



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 09:34 PM GMT

PDB ID : 1PPG
Title : The refined 2.3 angstroms crystal structure of human leukocyte elastase in a complex with a valine chloromethyl ketone inhibitor
Authors : Bode, W.; Wei, A-Z.
Deposited on : 1991-10-24
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
<http://wwpdb.org/validation/2016/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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

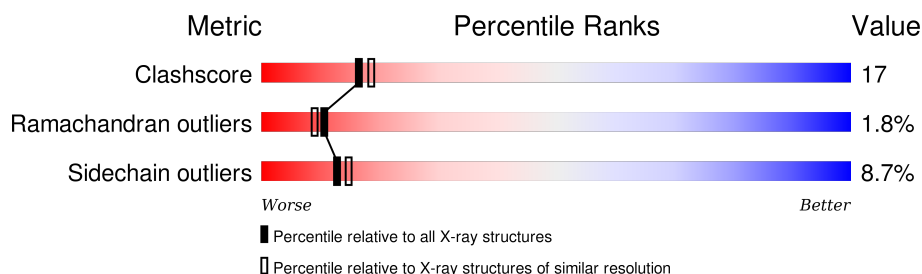
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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))
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (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 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 $\leq 5\%$. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	E	218	
2	I	6	

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	NAG	E	406	-	-	X	-
4	NDG	E	416	X	-	-	-
4	GLC	E	417	X	-	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 2053 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 HUMAN LEUKOCYTE ELASTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	E	218	Total	C	N	O	S	43	0	0
			1636	1026	316	283	11			

- Molecule 2 is a protein called MEO-SUCCINYL-ALA-ALA-PRO-VAL CHLOROMETHYLKETONE.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	I	6	Total	C	N	O	0	0	1
			33	22	4	7			

- Molecule 3 is a polymer of unknown type called SUGAR (8-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	E	8	Total	C	N	O	60	0
			96	54	3	39		

- Molecule 4 is a polymer of unknown type called SUGAR (8-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	E	8	Total	C	N	O	72	0
			96	54	3	39		

- Molecule 5 is water.

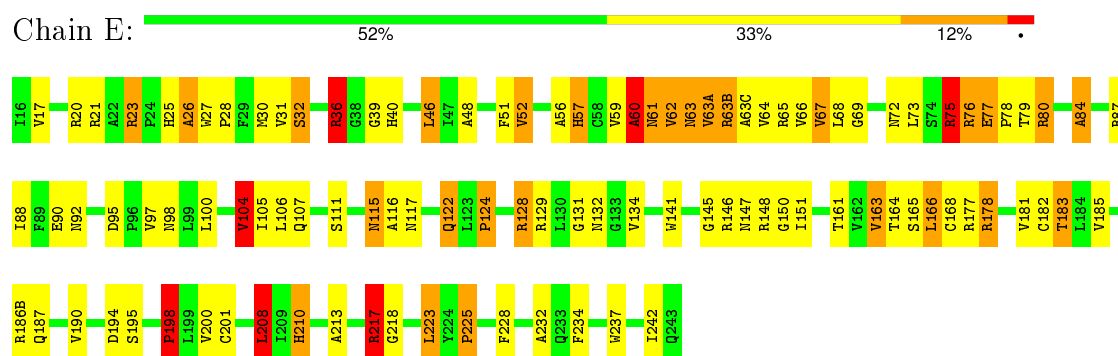
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	E	189	Total	O	29	0
			189	189		
5	I	3	Total	O	1	0
			3	3		

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 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.

Note EDS was not executed.

