

wwPDB X-ray Structure Validation Summary Report (i)

Aug 8, 2023 – 04:56 AM EDT

PDB ID : 1OS2

> Title Ternary enzyme-product-inhibitor complexes of human MMP12

Authors Bertini, I.; Calderone, V.; Fragai, M.; Luchinat, C.; Mangani, S.; Terni, B.

2003-03-18 Deposited on

2.15 Å(reported) Resolution

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 (i) 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 (1)) were used in the production of this report:

MolProbity 4.02b-467

> 1.8.5 (274361), CSD as541be (2020) Mogul

Xtriage (Phenix) 1.13

EDS 2.35

20191225.v01 (using entries in the PDB archive December 25th 2019) Percentile statistics

> Refmac 5.8.0158

CCP4 7.0.044 (Gargrove)

Ideal geometry (proteins) Engh & Huber (2001) Ideal geometry (DNA, RNA) Parkinson et al. (1996)

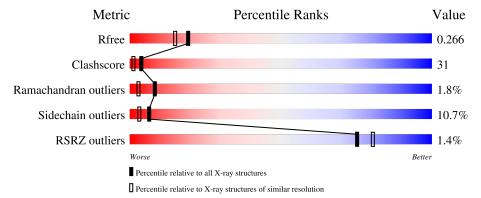
Validation Pipeline (wwPDB-VP) 2.35

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.15 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	130704	1479 (2.16-2.16)
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (2.16-2.16)

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 <=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 cha	nin	
1	A	165	62%	31%	6% •
1	В	165	% 	37%	13% •
1	С	165	2%	34%	12% •
1	D	165	62%	28%	7% •
1	Е	165	51%	38%	8% •



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Mol	Chain	Length	Quality	of chain	
			3%		
1	F	165	55%	34% 8% •	•

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
5	ACT	В	374	-	X	-	-



2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 8132 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 Macrophage metalloelastase.

Mol	Chain	Residues	${f Atoms}$			ZeroOcc	AltConf	Trace		
1	A	165	Total	С	N	О	S	0	7	0
1	A	105	1295	823	225	242	5	0	1	U
1	В	165	Total	С	N	О	S	0	7	0
1	Ъ	105	1295	823	225	242	5	0	'	0
1	С	165	Total	С	N	О	S	0	6	0
1		105	1295	823	225	242	5	0		0
1	D	165	Total	С	N	О	S	0	7	0
1	ע	105	1295	823	225	242	5	0	1	
1	Е	165	Total	С	N	О	S	0	7	0
1	12	105	1295	823	225	242	5	U	1	U
1	F	165	Total	С	N	О	S	0	7	0
1	Г	100	1295	823	225	242	5	0	7	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	104	MET	-	cloning artifact	UNP P39900
A	105	MET	-	cloning artifact	UNP P39900
A	171	ASP	PHE	engineered mutation	UNP P39900
В	104	MET	-	cloning artifact	UNP P39900
В	105	MET	-	cloning artifact	UNP P39900
В	171	ASP	PHE	engineered mutation	UNP P39900
С	104	MET	-	cloning artifact	UNP P39900
С	105	MET	-	cloning artifact	UNP P39900
С	171	ASP	PHE	engineered mutation	UNP P39900
D	104	MET	-	cloning artifact	UNP P39900
D	105	MET	-	cloning artifact	UNP P39900
D	171	ASP	PHE	engineered mutation	UNP P39900
E	104	MET	-	cloning artifact	UNP P39900
Е	105	MET	-	cloning artifact	UNP P39900
Е	171	ASP	PHE	engineered mutation	UNP P39900
F	104	MET	-	cloning artifact	UNP P39900
F	105	MET	-	cloning artifact	UNP P39900



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Chain	Residue	Modelled	Actual	Comment	Reference
F	171	ASP	PHE	engineered mutation	UNP P39900

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

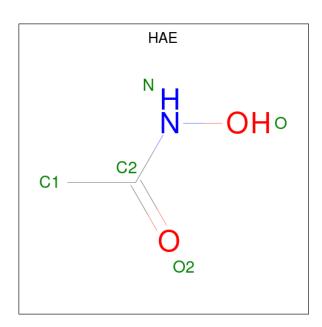
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Zn 2 2	0	0
2	В	2	Total Zn 2 2	0	0
2	С	2	Total Zn 2 2	0	0
2	D	2	Total Zn 2 2	0	0
2	E	2	Total Zn 2 2	0	0
2	F	2	Total Zn 2 2	0	0

• Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	3	Total Ca 3 3	0	0
3	В	3	Total Ca 3 3	0	0
3	С	3	Total Ca 3 3	0	0
3	D	3	Total Ca 3 3	0	0
3	E	3	Total Ca 3 3	0	0
3	F	3	Total Ca 3 3	0	0

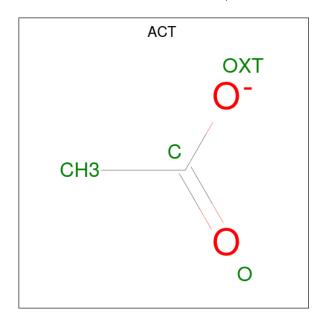
 \bullet Molecule 4 is ACETOHYDROXAMIC ACID (three-letter code: HAE) (formula: $\mathrm{C_2H_5NO_2}).$





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total 5		N 1		0	0
4	D	1	Total 5	C 2	N 1	O 2	0	0

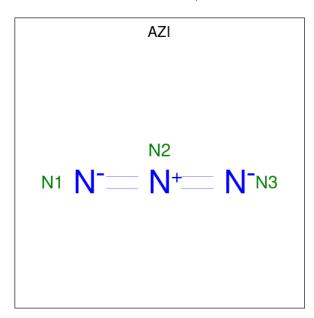
 \bullet Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: $\mathrm{C_2H_3O_2}).$



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	В	1	Total C O 4 2 2	0	0
5	Е	1	Total C O 4 2 2	0	0



 \bullet Molecule 6 is AZIDE ION (three-letter code: AZI) (formula: N3).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	С	1	Total N 3 3	0	0
6	F	1	Total N 3 3	0	0

• Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	46	Total O 46 46	0	0
7	В	67	Total O 67 67	0	0
7	С	51	Total O 51 51	0	0
7	D	44	Total O 44 44	0	0
7	Е	59	Total O 59 59	0	0
7	F	41	Total O 41 41	0	0

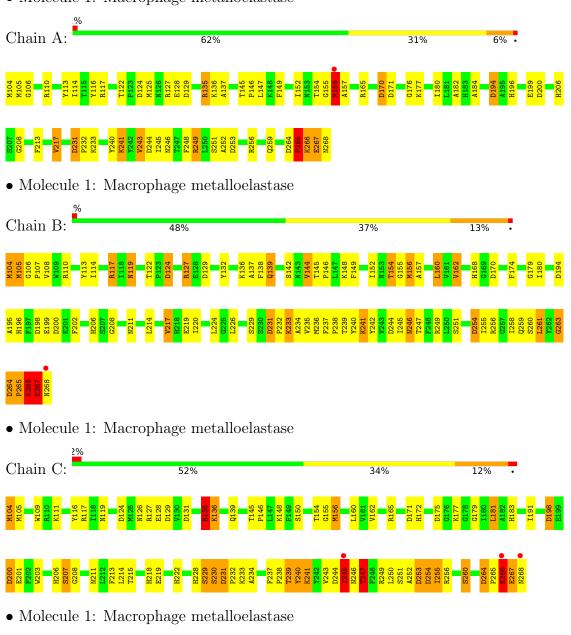


Chain D:

3 Residue-property plots (i)

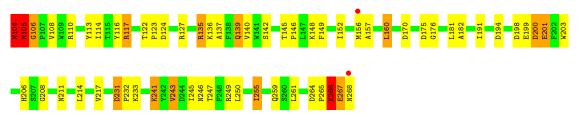
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

