
1:A:273:THR:HB	1:A:406:GLU:HB3	1.98	0.46
1:A:35:ARG:HA	1:A:41:TYR:CE2	2.51	0.45
1:A:55:PHE:CZ	1:A:57:GLU:HB3	2.53	0.44
1:A:209:TYR:O	1:A:212:GLU:HB3	2.18	0.43
1:A:232:ILE:HD13	1:A:245:THR:HG22	2.00	0.43
1:A:330:ILE:HG23	1:A:394:VAL:HG11	1.99	0.43
1:A:83:LEU:HA	1:A:83:LEU:HD23	1.80	0.43
1:A:241:ILE:HB	1:A:244:TYR:HB2	2.02	0.42
1:A:2:GLU:CG	1:A:3:ILE:H	2.21	0.42
1:A:12:ARG:O	1:A:16:VAL:HG23	2.19	0.42
1:A:197:ARG:NH2	4:A:682:HOH:O	2.51	0.42
1:A:60:ALA:HA	1:A:77:PHE:O	2.20	0.42
1:A:217:HIS:CE1	1:A:221:ARG:HE	2.38	0.41
1:A:232:ILE:HD12	1:A:243:HIS:HA	2.02	0.41
1:A:195:HIS:HE1	1:A:261:ALA:O	2.03	0.41
1:A:83:LEU:O	1:A:87:ILE:HG13	2.21	0.41
1:A:128:TYR:HA	1:A:163:ILE:O	2.21	0.41
1:A:260:ASP:OD2	3:A:443:ACT:H3	2.21	0.41
1:A:303:LEU:O	1:A:305:ARG:HG2	2.20	0.41
1:A:382:VAL:O	1:A:406:GLU:HA	2.21	0.41
1:A:272:ILE:HD11	1:A:420:THR:HB	2.02	0.40
1:A:276:PHE:HB2	1:A:277:PRO:HD2	2.03	0.40
1:A:185:ARG:O	1:A:189:GLU:HG3	2.21	0.40
1:A:394:VAL:HB	1:A:395:PRO:HD2	2.04	0.40
1:A:81:ARG:HG2	1:A:86:GLU:OE2	2.22	0.40

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	438/440 (100%)	416 (95%)	22 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	371/371 (100%)	357 (96%)	14 (4%)	33	62

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	38	ASP
1	A	56	ASN
1	A	69	ASP
1	A	70	THR
1	A	81	ARG
1	A	112	GLU
1	A	228	SER
1	A	253	ASP
1	A	279	ASN
1	A	287	ARG
1	A	319	ARG
1	A	360	VAL
1	A	380	LEU

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Mol	Chain	Res	Type
1	A	406	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	56	ASN
1	A	279	ASN
1	A	341	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 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	ACT	A	443	2	3,3,3	1.50	1 (33%)	3,3,3	2.76	2 (66%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	443	ACT	CH3-C	-2.34	1.39	1.49

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	443	ACT	OXT-C-O	-3.73	108.32	122.05
3	A	443	ACT	O-C-CH3	2.93	133.75	122.33

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	443	ACT	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	3

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	405:ILE	C	406:GLU	N	1.62
1	A	270:GLY	C	271:ASP	N	1.61
1	A	406:GLU	C	407:ASP	N	1.07

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	440/440 (100%)	-0.77	1 (0%) 95 96	17, 32, 57, 99	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	440	GLN	2.8

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 monosaccharides 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. 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	ACT	A	443	4/4	0.96	0.23	26,28,28,30	0
2	MN	A	441	1/1	0.99	0.12	30,30,30,30	0
2	MN	A	442	1/1	1.00	0.11	29,29,29,29	0

6.5 Other polymers [i](#)

There are no such residues in this entry.