• Molecule 1: HUMAN LEUKOCYTE ELASTASE



• Molecule 2: MEO-SUCCINYL-ALA-ALA-PRO-VAL CHLOROMETHYLKETONE



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	74.20 Å 74.20 Å 70.60 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	8.00 – 2.30	Depositor
% Data completeness (in resolution range)	(Not available) (8.00-2.30)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	EREF	Depositor
R, R_{free}	0.145 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2053	wwPDB-VP
Average B, all atoms (Å ²)	12.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: VAI, 0QE, GLC, NAG, NDG, GAL, BMA, MAN, HMB, FUC

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	E	1.35	9/1666 (0.5%)	1.81	37/2263 (1.6%)
2	I	1.24	0/17	1.27	0/23
All	All	1.35	9/1683 (0.5%)	1.81	37/2286 (1.6%)

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	E	0	24
2	I	1	0
4	E	2	0
All	All	3	24

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	141	TRP	NE1-CE2	-7.82	1.27	1.37
1	E	237	TRP	NE1-CE2	-6.85	1.28	1.37
1	E	75	ARG	NE-CZ	6.25	1.41	1.33
1	E	76	ARG	CZ-NH1	5.95	1.40	1.33
1	E	27	TRP	NE1-CE2	-5.91	1.29	1.37

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	217	ARG	NE-CZ-NH1	11.60	126.10	120.30
1	E	23	ARG	NE-CZ-NH1	-10.33	115.14	120.30
1	E	177	ARG	NE-CZ-NH2	-9.85	115.37	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	217	ARG	NH1-CZ-NH2	-8.41	110.15	119.40
1	E	194	ASP	CB-CG-OD2	7.70	125.23	118.30

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	E	416	NDG	C3
4	E	417	GLC	C3
2	I	1	HMB	CG

5 of 24 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	26	ALA	Mainchain
1	E	28	PRO	Mainchain
1	E	46	LEU	Mainchain
1	E	52	VAL	Mainchain
1	E	60	ALA	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	E	1636	0	1650	54	26
2	I	33	0	33	8	0
3	E	96	0	82	0	30
4	E	96	0	82	1	0
5	E	189	0	0	3	9
5	I	3	0	0	0	0
All	All	2053	0	1847	55	34

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 17.

The worst 5 of 55 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:E:195:SER:OG	2:I:6:0QE:C1	1.78	1.28
1:E:218:GLY:H	2:I:1:HMB:HB1	1.36	0.90
1:E:88:ILE:HG22	1:E:106:LEU:HD22	1.56	0.87
1:E:195:SER:CB	2:I:6:0QE:C1	2.55	0.85
1:E:105:ILE:HG13	5:E:1239:HOH:O	1.85	0.77

The worst 5 of 34 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)
1:E:97:VAL:CB	3:E:406:NAG:C5[4_564]	0.32	1.88
1:E:97:VAL:CA	3:E:406:NAG:C6[4_564]	0.62	1.58
3:E:405:MAN:C3	5:E:1234:HOH:O[4_565]	0.74	1.46
1:E:97:VAL:CG1	3:E:406:NAG:O5[4_564]	0.86	1.34
1:E:97:VAL:CG2	3:E:406:NAG:C4[4_564]	0.89	1.31

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	E	216/218 (99%)	201 (93%)	11 (5%)	4 (2%)	10	8
2	I	3/6 (50%)	3 (100%)	0	0	100	100
All	All	219/224 (98%)	204 (93%)	11 (5%)	4 (2%)	11	9

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	36	ARG
1	E	146	ARG
1	E	213	ALA
1	E	124	PRO

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	E	172/172 (100%)	157 (91%)	15 (9%)	13	15
2	I	1/1 (100%)	1 (100%)	0	100	100
All	All	173/173 (100%)	158 (91%)	15 (9%)	13	15

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	104	VAL
1	E	115	ASN
1	E	200	VAL
1	E	92	ASN
1	E	166	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	132	ASN
1	E	210	HIS
1	E	135	GLN
1	E	115	ASN
1	E	156	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](#)

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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	$\# Z > 2$
2	VAI	I	5	1,2	6,6,7	0.76	0	5,7,9	0.85	0

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
2	VAI	I	5	1,2	-	0/6/6/8	0/0/0/0

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	I	5	VAI	1	0

5.5 Carbohydrates

16 carbohydrates are modelled in this entry.