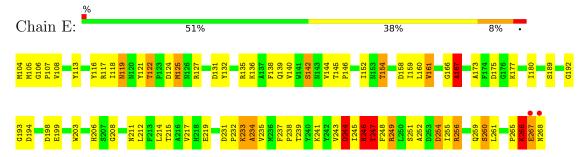




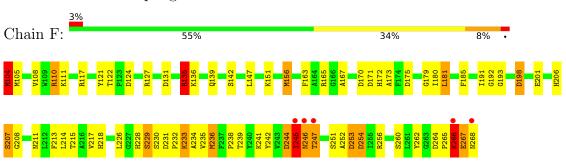
28%



• Molecule 1: Macrophage metalloelastase



• Molecule 1: Macrophage metalloelastase





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31	Depositor
Cell constants	123.84Å 123.84Å 69.73Å	Donositon
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	69.01 - 2.15	Depositor
rtesolution (A)	69.73 - 2.15	EDS
% Data completeness	100.0 (69.01-2.15)	Depositor
(in resolution range)	100.0 (69.73-2.15)	EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) > 1$	2.28 (at 2.14Å)	Xtriage
Refinement program	REFMAC 5.1.80	Depositor
R, R_{free}	0.212 , 0.271	Depositor
it, itfree	0.216 , 0.266	DCC
R_{free} test set	3296 reflections $(5.07%)$	wwPDB-VP
Wilson B-factor (Å ²)	31.2	Xtriage
Anisotropy	0.007	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.35, 42.3	EDS
L-test for twinning ²	$< L > = 0.49, < L^2> = 0.32$	Xtriage
	0.029 for -h,-k,l	
Estimated twinning fraction	0.488 for h,-h-k,-l	Xtriage
	0.029 for -k,-h,-l	
F_o, F_c correlation	0.94	EDS
Total number of atoms	8132	wwPDB-VP
Average B, all atoms (\mathring{A}^2)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.87% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of <|L|>, $<L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

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: CA, ZN, HAE, ACT, AZI

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	Bo	nd lengths	Bond angles		
MIOI	Mioi Chain		$\text{MSZ} \mid \# Z > 5$		# Z >5	
1	A	1.51	7/1333~(0.5%)	1.40	15/1805 (0.8%)	
1	В	1.67	19/1333 (1.4%)	1.49	17/1805 (0.9%)	
1	С	1.52	7/1333~(0.5%)	1.53	27/1805 (1.5%)	
1	D	1.50	12/1333~(0.9%)	1.35	11/1805 (0.6%)	
1	Е	1.68	$22/1333 \ (1.7\%)$	1.57	23/1805 (1.3%)	
1	F	1.45	4/1333~(0.3%)	1.47	19/1805 (1.1%)	
All	All	1.56	71/7998 (0.9%)	1.47	112/10830 (1.0%)	

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 maintenain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	1	2
1	В	0	2
1	С	0	2
1	Е	0	4
1	F	1	2
All	All	2	12

The worst 5 of 71 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
1	A	156	MET	C-O	8.71	1.39	1.23
1	D	139	GLN	CG-CD	7.84	1.69	1.51
1	Е	199	GLU	CD-OE1	-7.59	1.17	1.25
1	D	246	ASN	CB-CG	7.44	1.68	1.51
1	A	137	ALA	CA-CB	7.29	1.67	1.52

The worst 5 of 112 bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	Ε	166	GLY	C-N-CA	-12.70	89.94	121.70
1	Ε	194	ASP	CB-CG-OD2	12.05	129.15	118.30
1	F	175	ASP	CB-CG-OD2	11.76	128.88	118.30
1	С	175	ASP	CB-CG-OD2	11.17	128.35	118.30
1	В	194	ASP	CB-CG-OD2	10.57	127.82	118.30

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	266	LYS	CA
1	F	246	ASN	CA

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	156	MET	Mainchain
1	A	265	PRO	Peptide
1	В	265	PRO	Peptide
1	В	266	LYS	Peptide
1	С	245	ILE	Peptide

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	1295	0	1210	57	0
1	В	1295	0	1210	118	1
1	С	1295	0	1212	102	0
1	D	1295	0	1210	48	0
1	Ε	1295	0	1210	75	1
1	F	1295	0	1210	108	0
2	A	2	0	0	0	0
2	В	2	0	0	0	0
2	С	2	0	0	0	0
2	D	2	0	0	0	0
2	Е	2	0	0	0	0
2	F	2	0	0	0	0
3	A	3	0	0	0	0



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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	В	3	0	0	0	0
3	С	3	0	0	0	0
3	D	3	0	0	0	0
3	Е	3	0	0	0	0
3	F	3	0	0	0	0
4	A	5	0	4	0	0
4	D	5	0	4	0	0
5	В	4	0	3	1	0
5	Ε	4	0	3	1	0
6	С	3	0	0	1	0
6	F	3	0	0	1	0
7	A	46	0	0	11	0
7	В	67	0	0	10	0
7	С	51	0	0	2	0
7	D	44	0	0	4	0
7	Е	59	0	0	9	0
7	F	41	0	0	5	0
All	All	8132	0	7276	467	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 31.

The worst 5 of 467 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} \text{Interatomic} \\ \text{distance (Å)} \end{array}$	$egin{aligned} ext{Clash} \ ext{overlap } (ext{Å}) \end{aligned}$
1:F:136:LYS:CE	1:F:245:ILE:HD11	1.33	1.58
1:C:136:LYS:CE	1:C:245:ILE:HD11	1.32	1.55
1:F:136:LYS:HE2	1:F:245:ILE:CD1	1.42	1.49
1:C:136:LYS:HE2	1:C:245:ILE:CD1	1.58	1.32
1:C:136:LYS:CE	1:C:245:ILE:CD1	2.08	1.31

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	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
1:B:233:LYS:NZ	1:E:249:ARG:NH1[1_554]	2.07	0.13



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	163/165 (99%)	155 (95%)	6 (4%)	2 (1%)	13 7
1	В	163/165 (99%)	153 (94%)	7 (4%)	3 (2%)	8 3
1	С	163/165 (99%)	152 (93%)	7 (4%)	4 (2%)	5 1
1	D	163/165 (99%)	158 (97%)	3 (2%)	2 (1%)	13 7
1	E	163/165 (99%)	153 (94%)	7 (4%)	3 (2%)	8 3
1	F	163/165 (99%)	151 (93%)	8 (5%)	4 (2%)	5 1
All	All	978/990 (99%)	922 (94%)	38 (4%)	18 (2%)	8 3

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	266	LYS
1	В	266	LYS
1	С	245	ILE
1	С	266	LYS
1	С	267	GLU

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	Pe	erce	ntile	es
1	A	134/134 (100%)	123 (92%)	11 (8%)		11	7	
1	В	134/134 (100%)	118 (88%)	16 (12%)		5	2	
1	С	134/134 (100%)	117 (87%)	17 (13%)		4	1	



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Mol	Chain	Analysed	Rotameric Outliers		Percentiles		
1	D	134/134 (100%)	121 (90%)	13 (10%)	8 4		
1	E	134/134 (100%)	118 (88%)	16 (12%)	5 2		
1	F	134/134 (100%)	121 (90%)	13 (10%)	8 4		
All	All	804/804 (100%)	718 (89%)	86 (11%)	6 3		

5 of 86 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	Е	119	ASN
1	Е	266	LYS
1	Е	142[A]	SER
1	Е	241[A]	LYS
1	F	135	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	172	HIS
1	D	259	GLN
1	F	211[A]	ASN
1	D	211[A]	ASN
1	Е	172	HIS

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 36 ligands modelled in this entry, 30 are monoatomic - leaving 6 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	Mol Type Chain		Dog	Res Link	В	ond leng	$_{ m gths}$	Bond angles		
MIOI	Moi Type Chain	Chain	rtes	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	AZI	С	474	2	0,2,2	-	-	0,1,1	-	-
4	HAE	A	874	2	4,4,4	1.18	0	2,4,4	4.31	2 (100%)
5	ACT	В	374	2	3,3,3	1.76	1 (33%)	3,3,3	5.38	3 (100%)
6	AZI	F	774	2	0,2,2	-	-	0,1,1	-	-
5	ACT	E	674	2	3,3,3	2.02	1 (33%)	3,3,3	0.92	0
4	HAE	D	574	2	4,4,4	1.33	1 (25%)	2,4,4	5.71	2 (100%)

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
4	HAE	D	574	2	-	0/1/2/2	-
4	HAE	A	874	2	-	0/1/2/2	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	Observed(A)	$\operatorname{Ideal}(\text{\AA})$
5	Е	674	ACT	O-C	2.86	1.35	1.22
5	В	374	ACT	OXT-C	-2.46	1.19	1.30
4	D	574	HAE	C2-N	2.14	1.36	1.33

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^o)$	$\mathbf{Ideal}(^{o})$
5	В	374	ACT	OXT-C-O	-7.73	93.56	122.05
4	D	574	HAE	C1-C2-N	5.82	125.96	116.08
4	D	574	HAE	O2-C2-C1	-5.60	111.66	122.06
4	A	874	HAE	C1-C2-N	4.90	124.39	116.08



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Mol	Chain	Res	Type	Atoms	${f Z}$	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}({}^{o})$
5	В	374	ACT	OXT-C-CH3	4.49	133.73	115.18