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	NAG	E	401	1,3	14,14,15	0.97	0	15,19,21	2.54	7 (46%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	FUC	E	402	3	10,10,11	1.15	1 (10%)	14,14,16	1.99	4 (28%)
3	NAG	E	403	3	14,14,15	0.71	0	15,19,21	1.56	2 (13%)
3	BMA	E	404	3	11,11,12	0.81	1 (9%)	14,15,17	1.97	2 (14%)
3	MAN	E	405	3	11,11,12	0.41	0	14,15,17	2.12	2 (14%)
3	NAG	E	406	3	14,14,15	0.64	0	15,19,21	1.50	1 (6%)
3	GAL	E	407	3	11,11,12	0.58	0	14,15,17	1.54	1 (7%)
3	MAN	E	408	3	11,11,12	0.56	0	14,15,17	1.82	1 (7%)
4	NAG	E	411	1,4	14,14,15	1.57	5 (35%)	15,19,21	1.95	2 (13%)
4	FUC	E	412	4	10,10,11	1.32	1 (10%)	14,14,16	2.33	6 (42%)
4	NAG	E	413	4	14,14,15	0.92	0	15,19,21	1.59	3 (20%)
4	BMA	E	414	4	11,11,12	0.82	1 (9%)	14,15,17	1.78	5 (35%)
4	BMA	E	415	4	11,11,12	0.63	0	14,15,17	1.75	4 (28%)
4	NDG	E	416	4	14,14,15	0.87	1 (7%)	15,19,21	3.04	8 (53%)
4	GLC	E	417	4	11,11,12	0.65	0	14,15,17	2.05	2 (14%)
4	MAN	E	418	4	11,11,12	0.57	0	14,15,17	2.20	2 (14%)

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	NAG	E	401	1,3	-	0/6/23/26	0/1/1/1
3	FUC	E	402	3	-	0/0/17/20	0/1/1/1
3	NAG	E	403	3	-	0/6/23/26	0/1/1/1
3	BMA	E	404	3	-	0/2/19/22	0/1/1/1
3	MAN	E	405	3	-	0/2/19/22	0/1/1/1
3	NAG	E	406	3	-	0/6/23/26	0/1/1/1
3	GAL	E	407	3	-	0/2/19/22	0/1/1/1
3	MAN	E	408	3	-	0/2/19/22	0/1/1/1
4	NAG	E	411	1,4	-	0/6/23/26	0/1/1/1
4	FUC	E	412	4	-	0/0/17/20	0/1/1/1
4	NAG	E	413	4	-	0/6/23/26	0/1/1/1
4	BMA	E	414	4	-	0/2/19/22	0/1/1/1
4	BMA	E	415	4	-	0/2/19/22	0/1/1/1
4	NDG	E	416	4	1/1/5/7	0/6/23/26	0/1/1/1
4	GLC	E	417	4	1/1/4/5	0/2/19/22	0/1/1/1
4	MAN	E	418	4	-	0/2/19/22	1/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	402	FUC	O5-C1	-2.06	1.40	1.43
4	E	414	BMA	C2-C3	2.02	1.55	1.52
4	E	416	NDG	C1-C2	2.12	1.55	1.52
4	E	412	FUC	O3-C3	2.20	1.48	1.43
3	E	404	BMA	C1-C2	2.22	1.57	1.52

The worst 5 of 52 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	416	NDG	C3-C4-C5	-5.84	100.02	110.20
4	E	411	NAG	C2-N2-C7	-5.50	115.97	123.04
4	E	412	FUC	C2-C3-C4	-4.53	103.35	111.04
3	E	403	NAG	C2-N2-C7	-4.28	117.54	123.04
3	E	401	NAG	O4-C4-C3	-4.00	101.33	110.34

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	E	416	NDG	C3
4	E	417	GLC	C3

There are no torsion outliers.

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	E	418	MAN	C1-C2-C3-C4-C5-O5

6 monomers are involved in 31 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	404	BMA	0	1
3	E	405	MAN	0	5
3	E	406	NAG	0	20
3	E	407	GAL	0	2
3	E	408	MAN	0	2
4	E	412	FUC	1	0

5.6 Ligand geometry

There are no ligands in this entry.

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](#)

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.