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	С	474	AZI	1	0
5	В	374	ACT	1	0
6	F	774	AZI	1	0
5	Е	674	ACT	1	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, 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>	$\#\mathrm{RSRZ}{>}2$		$\mathbf{OWAB}(\mathbf{\mathring{A}}^2)$	Q < 0.9
1	A	165/165~(100%)	-0.36	1 (0%) 89	91	19, 36, 52, 62	9 (5%)
1	В	$165/165 \; (100\%)$	-0.31	1 (0%) 89	91	16, 31, 51, 82	9 (5%)
1	С	165/165 (100%)	-0.22	3 (1%) 68	75	18, 34, 56, 86	8 (4%)
1	D	165/165 (100%)	-0.33	2 (1%) 79	83	18, 36, 52, 66	9 (5%)
1	E	165/165 (100%)	-0.30	2 (1%) 79	83	16, 30, 52, 89	9 (5%)
1	F	165/165 (100%)	-0.17	5 (3%) 50	59	18, 35, 56, 82	9 (5%)
All	All	990/990 (100%)	-0.28	14 (1%) 75	80	16, 34, 54, 89	53 (5%)

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	С	245	ILE	5.4
1	Е	268	ASN	4.7
1	F	245	ILE	4.4
1	С	268	ASN	3.7
1	Е	267	GLU	3.6

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, 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	$\operatorname{B-factors}({}^{\mathrm{A}^2})$	Q < 0.9
3	CA	В	372	1/1	0.90	0.14	35,35,35,35	0
5	ACT	В	374	4/4	0.93	0.16	33,35,37,40	0
3	CA	D	573	1/1	0.94	0.13	51,51,51,51	0
3	CA	A	872	1/1	0.94	0.13	39,39,39,39	0
5	ACT	Е	674	4/4	0.95	0.16	28,33,36,36	0
3	CA	F	773	1/1	0.96	0.11	37,37,37,37	0
3	CA	С	473	1/1	0.97	0.10	38,38,38,38	0
3	CA	A	871	1/1	0.97	0.07	44,44,44,44	0
3	CA	E	672	1/1	0.97	0.14	32,32,32,32	0
2	ZN	Е	669	1/1	0.98	0.12	33,33,33,33	0
3	CA	A	873	1/1	0.98	0.13	47,47,47,47	0
2	ZN	F	770	1/1	0.98	0.14	33,33,33,33	0
2	ZN	A	870	1/1	0.98	0.09	43,43,43,43	0
3	CA	D	572	1/1	0.98	0.08	40,40,40,40	0
6	AZI	С	474	3/3	0.98	0.12	29,29,47,47	0
6	AZI	F	774	3/3	0.98	0.09	29,29,44,48	0
3	CA	С	472	1/1	0.99	0.09	31,31,31,31	0
2	ZN	F	769	1/1	0.99	0.09	33,33,33,33	0
3	CA	D	571	1/1	0.99	0.10	43,43,43,43	0
2	ZN	С	469	1/1	0.99	0.09	32,32,32,32	0
2	ZN	С	470	1/1	0.99	0.12	33,33,33,33	0
3	CA	Е	671	1/1	0.99	0.09	27,27,27,27	0
2	ZN	D	570	1/1	0.99	0.10	42,42,42,42	0
3	CA	Е	673	1/1	0.99	0.07	30,30,30,30	0
3	CA	F	771	1/1	0.99	0.10	29,29,29,29	0
3	CA	F	772	1/1	0.99	0.07	30,30,30,30	0
2	ZN	В	369	1/1	0.99	0.12	34,34,34,34	0
4	HAE	A	874	5/5	0.99	0.13	27,34,38,43	0
4	HAE	D	574	5/5	0.99	0.13	28,34,42,43	0
3	CA	В	371	1/1	0.99	0.10	26,26,26,26	0
2	ZN	E	670	1/1	0.99	0.12	30,30,30,30	0
3	CA	В	373	1/1	0.99	0.08	28,28,28,28	0
3	CA	С	471	1/1	0.99	0.10	28,28,28,28	0
2	ZN	D	569	1/1	1.00	0.12	28,28,28,28	0
2	ZN	A	869	1/1	1.00	0.12	29,29,29,29	0
2	ZN	В	370	1/1	1.00	0.10	29,29,29,29	0



6.5 Other polymers (i)

There are no such residues in this entry.

